

# Ecosystem

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## 1 Introduction

### 1.1 Copyright Statement

#### Copyright

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

### 1.2 General Information

The source code contained within the ecosystem project was designed as a standalone tool set for performing numerical modeling and data analyses associated with adsorption phenomena in both gaseous and aqueous systems. Many of the lower level tools are general enough to be applied to any system you desire to be modeled. Such algorithms included are Krylov subspace methods for linear systems and a Jacobian-Free Newton-Krylov method for non-linear systems. There is also a templated matrix object for generic matrix construction and modification. For specific information on each individual kernel, navigate through the class and file indices or table of contents.

#### Warning

Many of these algorithms may still be under development. This library is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE.

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## 5 Class Documentation

### 5.1 AdsorptionReaction Class Reference

Adsorption [Reaction](#) Object.

```
#include <shark.h>
```

#### Public Member Functions

- [AdsorptionReaction](#) ()  
*Default Constructor.*
- [~AdsorptionReaction](#) ()  
*Default Destructor.*
- void [Initialize\\_Object](#) ([MasterSpeciesList](#) &List, int i)  
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- void [Display\\_Info](#) ()  
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- int [setAqueousIndexAuto](#) ()

- Automatically sets the primary aqueous species index based on reactions.*

  - void [setMolarFactor](#) (int rxn\_i, double m)
 

*Set the molar factor for the ith reaction (mol/mol)*
  - void [setVolumeFactor](#) (int i, double v)
 

*Set the ith volume factor for the species list (cm<sup>3</sup>/mol)*
  - void [setAreaFactor](#) (int i, double a)
 

*Set the ith area factor for the species list (m<sup>2</sup>/mol)*
  - void [setSpecificArea](#) (double a)
 

*Set the specific area for the adsorbent (m<sup>2</sup>/kg)*
  - void [setSpecificMolality](#) (double a)
 

*Set the specific molality for the adsorbent (mol/kg)*
  - void [setSurfaceCharge](#) (double c)
 

*Set the surface charge of the uncomplexed ligands.*
  - void [setTotalMass](#) (double m)
 

*Set the total mass of the adsorbent (kg)*
  - void [setTotalVolume](#) (double v)
 

*Set the total volume of the system (L)*
  - void [setAreaBasisBool](#) (bool opt)
 

*Set the basis boolean directly.*
  - void [setBasis](#) (std::string option)
 

*Set the basis of the adsorption problem from the given string arg.*
  - void [setAdsorbentName](#) (std::string name)
 

*Set the name of the adsorbent to the given string.*
  - void [calculateAreaFactors](#) ()
 

*Calculates the area factors used from the van der Waals volumes.*
  - void [calculateEquilibria](#) (double T)
 

*Calculates all equilibrium parameters as a function of temperature.*
  - void [setChargeDensity](#) (const [Matrix](#)< double > &x)
 

*Calculates and sets the current value of charge density.*
  - void [setIonicStrength](#) (const [Matrix](#)< double > &x)
 

*Calculates and sets the current value of ionic strength.*
  - int [callSurfaceActivity](#) (const [Matrix](#)< double > &x)
 

*Calls the activity model and returns an int flag for success or failure.*
  - double [calculateActiveFraction](#) (const [Matrix](#)< double > &x)
 

*Calculates the fraction of the surface that is active and available.*
  - double [calculateSurfaceChargeDensity](#) (const [Matrix](#)< double > &x)
 

*Function to calculate the surface charge density based on concentrations.*
  - double [calculateLangmuirMaxCapacity](#) (int i)
 

*Calculates the theoretical maximum capacity for adsorption in reaction i.*
  - double [calculateLangmuirEquParam](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama, int i)
 

*Calculates the equivalent Langmuir isotherm equilibrium parameter.*
  - double [calculateLangmuirAdsorption](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama, int i)
 

*Calculates the equivalent Langmuir adsorption by forming the Langmuir-like parameters.*
  - double [calculateCubicPsiApprox](#) (double sigma, double T, double I, double rel\_epsilon)
 

*Function calculates the Psi (electric surface potential) given a set of arguments.*
  - double [calculateAqueousChargeExchange](#) (int i)
 

*Function to calculate the net exchange of charges of the aqueous species involved in a given reaction.*
  - double [calculateEquilibriumCorrection](#) (double sigma, double T, double I, double rel\_epsilon, int i)
 

*Function to calculate the correction term for the equilibrium parameter.*
  - double [Eval\\_Residual](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama, double T, double rel\_perm, int i)



- Calculates the residual for the ith reaction in the system.*

  - [Reaction & getReaction](#) (int i)

*Return reference to the ith reaction object in the adsorption object.*
- double [getMolarFactor](#) (int i)

*Get the ith reaction's molar factor for adsorption (mol/mol)*
- double [getVolumeFactor](#) (int i)

*Get the ith volume factor (species not involved return zeros) ( $\text{cm}^3/\text{mol}$ )*
- double [getAreaFactor](#) (int i)

*Get the ith area factor (species not involved return zeros) ( $\text{m}^2/\text{mol}$ )*
- double [getActivity](#) (int i)

*Get the ith activity factor for the surface species.*
- double [getSpecificArea](#) ()

*Get the specific area of the adsorbent ( $\text{m}^2/\text{kg}$ ) or (mol/kg)*
- double [getSpecificMolality](#) ()

*Get the specific molality of the adsorbent (mol/kg)*
- double [getSurfaceCharge](#) ()

*Get the surface charge of the adsorbent.*
- double [getBulkDensity](#) ()

*Calculate and return bulk density of adsorbent in system (kg/L)*
- double [getTotalMass](#) ()

*Get the total mass of adsorbent in the system (kg)*
- double [getTotalVolume](#) ()

*Get the total volume of the system (L)*
- double [getChargeDensity](#) ()

*Get the value of the surface charge density ( $\text{C}/\text{m}^2$ )*
- double [getIonicStrength](#) ()

*Get the value of the ionic strength of solution (mol/L)*
- int [getNumberRxns](#) ()

*Get the number of reactions involved in the adsorption object.*
- int [getAdsorbIndex](#) (int i)

*Get the index of the adsorbed species in the ith reaction.*
- int [getAqueousIndex](#) (int i)

*Get the index of the primary aqueous species in the ith reaction.*
- bool [isAreaBasis](#) ()

*Returns true if we are in the Area Basis, False if in Molar Basis.*
- std::string [getAdsorbentName](#) ()

*Returns the name of the adsorbent as a string.*

#### Protected Attributes

- [MasterSpeciesList](#) \* [List](#)
- Pointer to the [MasterSpeciesList](#) object.*
- int(\* [surface\\_activity](#) )(const [Matrix](#)< double > &logq, [Matrix](#)< double > &activity, const void \*data)
- Pointer to a surface activity model.*
- const void \* [activity\\_data](#)
- Pointer to the data structure needed for surface activities.*
- std::vector< double > [area\\_factors](#)
- List of area factors associated with surface species ( $\text{m}^2/\text{mol}$ )*
- std::vector< double > [volume\\_factors](#)
- List of the van der Waals volumes of each surface species ( $\text{cm}^3/\text{mol}$ )*
- std::vector< int > [adsorb\\_index](#)

*List of the indices for the adsorbed species in the reactions.*

- `std::vector< int > aqueous_index`

*List of the indices for the primary aqueous species in the reactions.*

- `std::vector< double > molar_factor`

*List of the number of ligands needed to form one mole of adsorption in each reaction.*

- `Matrix< double > activities`

*List of the activities calculated by the activity model.*

- `double specific_area`

*Specific surface area of the adsorbent ( $m^2/kg$ )*

- `double specific_molality`

*Specific molality of the adsorbent - moles of ligand per kg sorbent ( $mol/kg$ )*

- `double surface_charge`

*Charge of the uncomplexed surface ligand species.*

- `double total_mass`

*Total mass of the adsorbent in the system ( $kg$ )*

- `double total_volume`

*Total volume of the system ( $L$ )*

- `double ionic_strength`

*Ionic Strength of the system used to adjust equilibria constants ( $mol/L$ )*

- `double charge_density`

*Surface charge density of the adsorbent used to adjust equilibria ( $C/m^2$ )*

- `int num_rxns`

*Number of reactions involved in the adsorption equilibria.*

- `bool AreaBasis`

*True = Adsorption on an area basis, False = Adsorption on a ligand basis.*

- `std::string adsorbent_name`

*Name of the adsorbent for this object.*

#### Private Attributes

- `std::vector< Reaction > ads_rxn`

*List of reactions involved with adsorption.*

#### 5.1.1 Detailed Description

Adsorption [Reaction](#) Object.

C++ Object to handle data and functions associated with formulating adsorption equilibrium reactions in a aqueous mixture. Each unique surface in a system will require an instance of this structure.

#### Warning

THIS OBJECT IS NOT YET FUNCTIONAL!

#### 5.1.2 Constructor & Destructor Documentation

##### 5.1.2.1 AdsorptionReaction::AdsorptionReaction ( )

Default Constructor.

##### 5.1.2.2 AdsorptionReaction::~~AdsorptionReaction ( )

Default Destructor.

## 5.1.3 Member Function Documentation

## 5.1.3.1 void AdsorptionReaction::Initialize.Object ( MasterSpeciesList &amp; List, int i )

Function to call the initialization of objects sequentially.

## 5.1.3.2 void AdsorptionReaction::Display\_Info ( )

Display the adsorption reaction information (PLACE HOLDER)

## 5.1.3.3 void AdsorptionReaction::modifyDeltas ( MassBalance &amp; mbo )

Modify the Deltas in the [MassBalance](#) Object.

This function will take a mass balance object as an argument and modify the deltas in that object to correct for how adsorption affects that particular mass balance. Since adsorption can effect multiple mass balances, this function must be called for each mass balance in the system.

## Parameters

<i>mbo</i>	reference to the <a href="#">MassBalance</a> Object the adsorption is acting on
------------	---

## 5.1.3.4 int AdsorptionReaction::setAdsorbIndices ( )

Find and set the adsorbed species indices for each reaction object.

This function searches through the [Reaction](#) objects in [AdsorptionReaction](#) to find the solid species and their indices to set that information in the adsorb\_index structure. That information will be used later to approximate maximum capacities and equilibrium parameters for use in a modified extended Langmuir type expression. Function will return 0 if successful and -1 on a failure.

## 5.1.3.5 int AdsorptionReaction::checkAqueousIndices ( )

Function to check and report errors in the aqueous species indices.

## 5.1.3.6 void AdsorptionReaction::setActivityModelInfo ( int(\*) (const Matrix&lt; double &gt; &amp;logq, Matrix&lt; double &gt; &amp;activity, const void \*data) act, const void \* act\_data )

Function to set the surface activity model and data pointer.

This function will setup the surface activity model based on the given pointer arguments. If no arguments are given, or are given as NULL, then the activity model will default to ideal solution assumption.

## 5.1.3.7 void AdsorptionReaction::setAqueousIndex ( int rxn\_i, int species\_i )

Set the primary aqueous species index for the ith reaction.

## 5.1.3.8 int AdsorptionReaction::setAqueousIndexAuto ( )

Automatically sets the primary aqueous species index based on reactions.

This function will go through all species and all reactions in the adsorption object and automatically set the primary aqueous species index based on the stoichiometry of the reaction. It will also check and make sure that the primary aqueous index species appears opposite of the adsorbed species in the reactions. Note: This function assumes that the adsorbed indices have already been set.

## 5.1.3.9 void AdsorptionReaction::setMolarFactor ( int rxn\_i, double m )

Set the molar factor for the ith reaction (mol/mol)

## 5.1.3.10 void AdsorptionReaction::setVolumeFactor ( int i, double v )

Set the ith volume factor for the species list (cm<sup>3</sup>/mol)

5.1.3.11 void AdsorptionReaction::setAreaFactor ( int *i*, double *a* )

Set the *i*th area factor for the species list ( $\text{m}^2/\text{mol}$ )

5.1.3.12 void AdsorptionReaction::setSpecificArea ( double *a* )

Set the specific area for the adsorbent ( $\text{m}^2/\text{kg}$ )

5.1.3.13 void AdsorptionReaction::setSpecificMolality ( double *a* )

Set the specific molality for the adsorbent ( $\text{mol}/\text{kg}$ )

5.1.3.14 void AdsorptionReaction::setSurfaceCharge ( double *c* )

Set the surface charge of the uncomplexed ligands.

5.1.3.15 void AdsorptionReaction::setTotalMass ( double *m* )

Set the total mass of the adsorbent (kg)

5.1.3.16 void AdsorptionReaction::setTotalVolume ( double *v* )

Set the total volume of the system (L)

5.1.3.17 void AdsorptionReaction::setAreaBasisBool ( bool *opt* )

Set the basis boolean directly.

5.1.3.18 void AdsorptionReaction::setBasis ( std::string *option* )

Set the basis of the adsorption problem from the given string arg.

5.1.3.19 void AdsorptionReaction::setAdsorbentName ( std::string *name* )

Set the name of the adsorbent to the given string.

5.1.3.20 void AdsorptionReaction::calculateAreaFactors ( )

Calculates the area factors used from the van der Waals volumes.

5.1.3.21 void AdsorptionReaction::calculateEquilibria ( double *T* )

Calculates all equilibrium parameters as a function of temperature.

5.1.3.22 void AdsorptionReaction::setChargeDensity ( const Matrix< double > & *x* )

Calculates and sets the current value of charge density.

5.1.3.23 void AdsorptionReaction::setIonicStrength ( const Matrix< double > & *x* )

Calculates and sets the current value of ionic strength.

5.1.3.24 int AdsorptionReaction::callSurfaceActivity ( const Matrix< double > & *x* )

Calls the activity model and returns an int flag for success or failure.

5.1.3.25 double AdsorptionReaction::calculateActiveFraction ( const Matrix< double > & *x* )

Calculates the fraction of the surface that is active and available.

#### 5.1.3.26 double AdsorptionReaction::calculateSurfaceChargeDensity ( const Matrix< double > & x )

Function to calculate the surface charge density based on concentrations.

This function is used to calculate the surface charge density of the adsorbed species based on the charges and concentrations of the adsorbed species. The calculation is used to correct the adsorption equilibria constant based on a localized surface charge balance. This requires that you know the molality of the uncomplexed ligand species on the surface, as well as the specific surface area for the adsorbent.

##### Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
----------	--

#### 5.1.3.27 double AdsorptionReaction::calculateLangmuirMaxCapacity ( int i )

Calculates the theoretical maximum capacity for adsorption in reaction i.

This function is used to calculate the current maximum capacity of a species for a given adsorption reaction using the concentrations and activities of other species in the system. You must pass the index of the reaction of interest. The index of the species of interest is determined from the adsorb\_index object. Note: This is only true if the stoichiometry for the adsorbed species is 1.

##### Parameters

<i>i</i>	index of the reaction of interest for the adsorption object
----------	---

#### 5.1.3.28 double AdsorptionReaction::calculateLangmuirEquParam ( const Matrix< double > & x, const Matrix< double > & gama, int i )

Calculates the equivalent Langmuir isotherm equilibrium parameter.

This function will take in the current aqueous activities and calculate an effective Langmuir adsorption parameter for use in determining the adsorption in the system. It uses the system temperature as well to calculate equilibrium. Note: This is only true if the stoichiometry for the adsorbed species is 1.

##### Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>gama</i>	matrix of activity coefficients for each species at the current non-linear step
<i>i</i>	index of the reaction of interest for the adsorption object

#### 5.1.3.29 double AdsorptionReaction::calculateLangmuirAdsorption ( const Matrix< double > & x, const Matrix< double > & gama, int i )

Calculates the equivalent Langmuir adsorption by forming the Langmuir-like parameters.

This function will use the calculateLangmuirMaxCapacity and calculateLangmuirEquParam functions to approximate the adsorption of the ith reaction given the concentration of aqueous species, activities, and temperature. Note: This is only true if the stoichiometry for the adsorbed species is 1.

##### Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>gama</i>	matrix of activity coefficients for each species at the current non-linear step
<i>i</i>	index of the reaction of interest for the adsorption object

#### 5.1.3.30 double AdsorptionReaction::calculateCubicPsiApprox ( double sigma, double T, double I, double rel\_epsilon )

Function calculates the Psi (electric surface potential) given a set of arguments.

This function will approximate the electric surface potential of the adsorbent under the current conditions of charge

density, temperature, ionic strength, and relative permittivity. Approximations are made via the cubic representations of the hyperbolic sine function. As a result, this approximation is fourth order accurate and is a faster approximation then solving with derivatives of the function.

## Parameters

<i>sigma</i>	charge density of the surface (C/m <sup>2</sup> )
<i>T</i>	temperature of the system in question (K)
<i>I</i>	ionic strength of the medium the surface is in (mol/L)
<i>rel_epsilon</i>	relative permittivity of the medium (Unitless)

5.1.3.31 double AdsorptionReaction::calculateAqueousChargeExchange ( int *i* )

Function to calculate the net exchange of charges of the aqueous species involved in a given reaction.

This function will look at all aqueous species involved in the *i*th adsorption reaction and sum up their stoichiometries and charges to see what the net change in charge is caused by the adsorption of charged species in solution. It is then used to adjust or correct the equilibrium constant for the given adsorption reaction.

## Parameters

<i>i</i>	index of the reaction of interest for the adsorption object
----------	---

5.1.3.32 double AdsorptionReaction::calculateEquilibriumCorrection ( double *sigma*, double *T*, double *I*, double *rel\_epsilon*, int *i* )

Function to calculate the correction term for the equilibrium parameter.

This function calculates the correction term that gets applied to the equilibrium parameter to correct for surface charge and charge accumulation/depletion effects. It will call the psi approximation and charge exchange functions, therefore it needs to have those functions arguments passed to it as well.

## Parameters

<i>sigma</i>	charge density of the surface (C/m <sup>2</sup> )
<i>T</i>	temperature of the system in question (K)
<i>I</i>	ionic strength of the medium the surface is in (mol/L)
<i>rel_epsilon</i>	relative permittivity of the medium (Unitless)
<i>i</i>	index of the reaction of interest for the adsorption object

5.1.3.33 double AdsorptionReaction::Eval\_Residual ( const Matrix< double > & *x*, const Matrix< double > & *gama*, double *T*, double *rel\_perm*, int *i* )

Calculates the residual for the *i*th reaction in the system.

This function will provide a system residual for the *i*th reaction object involved in the Adsorption [Reaction](#). The residual is fed into the SHARK solver to find the solution to solid and aqueous phase concentrations simultaneously. This function will also adjust the equilibrium parameter for the reaction

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>gama</i>	matrix of activity coefficients for each species at the current non-linear step
<i>T</i>	temperature of the system in question (K)
<i>rel_perm</i>	relative permittivity of the media (unitless)
<i>i</i>	index of the reaction of interest for the adsorption object

**5.1.3.34 Reaction& AdsorptionReaction::getReaction ( int i )**

Return reference to the ith reaction object in the adsorption object.

**5.1.3.35 double AdsorptionReaction::getMolarFactor ( int i )**

Get the ith reaction's molar factor for adsorption (mol/mol)

**5.1.3.36 double AdsorptionReaction::getVolumeFactor ( int i )**

Get the ith volume factor (species not involved return zeros) ( $\text{cm}^3/\text{mol}$ )

**5.1.3.37 double AdsorptionReaction::getAreaFactor ( int i )**

Get the ith area factor (species not involved return zeros) ( $\text{m}^2/\text{mol}$ )

**5.1.3.38 double AdsorptionReaction::getActivity ( int i )**

Get the ith activity factor for the surface species.

**5.1.3.39 double AdsorptionReaction::getSpecificArea ( )**

Get the specific area of the adsorbent ( $\text{m}^2/\text{kg}$ ) or ( $\text{mol}/\text{kg}$ )

**5.1.3.40 double AdsorptionReaction::getSpecificMolality ( )**

Get the specific molality of the adsorbent ( $\text{mol}/\text{kg}$ )

**5.1.3.41 double AdsorptionReaction::getSurfaceCharge ( )**

Get the surface charge of the adsorbent.

**5.1.3.42 double AdsorptionReaction::getBulkDensity ( )**

Calculate and return bulk density of adsorbent in system ( $\text{kg}/\text{L}$ )

**5.1.3.43 double AdsorptionReaction::getTotalMass ( )**

Get the total mass of adsorbent in the system ( $\text{kg}$ )

**5.1.3.44 double AdsorptionReaction::getTotalVolume ( )**

Get the total volume of the system ( $\text{L}$ )

**5.1.3.45 double AdsorptionReaction::getChargeDensity ( )**

Get the value of the surface charge density ( $\text{C}/\text{m}^2$ )

**5.1.3.46 double AdsorptionReaction::getIonicStrength ( )**

Get the value of the ionic strength of solution ( $\text{mol}/\text{L}$ )

**5.1.3.47 int AdsorptionReaction::getNumberRxns ( )**

Get the number of reactions involved in the adsorption object.

**5.1.3.48 int AdsorptionReaction::getAdsorbIndex ( int i )**

Get the index of the adsorbed species in the ith reaction.

5.1.3.49 `int AdsorptionReaction::getAqueousIndex ( int i )`

Get the index of the primary aqueous species in the ith reaction.

5.1.3.50 `bool AdsorptionReaction::isAreaBasis ( )`

Returns true if we are in the Area Basis, False if in Molar Basis.

5.1.3.51 `std::string AdsorptionReaction::getAdsorbentName ( )`

Returns the name of the adsorbent as a string.

#### 5.1.4 Member Data Documentation

5.1.4.1 `MasterSpeciesList* AdsorptionReaction::List` [protected]

Pointer to the [MasterSpeciesList](#) object.

5.1.4.2 `int(* AdsorptionReaction::surface_activity)(const Matrix< double > &logq, Matrix< double > &activity, const void *data)` [protected]

Pointer to a surface activity model.

This is a function pointer for a surface activity model. The function must accept the log of the surface concentrations as an argument (logq) and provide the activities for each species (activity). The pointer data is used to pass any additional arguments needed.

##### Parameters

<i>logq</i>	matrix of the log (base 10) of surface concentrations of all species
<i>activity</i>	matrix of activity coefficients for all surface species (must be overridden)
<i>data</i>	pointer to a data structure needed to calculate activities

5.1.4.3 `const void* AdsorptionReaction::activity_data` [protected]

Pointer to the data structure needed for surface activities.

5.1.4.4 `std::vector<double> AdsorptionReaction::area_factors` [protected]

List of area factors associated with surface species ( $\text{m}^2/\text{mol}$ )

5.1.4.5 `std::vector<double> AdsorptionReaction::volume_factors` [protected]

List of the van der Waals volumes of each surface species ( $\text{cm}^3/\text{mol}$ )

5.1.4.6 `std::vector<int> AdsorptionReaction::adsorb_index` [protected]

List of the indices for the adsorbed species in the reactions.

5.1.4.7 `std::vector<int> AdsorptionReaction::aqueous_index` [protected]

List of the indices for the primary aqueous species in the reactions.

5.1.4.8 `std::vector<double> AdsorptionReaction::molar_factor` [protected]

List of the number of ligands needed to form one mole of adsorption in each reaction.

5.1.4.9 `Matrix<double> AdsorptionReaction::activities` [protected]

List of the activities calculated by the activity model.



5.1.4.10 `double AdsorptionReaction::specific_area` [protected]

Specific surface area of the adsorbent ( $\text{m}^2/\text{kg}$ )

5.1.4.11 `double AdsorptionReaction::specific_molality` [protected]

Specific molality of the adsorbent - moles of ligand per kg sorbent ( $\text{mol}/\text{kg}$ )

5.1.4.12 `double AdsorptionReaction::surface_charge` [protected]

Charge of the uncomplexed surface ligand species.

5.1.4.13 `double AdsorptionReaction::total_mass` [protected]

Total mass of the adsorbent in the system (kg)

5.1.4.14 `double AdsorptionReaction::total_volume` [protected]

Total volume of the system (L)

5.1.4.15 `double AdsorptionReaction::ionic_strength` [protected]

Ionic Strength of the system used to adjust equilibria constants ( $\text{mol}/\text{L}$ )

5.1.4.16 `double AdsorptionReaction::charge_density` [protected]

Surface charge density of the adsorbent used to adjust equilibria ( $\text{C}/\text{m}^2$ )

5.1.4.17 `int AdsorptionReaction::num_rxns` [protected]

Number of reactions involved in the adsorption equilibria.

5.1.4.18 `bool AdsorptionReaction::AreaBasis` [protected]

True = Adsorption on an area basis, False = Adsorption on a ligand basis.

5.1.4.19 `std::string AdsorptionReaction::adsorbent_name` [protected]

Name of the adsorbent for this object.

5.1.4.20 `std::vector<Reaction> AdsorptionReaction::ads_rxn` [private]

List of reactions involved with adsorption.

The documentation for this class was generated from the following file:

- [shark.h](#)

## 5.2 ARNOLDI\_DATA Struct Reference

Data structure for the construction of the Krylov subspaces for a linear system.

```
#include <lark.h>
```

### Public Attributes

- `int k`  
*Desired size of the Krylov subspace.*
- `int iter`  
*Actual size of the Krylov subspace.*

- double `beta`  
*Normalization parameter.*
- double `hp1`  
*Additional row element of H (separate storage for holding)*
- bool `Output = true`  
*True = print messages to console.*
- `std::vector< Matrix< double > > Vk`  
*(N) x (k) orthonormal vector basis stored as a vector of column matrices*
- `Matrix< double > Hk+1`  
*(k+1) x (k) upper Hessenberg matrix*
- `Matrix< double > yk`  
*(k) x (1) vector search direction*
- `Matrix< double > e1`  
*(k) x (1) orthonormal vector with 1 in first position*
- `Matrix< double > w`  
*(N) x (1) interim result of the matrix\_vector multiplication*
- `Matrix< double > v`  
*(N) x (1) holding cell for the column entries of V<sub>k</sub> and other interims*
- `Matrix< double > sum`  
*(N) x (1) running sum of subspace vectors for use in altering w*

### 5.2.1 Detailed Description

Data structure for the construction of the Krylov subspaces for a linear system.

C-style object used in conjunction with the Arnoldi algorithm to construct an orthonormal basis and upper Hessenberg representation of a given linear operator. This is used to solve a linear system both iteratively (i.e., in conjunction with GMRESLP) and directly (i.e., in conjunction with FOM). Alternatively, you can just store the factorized components for later use in another routine.

### 5.2.2 Member Data Documentation

#### 5.2.2.1 int ARNOLDI\_DATA::k

Desired size of the Krylov subspace.

#### 5.2.2.2 int ARNOLDI\_DATA::iter

Actual size of the Krylov subspace.

#### 5.2.2.3 double ARNOLDI\_DATA::beta

Normalization parameter.

#### 5.2.2.4 double ARNOLDI\_DATA::hp1

Additional row element of H (separate storage for holding)

#### 5.2.2.5 bool ARNOLDI\_DATA::Output = true

True = print messages to console.

#### 5.2.2.6 std::vector< Matrix<double> > ARNOLDI\_DATA::V<sub>k</sub>

(N) x (k) orthonormal vector basis stored as a vector of column matrices

**5.2.2.7 Matrix<double> ARNOLDI\_DATA::Hkp1**

(k+1) x (k) upper Hessenberg matrix

**5.2.2.8 Matrix<double> ARNOLDI\_DATA::yk**

(k) x (1) vector search direction

**5.2.2.9 Matrix<double> ARNOLDI\_DATA::e1**

(k) x (1) orthonormal vector with 1 in first position

**5.2.2.10 Matrix<double> ARNOLDI\_DATA::w**

(N) x (1) interim result of the matrix\_vector multiplication

**5.2.2.11 Matrix<double> ARNOLDI\_DATA::v**

(N) x (1) holding cell for the column entries of  $V_k$  and other interims

**5.2.2.12 Matrix<double> ARNOLDI\_DATA::sum**

(N) x (1) running sum of subspace vectors for use in altering w

The documentation for this struct was generated from the following file:

- [lark.h](#)

**5.3 Atom Class Reference**

[Atom](#) object to hold information about specific atoms in the periodic table (click [Atom](#) to go to function definitions)

```
#include <eel.h>
```

**Public Member Functions**

- [Atom](#) ()  
*Default Constructor.*
- [~Atom](#) ()  
*Default Destructor.*
- [Atom](#) (std::string [Name](#))  
*Constructor by [Atom](#) Name.*
- [Atom](#) (int number)  
*Constructor by Atomic number.*
- void [Register](#) (std::string [Symbol](#))  
*Register an atom object by symbol.*
- void [Register](#) (int number)  
*Register an atom object by number.*
- void [editAtomicWeight](#) (double AW)  
*Manually changes the atomic weight.*
- void [editOxidationState](#) (int state)  
*Manually changes the oxidation state.*
- void [editProtons](#) (int proton)  
*Manually changes the number of protons.*
- void [editNeutrons](#) (int neutron)  
*Manually changes the number of neutrons.*

- void `editElectrons` (int electron)  
*Manually changes the number of electrons.*
- void `editValence` (int val)  
*Manually changes the number of valence electrons.*
- void `removeProton` ()  
*Manually removes 1 proton and adjusts weight.*
- void `removeNeutron` ()  
*Manually removes 1 neutron and adjusts weight.*
- void `removeElectron` ()  
*Manually removes 1 electron from valence.*
- double `AtomicWeight` ()  
*Returns the current atomic weight (g/mol)*
- int `OxidationState` ()  
*Returns the current oxidation state.*
- int `Protons` ()  
*Returns the current number of protons.*
- int `Neutrons` ()  
*Returns the current number of neutrons.*
- int `Electrons` ()  
*Returns the current number of electrons.*
- int `BondingElectrons` ()  
*Returns the number of electrons available for bonding.*
- std::string `AtomName` ()  
*Returns the name of the atom.*
- std::string `AtomSymbol` ()  
*Returns the symbol of the atom.*
- std::string `AtomCategory` ()  
*Returns the category of the atom.*
- std::string `AtomState` ()  
*Returns the state of the atom.*
- int `AtomicNumber` ()  
*Returns the atomic number of the atom.*
- void `DisplayInfo` ()  
*Displays `Atom` information to console.*

#### Protected Attributes

- double `atomic_weight`  
*Holds the atomic weight of the atom.*
- int `oxidation_state`  
*Holds the oxidation state of the atom.*
- int `protons`  
*Holds the number of protons in the atom.*
- int `neutrons`  
*Holds the number of neutrons in the atom.*
- int `electrons`  
*Holds the number of electrons in the atom.*
- int `valence_e`  
*Holds the number of valence electrons in the atom.*

#### Private Attributes

- std::string [Name](#)  
*Holds the name of the atom.*
- std::string [Symbol](#)  
*Holds the atomic symbol for the atom.*
- std::string [Category](#)  
*Holds the category of the atom (e.g., Alkali Metal)*
- std::string [NaturalState](#)  
*Holds the natural state of the atom (e.g., Gas)*
- int [atomic\\_number](#)  
*Holds the atomic number of the atom.*

#### 5.3.1 Detailed Description

[Atom](#) object to hold information about specific atoms in the periodic table (click [Atom](#) to go to function definitions)

C++ class object holding data and functions associated with atoms. Objects can be registered at the time of object construction, or after declaring an [Atom](#) object. Registration can be done via the atomic symbol or atomic number. Valid atoms go from Hydrogen (1) to Ununoctium (118).

#### 5.3.2 Constructor & Destructor Documentation

##### 5.3.2.1 `Atom::Atom ( )`

Default Constructor.

##### 5.3.2.2 `Atom::~~Atom ( )`

Default Destructor.

##### 5.3.2.3 `Atom::Atom ( std::string Name )`

Constructor by [Atom](#) Name.

##### 5.3.2.4 `Atom::Atom ( int number )`

Constructor by Atomic number.

#### 5.3.3 Member Function Documentation

##### 5.3.3.1 `void Atom::Register ( std::string Symbol )`

Register an atom object by symbol.

##### 5.3.3.2 `void Atom::Register ( int number )`

Register an atom object by number.

##### 5.3.3.3 `void Atom::editAtomicWeight ( double AW )`

Manually changes the atomic weight.

##### 5.3.3.4 `void Atom::editOxidationState ( int state )`

Manually changes the oxidation state.

5.3.3.5 void Atom::editProtons ( int *proton* )

Manually changes the number of protons.

5.3.3.6 void Atom::editNeutrons ( int *neutron* )

Manually changes the number of neutrons.

5.3.3.7 void Atom::editElectrons ( int *electron* )

Manually changes the number of electrons.

5.3.3.8 void Atom::editValence ( int *val* )

Manually changes the number of valence electrons.

5.3.3.9 void Atom::removeProton ( )

Manually removes 1 proton and adjusts weight.

5.3.3.10 void Atom::removeNeutron ( )

Manually removes 1 neutron and adjusts weight.

5.3.3.11 void Atom::removeElectron ( )

Manually removes 1 electron from valence.

5.3.3.12 double Atom::AtomicWeight ( )

Returns the current atomic weight (g/mol)

5.3.3.13 int Atom::OxidationState ( )

Returns the current oxidation state.

5.3.3.14 int Atom::Protons ( )

Returns the current number of protons.

5.3.3.15 int Atom::Neutrons ( )

Returns the current number of neutrons.

5.3.3.16 int Atom::Electrons ( )

Returns the current number of electrons.

5.3.3.17 int Atom::BondingElectrons ( )

Returns the number of electrons available for bonding.

5.3.3.18 std::string Atom::AtomName ( )

Returns the name of the atom.

5.3.3.19 std::string Atom::AtomSymbol ( )

Returns the symbol of the atom.

#### 5.3.3.20 `std::string Atom::AtomCategory ( )`

Returns the category of the atom.

#### 5.3.3.21 `std::string Atom::AtomState ( )`

Returns the state of the atom.

#### 5.3.3.22 `int Atom::AtomicNumber ( )`

Returns the atomic number of the atom.

#### 5.3.3.23 `void Atom::DisplayInfo ( )`

Displays [Atom](#) information to console.

### 5.3.4 Member Data Documentation

#### 5.3.4.1 `double Atom::atomic_weight` `[protected]`

Holds the atomic weight of the atom.

#### 5.3.4.2 `int Atom::oxidation_state` `[protected]`

Holds the oxidation state of the atom.

#### 5.3.4.3 `int Atom::protons` `[protected]`

Holds the number of protons in the atom.

#### 5.3.4.4 `int Atom::neutrons` `[protected]`

Holds the number of neutrons in the atom.

#### 5.3.4.5 `int Atom::electrons` `[protected]`

Holds the number of electrons in the atom.

#### 5.3.4.6 `int Atom::valence_e` `[protected]`

Holds the number of valence electrons in the atom.

#### 5.3.4.7 `std::string Atom::Name` `[private]`

Holds the name of the atom.

#### 5.3.4.8 `std::string Atom::Symbol` `[private]`

Holds the atomic symbol for the atom.

#### 5.3.4.9 `std::string Atom::Category` `[private]`

Holds the category of the atom (e.g., Alkali Metal)

#### 5.3.4.10 `std::string Atom::NaturalState` `[private]`

Holds the natural state of the atom (e.g., Gas)

#### 5.3.4.11 `int Atom::atomic_number` `[private]`

Holds the atomic number of the atom.

The documentation for this class was generated from the following file:

- [eel.h](#)

## 5.4 BACKTRACK\_DATA Struct Reference

Data structure for the implementation of Backtracking Linesearch.

```
#include <lark.h>
```

### Public Attributes

- int [fun\\_call](#) = 0  
*Number of function calls made during line search.*
- double [alpha](#) = 1e-4  
*Scaling parameter for determination of search step size.*
- double [rho](#) = 0.1  
*Scaling parameter for to change step size by.*
- double [lambdaMin](#) = DBL\_EPSILON  
*Smallest allowable step length.*
- double [normFkp1](#)  
*New residual norm of the Newton step.*
- bool [constRho](#) = false  
*True = use a constant value for rho.*
- [Matrix](#)< double > [Fk](#)  
*Old residual vector of the Newton step.*
- [Matrix](#)< double > [xk](#)  
*Old solution vector of the Newton step.*

### 5.4.1 Detailed Description

Data structure for the implementation of Backtracking Linesearch.

C-style object used in conjunction with the Backtracking Linesearch algorithm to smooth out convergence of Newton based iterative methods for non-linear systems of equations. The actual algorithm has been separated from the interior of the Newton method so that it can be included in any future Newton based iterative methods being developed.

### 5.4.2 Member Data Documentation

#### 5.4.2.1 int BACKTRACK\_DATA::fun\_call = 0

Number of function calls made during line search.

#### 5.4.2.2 double BACKTRACK\_DATA::alpha = 1e-4

Scaling parameter for determination of search step size.

#### 5.4.2.3 double BACKTRACK\_DATA::rho = 0.1

Scaling parameter for to change step size by.

#### 5.4.2.4 double BACKTRACK\_DATA::lambdaMin = DBL\_EPSILON

Smallest allowable step length.



## 5.4.2.5 double BACKTRACK\_DATA::normFkp1

New residual norm of the Newton step.

## 5.4.2.6 bool BACKTRACK\_DATA::constRho = false

True = use a constant value for rho.

## 5.4.2.7 Matrix&lt;double&gt; BACKTRACK\_DATA::Fk

Old residual vector of the Newton step.

## 5.4.2.8 Matrix&lt;double&gt; BACKTRACK\_DATA::xk

Old solution vector of the Newton step.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.5 BiCGSTAB\_DATA Struct Reference

Data structure for the implementation of the BiCGSTAB algorithm for non-symmetric linear systems.

```
#include <lark.h>
```

## Public Attributes

- int [maxit](#) = 0  
*Maximum allowable iterations - default = min(2\*vector\_size,1000)*
- int [iter](#) = 0  
*Actual number of iterations.*
- bool [breakdown](#)  
*Boolean to determine if the method broke down.*
- double [alpha](#)  
*Step size parameter for next solution.*
- double [beta](#)  
*Step size parameter for search direction.*
- double [rho](#)  
*Scaling parameter for alpha and beta.*
- double [rho\\_old](#)  
*Previous scaling parameter for alpha and beta.*
- double [omega](#)  
*Scaling parameter and additional step length.*
- double [omega\\_old](#)  
*Previous scaling parameter and step length.*
- double [tol\\_rel](#) = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double [tol\\_abs](#) = 1e-6  
*Absolute tolerance for convergence - default = 1e-6.*
- double [res](#)  
*Absolute residual norm.*
- double [relres](#)  
*Relative residual norm.*
- double [relres\\_base](#)

- Initial residual norm.*
- double `bestres`
- Best found residual norm.*
- bool `Output` = true
- True = print messages to console.*
- `Matrix< double > x`
- Current solution to the linear system.*
- `Matrix< double > bestx`
- Best found solution to the linear system.*
- `Matrix< double > r`
- Residual vector for the linear system.*
- `Matrix< double > r0`
- Initial residual vector.*
- `Matrix< double > v`
- Search direction for p.*
- `Matrix< double > p`
- Search direction for updating.*
- `Matrix< double > y`
- Preconditioned search direction.*
- `Matrix< double > s`
- Residual updating vector.*
- `Matrix< double > z`
- Preconditioned residual updating vector.*
- `Matrix< double > t`
- Search direction for residual updates.*

### 5.5.1 Detailed Description

Data structure for the implementation of the BiCGSTAB algorithm for non-symmetric linear systems.

C-style object used in conjunction with the Bi-Conjugate Gradient STABalized (BiCGSTAB) algorithm to solve a linear system of equations. This algorithm is generally more efficient than any GMRES or GCR variant, but may not always reduce the residual at each step. However, if used with preconditioning, then this algorithm is very efficient, especially when used for solving grid-based linear systems.

### 5.5.2 Member Data Documentation

#### 5.5.2.1 int BiCGSTAB\_DATA::maxit = 0

Maximum allowable iterations - default = min(2\*vector\_size,1000)

#### 5.5.2.2 int BiCGSTAB\_DATA::iter = 0

Actual number of iterations.

#### 5.5.2.3 bool BiCGSTAB\_DATA::breakdown

Boolean to determine if the method broke down.

#### 5.5.2.4 double BiCGSTAB\_DATA::alpha

Step size parameter for next solution.

**5.5.2.5 double BiCGSTAB\_DATA::beta**

Step size parameter for search direction.

**5.5.2.6 double BiCGSTAB\_DATA::rho**

Scaling parameter for alpha and beta.

**5.5.2.7 double BiCGSTAB\_DATA::rho\_old**

Previous scaling parameter for alpha and beta.

**5.5.2.8 double BiCGSTAB\_DATA::omega**

Scaling parameter and additional step length.

**5.5.2.9 double BiCGSTAB\_DATA::omega\_old**

Previous scaling parameter and step length.

**5.5.2.10 double BiCGSTAB\_DATA::tol\_rel = 1e-6**

Relative tolerance for convergence - default = 1e-6.

**5.5.2.11 double BiCGSTAB\_DATA::tol\_abs = 1e-6**

Absolution tolerance for convergence - default = 1e-6.

**5.5.2.12 double BiCGSTAB\_DATA::res**

Absolute residual norm.

**5.5.2.13 double BiCGSTAB\_DATA::relres**

Relative residual norm.

**5.5.2.14 double BiCGSTAB\_DATA::relres\_base**

Initial residual norm.

**5.5.2.15 double BiCGSTAB\_DATA::bestres**

Best found residual norm.

**5.5.2.16 bool BiCGSTAB\_DATA::Output = true**

True = print messages to console.

**5.5.2.17 Matrix<double> BiCGSTAB\_DATA::x**

Current solution to the linear system.

**5.5.2.18 Matrix<double> BiCGSTAB\_DATA::bestx**

Best found solution to the linear system.

**5.5.2.19 Matrix<double> BiCGSTAB\_DATA::r**

Residual vector for the linear system.

**5.5.2.20 Matrix<double> BiCGSTAB\_DATA::r0**

Initial residual vector.

**5.5.2.21 Matrix<double> BiCGSTAB\_DATA::v**

Search direction for p.

**5.5.2.22 Matrix<double> BiCGSTAB\_DATA::p**

Search direction for updating.

**5.5.2.23 Matrix<double> BiCGSTAB\_DATA::y**

Preconditioned search direction.

**5.5.2.24 Matrix<double> BiCGSTAB\_DATA::s**

Residual updating vector.

**5.5.2.25 Matrix<double> BiCGSTAB\_DATA::z**

Preconditioned residual updating vector.

**5.5.2.26 Matrix<double> BiCGSTAB\_DATA::t**

Search direction for residual updates.

The documentation for this struct was generated from the following file:

- [lark.h](#)

**5.6 CGS\_DATA Struct Reference**

Data structure for the implementation of the CGS algorithm for non-symmetric linear systems.

```
#include <lark.h>
```

**Public Attributes**

- int [maxit](#) = 0  
*Maximum allowable iterations - default = min(2\*vector\_size, 1000)*
- int [iter](#) = 0  
*Actual number of iterations.*
- bool [breakdown](#)  
*Boolean to determine if the method broke down.*
- double [alpha](#)  
*Step size parameter for next solution.*
- double [beta](#)  
*Step size parameter for search direction.*
- double [rho](#)  
*Scaling parameter for alpha and beta.*
- double [sigma](#)  
*Scaling parameter and additional step length.*
- double [tol\\_rel](#) = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double [tol\\_abs](#) = 1e-6

- double `res`  
*Absolute tolerance for convergence - default = 1e-6.*
- double `relres`  
*Absolute residual norm.*
- double `relres_base`  
*Relative residual norm.*
- double `relres_base`  
*Initial residual norm.*
- double `bestres`  
*Best found residual norm.*
- bool `Output` = true  
*True = print messages to console.*
- `Matrix`< double > `x`  
*Current solution to the linear system.*
- `Matrix`< double > `bestx`  
*Best found solution to the linear system.*
- `Matrix`< double > `r`  
*Residual vector for the linear system.*
- `Matrix`< double > `r0`  
*Initial residual vector.*
- `Matrix`< double > `u`  
*Search direction for v.*
- `Matrix`< double > `w`  
*Updates sigma and u.*
- `Matrix`< double > `v`  
*Search direction for x.*
- `Matrix`< double > `p`  
*Preconditioning result for w, z, and matvec for Ax.*
- `Matrix`< double > `c`  
*Holds the matvec result between A and p.*
- `Matrix`< double > `z`  
*Full search direction for x.*

### 5.6.1 Detailed Description

Data structure for the implementation of the CGS algorithm for non-symmetric linear systems.

C-style object to be used in conjunction with the Conjugate Gradient Squared (CGS) algorithm to solve linear systems of equations. This algorithm is slightly less computational work than BiCGSTAB, but is much less stable. As a result, I do not recommend using this algorithm unless you also use some form of preconditioning.

### 5.6.2 Member Data Documentation

#### 5.6.2.1 int CGS\_DATA::maxit = 0

Maximum allowable iterations - default = min(2\*vector\_size,1000)

#### 5.6.2.2 int CGS\_DATA::iter = 0

Actual number of iterations.

#### 5.6.2.3 bool CGS\_DATA::breakdown

Boolean to determine if the method broke down.

**5.6.2.4 double CGS\_DATA::alpha**

Step size parameter for next solution.

**5.6.2.5 double CGS\_DATA::beta**

Step size parameter for search direction.

**5.6.2.6 double CGS\_DATA::rho**

Scaling parameter for alpha and beta.

**5.6.2.7 double CGS\_DATA::sigma**

Scaling parameter and additional step length.

**5.6.2.8 double CGS\_DATA::tol\_rel = 1e-6**

Relative tolerance for convergence - default = 1e-6.

**5.6.2.9 double CGS\_DATA::tol\_abs = 1e-6**

Absolution tolerance for convergence - default = 1e-6.

**5.6.2.10 double CGS\_DATA::res**

Absolute residual norm.

**5.6.2.11 double CGS\_DATA::relres**

Relative residual norm.

**5.6.2.12 double CGS\_DATA::relres\_base**

Initial residual norm.

**5.6.2.13 double CGS\_DATA::bestres**

Best found residual norm.

**5.6.2.14 bool CGS\_DATA::Output = true**

True = print messages to console.

**5.6.2.15 Matrix<double> CGS\_DATA::x**

Current solution to the linear system.

**5.6.2.16 Matrix<double> CGS\_DATA::bestx**

Best found solution to the linear system.

**5.6.2.17 Matrix<double> CGS\_DATA::r**

Residual vector for the linear system.

**5.6.2.18 Matrix<double> CGS\_DATA::r0**

Initial residual vector.

**5.6.2.19 Matrix<double> CGS\_DATA::u**

Search direction for v.

**5.6.2.20 Matrix<double> CGS\_DATA::w**

Updates sigma and u.

**5.6.2.21 Matrix<double> CGS\_DATA::v**

Search direction for x.

**5.6.2.22 Matrix<double> CGS\_DATA::p**

Preconditioning result for w, z, and matvec for Ax.

**5.6.2.23 Matrix<double> CGS\_DATA::c**

Holds the matvec result between A and p.

**5.6.2.24 Matrix<double> CGS\_DATA::z**

Full search direction for x.

The documentation for this struct was generated from the following file:

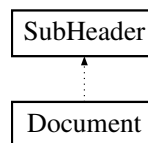
- [lark.h](#)

**5.7 Document Class Reference**

Object for the various documents in the yaml file.

```
#include <yaml_wrapper.h>
```

Inheritance diagram for Document:

**Public Member Functions**

- [Document](#) ()  
*Default constructor.*
- [~Document](#) ()  
*Default destructor.*
- [Document](#) (const [Document](#) &doc)  
*Copy constructor.*
- [Document](#) (std::string name)  
*Constructor by name.*
- [Document](#) (const [KeyValueMap](#) &map)  
*Constructor by existing map.*
- [Document](#) (std::string name, const [KeyValueMap](#) &map)  
*Constructor by name and map.*
- [Document](#) (std::string key, const [Header](#) &head)

- Constructor by single header.*

  - `Document & operator= (const Document &doc)`

*Equals overload.*
- `ValueTypePair & operator[] (const std::string key)`

*Return the ValueType reference at the given key.*
- `ValueTypePair operator[] (const std::string key) const`

*Return the ValueType at the given key.*
- `Header & operator() (const std::string key)`

*Return the Header reference at the given key.*
- `Header operator() (const std::string key) const`

*Return the Header at the given key.*
- `std::map< std::string, Header > & getHeadMap ()`

*Return the reference to the Header Map.*
- `KeyValueMap & getDataMap ()`

*Return the reference to the KeyValueMap.*
- `Header & getHeader (std::string key)`

*Return reference to the Header in map at the key.*
- `std::map< std::string, Header > ::const_iterator end () const`

*Returns a const iterator pointing to the end of the list.*
- `std::map< std::string, Header > ::iterator end ()`

*Returns an iterator pointing to the end of the list.*
- `std::map< std::string, Header > ::const_iterator begin () const`

*Returns a const iterator pointing to the beginning of the list.*
- `std::map< std::string, Header > ::iterator begin ()`

*Returns an iterator pointing to the beginning of the list.*
- `void clear ()`

*Clear out info in the Document.*
- `void resetKeys ()`

*Set all keys in the map to match names of the headers.*
- `void changeKey (std::string oldKey, std::string newKey)`

*Change a given oldKey in the header map to the newKey given.*
- `void revalidateAllKeys ()`

*Resets and validates keys in header and subheader maps.*
- `void addPair (std::string key, std::string val)`

*Adds a pair object to the map (with only strings)*
- `void addPair (std::string key, std::string val, int t)`

*Adds a pair object and asserts a type.*
- `void setName (std::string name)`

*Set the name of the Document.*
- `void setAlias (std::string alias)`

*Set the alias of the Document.*
- `void setNameAliasPair (std::string n, std::string a, int s)`

*Set the name, alias, and state of the document.*
- `void setState (int state)`

*Set the state of the Document.*
- `void DisplayContents ()`

*Display the contents of the Document.*



- void [addHeadKey](#) (std::string key)  
*Add a key to the [Header](#) without a header object.*
- void [copyAnchor2Alias](#) (std::string alias, [Header](#) &ref)  
*Find the anchor in the map, and copy to the [Header](#) reference given.*
- int [size](#) ()  
*Return the size of the header map.*
- std::string [getName](#) ()  
*Return the name of the document.*
- std::string [getAlias](#) ()  
*Return the alias of the document.*
- int [getState](#) ()  
*Return the state of the document.*
- bool [isAlias](#) ()  
*Returns true if the document is an alias.*
- bool [isAnchor](#) ()  
*Returns true if the document is an anchor.*
- [Header](#) & [getAnchoredHeader](#) (std::string alias)  
*Returns reference to the anchored header, if any.*
- [Header](#) & [getHeadFromSubAlias](#) (std::string alias)  
*Returns reference to the [Header](#) that contains a Sub with the given alias.*

#### Private Attributes

- std::map< std::string, [Header](#) > [Head\\_Map](#)  
*Map of headers contained within the document.*

#### Additional Inherited Members

##### 5.7.1 Detailed Description

Object for the various documents in the yaml file.

C++ Object for the documents in a yaml input file as denoted by a Key: followed by — (three dashes) and ending with a ... (three dots). A single yaml file can have multiple document structures and each document structure can have multiple headers (which have sub-headers and key-values) and key-value-pairs. This is the largest single object in the yaml file itself.

Just like [Header](#), this object also inherits from [SubHeader](#) and therefore has access to its protected members. You can use access to those members to establish the KeyValuePairs in the [Document](#), name the [Document](#), and give the [Document](#) an alias or anchor value.

##### 5.7.2 Constructor & Destructor Documentation

###### 5.7.2.1 Document::Document ( )

Default constructor.

###### 5.7.2.2 Document::~~Document ( )

Default destructor.

###### 5.7.2.3 Document::Document ( const Document & doc )

Copy constructor.

#### 5.7.2.4 Document::Document ( std::string *name* )

Constructor by name.

#### 5.7.2.5 Document::Document ( const KeyValueType & *map* )

Constructor by existing map.

#### 5.7.2.6 Document::Document ( std::string *name*, const KeyValueType & *map* )

Constructor by name and map.

#### 5.7.2.7 Document::Document ( std::string *key*, const Header & *head* )

Constructor by single header.

### 5.7.3 Member Function Documentation

#### 5.7.3.1 Document& Document::operator= ( const Document & *doc* )

Equals overload.

#### 5.7.3.2 ValuePair& Document::operator[] ( const std::string *key* )

Return the ValuePair reference at the given key.

#### 5.7.3.3 ValuePair Document::operator[] ( const std::string *key* ) const

Return the ValuePair at the given key.

#### 5.7.3.4 Header& Document::operator() ( const std::string *key* )

Return the [Header](#) reference at the given key.

#### 5.7.3.5 Header Document::operator() ( const std::string *key* ) const

Return the [Header](#) at the given key.

#### 5.7.3.6 std::map<std::string, Header>& Document::getHeadMap ( )

Return the reference to the [Header](#) Map.

#### 5.7.3.7 KeyValueType& Document::getDataMap ( )

Return the reference to the [KeyValueType](#).

#### 5.7.3.8 Header& Document::getHeader ( std::string *key* )

Return reference to the [Header](#) in map at the key.

#### 5.7.3.9 std::map<std::string, Header>::const\_iterator Document::end ( ) const

Returns a const iterator pointing to the end of the list.

#### 5.7.3.10 std::map<std::string, Header>::iterator Document::end ( )

Returns an iterator pointing to the end of the list.

#### 5.7.3.11 std::map<std::string, Header>::const\_iterator Document::begin ( ) const

Returns a const iterator pointing to the beginning of the list.

5.7.3.12 `std::map<std::string, Header>::iterator Document::begin ( )`

Returns an iterator pointing to the beginning of the list.

5.7.3.13 `void Document::clear ( )`

Clear out info in the [Document](#).

5.7.3.14 `void Document::resetKeys ( )`

Set all keys in the map to match names of the headers.

5.7.3.15 `void Document::changeKey ( std::string oldKey, std::string newKey )`

Change a given *oldKey* in the header map to the *newKey* given.

5.7.3.16 `void Document::revalidateAllKeys ( )`

Resets and validates keys in header and subheader maps.

5.7.3.17 `void Document::addPair ( std::string key, std::string val )`

Adds a pair object to the map (with only strings)

5.7.3.18 `void Document::addPair ( std::string key, std::string val, int t )`

Adds a pair object and asserts a type.

5.7.3.19 `void Document::setName ( std::string name )`

Set the name of the [Document](#).

5.7.3.20 `void Document::setAlias ( std::string alias )`

Set the alias of the [Document](#).

5.7.3.21 `void Document::setNameAliasPair ( std::string n, std::string a, int s )`

Set the name, alias, and state of the document.

5.7.3.22 `void Document::setState ( int state )`

Set the state of the [Document](#).

5.7.3.23 `void Document::DisplayContents ( )`

Display the contents of the [Document](#).

5.7.3.24 `void Document::addHeadKey ( std::string key )`

Add a key to the [Header](#) without a header object.

5.7.3.25 `void Document::copyAnchor2Alias ( std::string alias, Header & ref )`

Find the anchor in the map, and copy to the [Header](#) reference given.

5.7.3.26 `int Document::size ( )`

Return the size of the header map.

5.7.3.27 `std::string Document::getName ( )`

Return the name of the document.

5.7.3.28 `std::string Document::getAlias ( )`

Return the alias of the document.

5.7.3.29 `int Document::getState ( )`

Return the state of the document.

5.7.3.30 `bool Document::isAlias ( )`

Returns true if the document is an alias.

5.7.3.31 `bool Document::isAnchor ( )`

Returns true if the document is an anchor.

5.7.3.32 `Header& Document::getAnchoredHeader ( std::string alias )`

Returns reference to the anchored header, if any.

5.7.3.33 `Header& Document::getHeadFromSubAlias ( std::string alias )`

Returns reference to the [Header](#) that contains a Sub with the given alias.

## 5.7.4 Member Data Documentation

5.7.4.1 `std::map<std::string, Header> Document::Head_Map [private]`

Map of headers contained within the document.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 5.8 DOGFISH\_DATA Struct Reference

Primary data structure for running the DOGFISH application.

```
#include <dogfish.h>
```

## Public Attributes

- unsigned long int `total_steps` = 0  
*Total number of solver steps taken.*
- double `time_old` = 0.0  
*Old value of time (hrs)*
- double `time` = 0.0  
*Current value of time (hrs)*
- bool `Print2File` = true  
*True = results to .txt; False = no printing.*
- bool `Print2Console` = true  
*True = results to console; False = no printing.*
- bool `DirichletBC` = false

- False = uses film mass transfer for BC, True = Dirichlet BC.*

  - bool `NonLinear` = false
- False = Solve directly, True = Solve iteratively.*

  - double `t_counter` = 0.0
- Counter for the time output.*

  - double `t_print`
- Print output at every t\_print time (hrs)*

  - int `NumComp`
- Number of species to track.*

  - double `end_time`
- Units: hours.*

  - double `total_sorption_old`
- Per mass or volume of single fiber.*

  - double `total_sorption`
- Per mass or volume of single fiber.*

  - double `fiber_length`
- Units: um.*

  - double `fiber_diameter`
- Units: um.*

  - double `fiber_specific_area`
- Units: m<sup>2</sup>/kg.*

  - FILE \* `OutputFile`
- Output file pointer to the output file for postprocesses and results.*

  - double(\* `eval_R`)(int i, int l, const void \*data)
- Function pointer to evaluate retardation coefficient.*

  - double(\* `eval_DI`)(int i, int l, const void \*data)
- Function pointer to evaluate intraparticle diffusivity.*

  - double(\* `eval_kf`)(int i, const void \*data)
- Function pointer to evaluate film mass transfer coefficient.*

  - double(\* `eval_qs`)(int i, const void \*data)
- Function pointer to evaluate fiber surface concentration.*

  - const void \* `user_data`
- Data structure for users info to calculate all parameters.*

  - std::vector< `FINCH_DATA` > `finch_dat`
- Data structure for `FINCH_DATA` objects.*

  - std::vector< `DOGFISH_PARAM` > `param_dat`
- Data structure for `DOGFISH_PARAM` objects.*

### 5.8.1 Detailed Description

Primary data structure for running the DOGFISH application.

C-style object to hold information for the adsorption simulations. Contains function pointers and other data structures. This information is passed around to other functions used to simulate the fiber diffusion physics.

### 5.8.2 Member Data Documentation

#### 5.8.2.1 unsigned long int DOGFISH\_DATA::total\_steps = 0

Total number of solver steps taken.

5.8.2.2 double DOGFISH\_DATA::time\_old = 0.0

Old value of time (hrs)

5.8.2.3 double DOGFISH\_DATA::time = 0.0

Current value of time (hrs)

5.8.2.4 bool DOGFISH\_DATA::Print2File = true

True = results to .txt; False = no printing.

5.8.2.5 bool DOGFISH\_DATA::Print2Console = true

True = results to console; False = no printing.

5.8.2.6 bool DOGFISH\_DATA::DirichletBC = false

False = uses film mass transfer for BC, True = Dirichlet BC.

5.8.2.7 bool DOGFISH\_DATA::NonLinear = false

False = Solve directly, True = Solve iteratively.

5.8.2.8 double DOGFISH\_DATA::t\_counter = 0.0

Counter for the time output.

5.8.2.9 double DOGFISH\_DATA::t\_print

Print output at every t\_print time (hrs)

5.8.2.10 int DOGFISH\_DATA::NumComp

Number of species to track.

5.8.2.11 double DOGFISH\_DATA::end\_time

Units: hours.

5.8.2.12 double DOGFISH\_DATA::total\_sorption\_old

Per mass or volume of single fiber.

5.8.2.13 double DOGFISH\_DATA::total\_sorption

Per mass or volume of single fiber.

5.8.2.14 double DOGFISH\_DATA::fiber\_length

Units:  $\mu\text{m}$ .

5.8.2.15 double DOGFISH\_DATA::fiber\_diameter

Units:  $\mu\text{m}$ .

5.8.2.16 double DOGFISH\_DATA::fiber\_specific\_area

Units:  $\text{m}^2/\text{kg}$ .

## 5.8.2.17 FILE\* DOGFISH\_DATA::OutputFile

Output file pointer to the output file for postprocesses and results.

## 5.8.2.18 double(\* DOGFISH\_DATA::eval\_R)(int i, int l, const void \*data)

Function pointer to evaluate retardation coefficient.

## 5.8.2.19 double(\* DOGFISH\_DATA::eval\_DI)(int i, int l, const void \*data)

Function pointer to evaluate intraparticle diffusivity.

## 5.8.2.20 double(\* DOGFISH\_DATA::eval\_kf)(int i, const void \*data)

Function pointer to evaluate film mass transfer coefficient.

## 5.8.2.21 double(\* DOGFISH\_DATA::eval\_qs)(int i, const void \*data)

Function pointer to evaluate fiber surface concentration.

## 5.8.2.22 const void\* DOGFISH\_DATA::user\_data

Data structure for users info to calculate all parameters.

## 5.8.2.23 std::vector&lt;FINCH\_DATA&gt; DOGFISH\_DATA::finch\_dat

Data structure for [FINCH\\_DATA](#) objects.

## 5.8.2.24 std::vector&lt;DOGFISH\_PARAM&gt; DOGFISH\_DATA::param\_dat

Data structure for [DOGFISH\\_PARAM](#) objects.

The documentation for this struct was generated from the following file:

- [dogfish.h](#)

## 5.9 DOGFISH\_PARAM Struct Reference

Data structure for species-specific parameters.

```
#include <dogfish.h>
```

## Public Attributes

- double [intraparticle\\_diffusion](#)  
*Units:  $\mu\text{m}^2/\text{hr}$ .*
- double [film\\_transfer\\_coeff](#)  
*Units:  $\mu\text{m}/\text{hr}$ .*
- double [surface\\_concentration](#)  
*Units:  $\text{mol}/\text{kg}$ .*
- double [initial\\_sorption](#)  
*Units:  $\text{mol}/\text{kg}$ .*
- double [sorbed\\_molefraction](#)  
*Molefraction of sorbed species.*
- [Molecule species](#)  
*Adsorbed species [Molecule](#) Object.*

## 5.9.1 Detailed Description

Data structure for species-specific parameters.

C-style object to hold information on all adsorbing species. Parameters are given descriptive names to indicate what each is for.

## 5.9.2 Member Data Documentation

## 5.9.2.1 double DOGFISH\_PARAM::intraparticle\_diffusion

Units:  $\mu\text{m}^2/\text{hr}$ .

## 5.9.2.2 double DOGFISH\_PARAM::film\_transfer\_coeff

Units:  $\mu\text{m}/\text{hr}$ .

## 5.9.2.3 double DOGFISH\_PARAM::surface\_concentration

Units:  $\text{mol}/\text{kg}$ .

## 5.9.2.4 double DOGFISH\_PARAM::initial\_sorption

Units:  $\text{mol}/\text{kg}$ .

## 5.9.2.5 double DOGFISH\_PARAM::sorbed\_molefraction

Molefraction of sorbed species.

## 5.9.2.6 Molecule DOGFISH\_PARAM::species

Adsorbed species [Molecule](#) Object.

The documentation for this struct was generated from the following file:

- [dogfish.h](#)

## 5.10 FINCH\_DATA Struct Reference

Data structure for the FINCH object.

```
#include <finch.h>
```

## Public Attributes

- int [d](#) = 0  
*Dimension of the problem: 0 = cartesian, 1 = cylindrical, 2 = spherical.*
- double [dt](#) = 0.0125  
*Time step.*
- double [dt\\_old](#) = 0.0125  
*Previous time step.*
- double [T](#) = 1.0  
*Total time.*
- double [dz](#) = 0.1  
*Space step.*
- double [L](#) = 1.0  
*Total space.*



- double `s` = 1.0  
*Char quantity (spherical = 1, cylindrical = length, cartesian = area)*
- double `t` = 0.0  
*Current Time.*
- double `t_old` = 0.0  
*Previous Time.*
- double `uT` = 0.0  
*Total amount of conserved quantity in domain.*
- double `uT_old` = 0.0  
*Old Total amount of conserved quantity.*
- double `uAvg` = 0.0  
*Average amount of conserved quantity in domain.*
- double `uAvg_old` = 0.0  
*Old Average amount of conserved quantity.*
- double `uIC` = 0.0  
*Initial condition of Conserved Quantity (if constant)*
- double `vIC` = 1.0  
*Initial condition of Velocity (if constant)*
- double `DIC` = 1.0  
*Initial condition of Dispersion (if constant)*
- double `kIC` = 1.0  
*Initial condition of Reaction (if constant)*
- double `RIC` = 1.0  
*Initial condition of the Time Coefficient (if constant)*
- double `uo` = 1.0  
*Boundary Value of Conserved Quantity.*
- double `vo` = 1.0  
*Boundary Value of Velocity.*
- double `Do` = 1.0  
*Boundary Value of Dispersion.*
- double `ko` = 1.0  
*Boundary Value of Reaction.*
- double `Ro` = 1.0  
*Boundary Value of Time Coefficient.*
- double `kfn` = 1.0  
*Film mass transfer coefficient Old.*
- double `kfnp1` = 1.0  
*Film mass transfer coefficient New.*
- double `lambda_I`  
*Boundary Coefficient for Implicit Neumann (Calculated at Runtime)*
- double `lambda_E`  
*Boundary Coefficient for Explicit Neumann (Calculated at Runtime)*
- int `LN` = 10  
*Number of nodes.*
- bool `CN` = true  
*True if Crank-Nicholson, false if Implicit, never use explicit.*
- bool `Update` = false  
*Flag to check if the system needs updating.*
- bool `Dirichlet` = false  
*Flag to indicate use of Dirichlet or Neumann starting boundary.*
- bool `CheckMass` = false

- Flag to indicate whether or not mass is to be checked.*

  - bool `ExplicitFlux` = false
- Flag to indicate whether or not to use fully explicit flux limiters.*

  - bool `Iterative` = true
- Flag to indicate whether to solve directly, or iteratively.*

  - bool `SteadyState` = false
- Flag to determine whether or not to solve the steady-state problem.*

  - bool `NormTrack` = true
- Flag to determine whether or not to track the norms during simulation.*

  - double `beta` = 0.5
- Scheme type indicator: 0.5=CN & 1.0=Implicit; all else NULL.*

  - double `tol_rel` = 1e-6
- Relative Tolerance for Convergence.*

  - double `tol_abs` = 1e-6
- Absolute Tolerance for Convergence.*

  - int `max_iter` = 20
- Maximum number of iterations allowed.*

  - int `total_iter` = 0
- Total number of iterations made.*

  - int `nl_method` = `FINCH_Picard`
- Non-linear solution method - default = FINCH\_Picard.*

  - std::vector< double > `CL_I`
- Left side, implicit coefficients (Calculated at Runtime)*

  - std::vector< double > `CL_E`
- Left side, explicit coefficients (Calculated at Runtime)*

  - std::vector< double > `CC_I`
- Centered, implicit coefficients (Calculated at Runtime)*

  - std::vector< double > `CC_E`
- Centered, explicit coefficients (Calculated at Runtime)*

  - std::vector< double > `CR_I`
- Right side, implicit coefficients (Calculated at Runtime)*

  - std::vector< double > `CR_E`
- Right side, explicit coefficients (Calculated at Runtime)*

  - std::vector< double > `fL_I`
- Left side, implicit fluxes (Calculated at Runtime)*

  - std::vector< double > `fL_E`
- Left side, explicit fluxes (Calculated at Runtime)*

  - std::vector< double > `fC_I`
- Centered, implicit fluxes (Calculated at Runtime)*

  - std::vector< double > `fC_E`
- Centered, explicit fluxes (Calculated at Runtime)*

  - std::vector< double > `fR_I`
- Right side, implicit fluxes (Calculated at Runtime)*

  - std::vector< double > `fR_E`
- Right side, explicit fluxes (Calculated at Runtime)*

  - std::vector< double > `OI`
- Implicit upper diagonal matrix elements (Calculated at Runtime)*

  - std::vector< double > `OE`
- Explicit upper diagonal matrix elements (Calculated at Runtime)*

  - std::vector< double > `NI`
- Implicit diagonal matrix elements (Calculated at Runtime)*

- `std::vector< double > NE`  
*Explicit diagonal matrix elements (Calculated at Runtime)*
- `std::vector< double > MI`  
*Implicit lower diagonal matrix elements (Calculated at Runtime)*
- `std::vector< double > ME`  
*Explicit lower diagonal matrix elements (Calculated at Runtime)*
- `std::vector< double > uz_I_I`
- `std::vector< double > uz_lm1_I`
- `std::vector< double > uz_lp1_I`  
*Implicit local slopes (Calculated at Runtime)*
- `std::vector< double > uz_I_E`
- `std::vector< double > uz_lm1_E`
- `std::vector< double > uz_lp1_E`  
*Explicit local slopes (Calculated at Runtime)*
- `Matrix< double > unm1`  
*Conserved Quantity Older.*
- `Matrix< double > un`  
*Conserved Quantity Old.*
- `Matrix< double > unp1`  
*Conserved Quantity New.*
- `Matrix< double > u_star`  
*Conserved Quantity Projected New.*
- `Matrix< double > ubest`  
*Best found solution if solving iteratively.*
- `Matrix< double > vn`  
*Velocity Old.*
- `Matrix< double > vnp1`  
*Velocity New.*
- `Matrix< double > Dn`  
*Dispersion Old.*
- `Matrix< double > Dnp1`  
*Dispersion New.*
- `Matrix< double > kn`  
*Reaction Old.*
- `Matrix< double > knp1`  
*Reaction New.*
- `Matrix< double > Sn`  
*Forcing Function Old.*
- `Matrix< double > Snp1`  
*Forcing Function New.*
- `Matrix< double > Rn`  
*Time Coeff Old.*
- `Matrix< double > Rnp1`  
*Time Coeff New.*
- `Matrix< double > Fn`  
*Flux Limiter Old.*
- `Matrix< double > Fnp1`  
*Flux Limiter New.*
- `Matrix< double > gl`  
*Implicit Side Boundary Conditions.*
- `Matrix< double > gE`

*Explicit Side Boundary Conditions.*

- [Matrix< double > res](#)  
*Current residual.*
- [Matrix< double > pres](#)  
*Current search direction.*
- [int\(\\* callroutine \)\(const void \\*user\\_data\)](#)  
*Function pointer to executioner (DEFAULT = default\_execution)*
- [int\(\\* setic \)\(const void \\*user\\_data\)](#)  
*Function pointer to initial conditions (DEFAULT = default\_ic)*
- [int\(\\* settime \)\(const void \\*user\\_data\)](#)  
*Function pointer to set time step (DEFAULT = default\_timestep)*
- [int\(\\* setpreprocess \)\(const void \\*user\\_data\)](#)  
*Function pointer to preprocesses (DEFAULT = default\_preprocess)*
- [int\(\\* solve \)\(const void \\*user\\_data\)](#)  
*Function pointer to the solver (DEFAULT = default\_solve)*
- [int\(\\* setparams \)\(const void \\*user\\_data\)](#)  
*Function pointer to set parameters (DEFAULT = default\_params)*
- [int\(\\* discretize \)\(const void \\*user\\_data\)](#)  
*Function pointer to discretization (DEFAULT = ospre\_discretization)*
- [int\(\\* setbcs \)\(const void \\*user\\_data\)](#)
- [int\(\\* evalres \)\(const \[Matrix< double > &x\]\(#\), \[Matrix< double > &res\]\(#\), const void \\*user\\_data\)](#)  
*Function pointer to the residual function (DEFAULT = default\_res)*
- [int\(\\* evalprecon \)\(const \[Matrix< double > &b\]\(#\), \[Matrix< double > &p\]\(#\), const void \\*user\\_data\)](#)  
*Function pointer to the preconditioning function (DEFAULT = default\_precon)*
- [int\(\\* setpostprocess \)\(const void \\*user\\_data\)](#)  
*Function pointer to the postprocesses (DEFAULT = default\_postprocess)*
- [int\(\\* resettime \)\(const void \\*user\\_data\)](#)  
*Function pointer to reset time (DEFAULT = default\_reset)*
- [PICARD\\_DATA picard\\_dat](#)  
*Data structure for PICARD method (no need to use this)*
- [PJFNK\\_DATA pjfnk\\_dat](#)  
*Data structure for PJFNK method (more rigours method)*
- [const void \\* param\\_data](#)  
*User's data structure used to evaluate the parameter function (Must override if setparams is overridden)*

### 5.10.1 Detailed Description

Data structure for the FINCH object.

C-style object that holds data, functions, and other structures necessary to discretize and solve a FINCH problem. All of this information must be overridden or initialized prior to running a FINCH simulation. Many, many default functions are provided to make it easier to incorporate FINCH into other problems. The main function to override will be the setparams function. This will be a function that the user provides to tell the FINCH simulation how the parameters of the problem vary in time and space and whether or not they are coupled the the variable u. All functions are overridable and several can be skipped entirely, or called directly at different times in the execution of a particular routine. This make FINCH extremely flexible to the user.

#### Note

All parameters and dimensions do not carry any units with them. The user is required to keep track of all their own units in their particular problem and ensure that units will cancel and be consistent in their own physical model.

### 5.10.2 Member Data Documentation

#### 5.10.2.1 int FINCH\_DATA::d = 0

Dimension of the problem: 0 = cartesian, 1 = cylindrical, 2 = spherical.

#### 5.10.2.2 double FINCH\_DATA::dt = 0.0125

Time step.

#### 5.10.2.3 double FINCH\_DATA::dt\_old = 0.0125

Previous time step.

#### 5.10.2.4 double FINCH\_DATA::T = 1.0

Total time.

#### 5.10.2.5 double FINCH\_DATA::dz = 0.1

Space step.

#### 5.10.2.6 double FINCH\_DATA::L = 1.0

Total space.

#### 5.10.2.7 double FINCH\_DATA::s = 1.0

Char quantity (spherical = 1, cylindrical = length, cartesian = area)

#### 5.10.2.8 double FINCH\_DATA::t = 0.0

Current Time.

#### 5.10.2.9 double FINCH\_DATA::t\_old = 0.0

Previous Time.

#### 5.10.2.10 double FINCH\_DATA::uT = 0.0

Total amount of conserved quantity in domain.

#### 5.10.2.11 double FINCH\_DATA::uT\_old = 0.0

Old Total amount of conserved quantity.

#### 5.10.2.12 double FINCH\_DATA::uAvg = 0.0

Average amount of conserved quantity in domain.

#### 5.10.2.13 double FINCH\_DATA::uAvg\_old = 0.0

Old Average amount of conserved quantity.

#### 5.10.2.14 double FINCH\_DATA::uIC = 0.0

Initial condition of Conserved Quantity (if constant)

#### 5.10.2.15 double FINCH\_DATA::vIC = 1.0

Initial condition of Velocity (if constant)

5.10.2.16 double FINCH\_DATA::DIC = 1.0

Initial condition of Dispersion (if constant)

5.10.2.17 double FINCH\_DATA::kIC = 1.0

Initial condition of [Reaction](#) (if constant)

5.10.2.18 double FINCH\_DATA::RIC = 1.0

Initial condition of the Time Coefficient (if constant)

5.10.2.19 double FINCH\_DATA::uo = 1.0

Boundary Value of Conserved Quantity.

5.10.2.20 double FINCH\_DATA::vo = 1.0

Boundary Value of Velocity.

5.10.2.21 double FINCH\_DATA::Do = 1.0

Boundary Value of Dispersion.

5.10.2.22 double FINCH\_DATA::ko = 1.0

Boundary Value of [Reaction](#).

5.10.2.23 double FINCH\_DATA::Ro = 1.0

Boundary Value of Time Coefficient.

5.10.2.24 double FINCH\_DATA::kfn = 1.0

Film mass transfer coefficient Old.

5.10.2.25 double FINCH\_DATA::kfnp1 = 1.0

Film mass transfer coefficient New.

5.10.2.26 double FINCH\_DATA::lambda\_I

Boundary Coefficient for Implicit Neumann (Calculated at Runtime)

5.10.2.27 double FINCH\_DATA::lambda\_E

Boundary Coefficient for Explicit Neumann (Calculated at Runtime)

5.10.2.28 int FINCH\_DATA::LN = 10

Number of nodes.

5.10.2.29 bool FINCH\_DATA::CN = true

True if Crank-Nicholson, false if Implicit, never use explicit.

5.10.2.30 bool FINCH\_DATA::Update = false

Flag to check if the system needs updating.

5.10.2.31 `bool FINCH_DATA::Dirichlet = false`

Flag to indicate use of Dirichlet or Neumann starting boundary.

5.10.2.32 `bool FINCH_DATA::CheckMass = false`

Flag to indicate whether or not mass is to be checked.

5.10.2.33 `bool FINCH_DATA::ExplicitFlux = false`

Flag to indicate whether or not to use fully explicit flux limiters.

5.10.2.34 `bool FINCH_DATA::Iterative = true`

Flag to indicate whether to solve directly, or iteratively.

5.10.2.35 `bool FINCH_DATA::SteadyState = false`

Flag to determine whether or not to solve the steady-state problem.

5.10.2.36 `bool FINCH_DATA::NormTrack = true`

Flag to determine whether or not to track the norms during simulation.

5.10.2.37 `double FINCH_DATA::beta = 0.5`

Scheme type indicator: 0.5=CN & 1.0=Implicit; all else NULL.

5.10.2.38 `double FINCH_DATA::tol_rel = 1e-6`

Relative Tolerance for Convergence.

5.10.2.39 `double FINCH_DATA::tol_abs = 1e-6`

Absolute Tolerance for Convergence.

5.10.2.40 `int FINCH_DATA::max_iter = 20`

Maximum number of iterations allowed.

5.10.2.41 `int FINCH_DATA::total_iter = 0`

Total number of iterations made.

5.10.2.42 `int FINCH_DATA::nl_method = FINCH_Picard`

Non-linear solution method - default = FINCH\_Picard.

5.10.2.43 `std::vector<double> FINCH_DATA::CL_I`

Left side, implicit coefficients (Calculated at Runtime)

5.10.2.44 `std::vector<double> FINCH_DATA::CL_E`

Left side, explicit coefficients (Calculated at Runtime)

5.10.2.45 `std::vector<double> FINCH_DATA::CC_I`

Centered, implicit coefficients (Calculated at Runtime)

5.10.2.46 `std::vector<double> FINCH_DATA::CC_E`

Centered, explicit coefficients (Calculated at Runtime)

5.10.2.47 `std::vector<double> FINCH_DATA::CR_I`

Right side, implicit coefficients (Calculated at Runtime)

5.10.2.48 `std::vector<double> FINCH_DATA::CR_E`

Right side, explicit coefficients (Calculated at Runtime)

5.10.2.49 `std::vector<double> FINCH_DATA::fL_I`

Left side, implicit fluxes (Calculated at Runtime)

5.10.2.50 `std::vector<double> FINCH_DATA::fL_E`

Left side, explicit fluxes (Calculated at Runtime)

5.10.2.51 `std::vector<double> FINCH_DATA::fC_I`

Centered, implicit fluxes (Calculated at Runtime)

5.10.2.52 `std::vector<double> FINCH_DATA::fC_E`

Centered, explicit fluxes (Calculated at Runtime)

5.10.2.53 `std::vector<double> FINCH_DATA::fR_I`

Right side, implicit fluxes (Calculated at Runtime)

5.10.2.54 `std::vector<double> FINCH_DATA::fR_E`

Right side, explicit fluxes (Calculated at Runtime)

5.10.2.55 `std::vector<double> FINCH_DATA::OI`

Implicit upper diagonal matrix elements (Calculated at Runtime)

5.10.2.56 `std::vector<double> FINCH_DATA::OE`

Explicit upper diagonal matrix elements (Calculated at Runtime)

5.10.2.57 `std::vector<double> FINCH_DATA::NI`

Implicit diagonal matrix elements (Calculated at Runtime)

5.10.2.58 `std::vector<double> FINCH_DATA::NE`

Explicit diagonal matrix elements (Calculated at Runtime)

5.10.2.59 `std::vector<double> FINCH_DATA::MI`

Implicit lower diagonal matrix elements (Calculated at Runtime)

5.10.2.60 `std::vector<double> FINCH_DATA::ME`

Explicit lower diagonal matrix elements (Calculated at Runtime)

5.10.2.61 `std::vector<double> FINCH_DATA::uz_I_I`



5.10.2.62 `std::vector<double> FINCH_DATA::uz_lm1_I`

5.10.2.63 `std::vector<double> FINCH_DATA::uz_lp1_I`

Implicit local slopes (Calculated at Runtime)

5.10.2.64 `std::vector<double> FINCH_DATA::uz_I_E`

5.10.2.65 `std::vector<double> FINCH_DATA::uz_lm1_E`

5.10.2.66 `std::vector<double> FINCH_DATA::uz_lp1_E`

Explicit local slopes (Calculated at Runtime)

5.10.2.67 `Matrix<double> FINCH_DATA::unm1`

Conserved Quantity Older.

5.10.2.68 `Matrix<double> FINCH_DATA::un`

Conserved Quantity Old.

5.10.2.69 `Matrix<double> FINCH_DATA::unp1`

Conserved Quantity New.

5.10.2.70 `Matrix<double> FINCH_DATA::u_star`

Conserved Quantity Projected New.

5.10.2.71 `Matrix<double> FINCH_DATA::ubest`

Best found solution if solving iteratively.

5.10.2.72 `Matrix<double> FINCH_DATA::vn`

Velocity Old.

5.10.2.73 `Matrix<double> FINCH_DATA::vnp1`

Velocity New.

5.10.2.74 `Matrix<double> FINCH_DATA::Dn`

Dispersion Old.

5.10.2.75 `Matrix<double> FINCH_DATA::Dnp1`

Dispersion New.

5.10.2.76 `Matrix<double> FINCH_DATA::kn`

[Reaction](#) Old.

5.10.2.77 `Matrix<double> FINCH_DATA::knp1`

[Reaction](#) New.

5.10.2.78 `Matrix<double> FINCH_DATA::Sn`

Forcing Function Old.

**5.10.2.79** Matrix<double> FINCH\_DATA::Snp1

Forcing Function New.

**5.10.2.80** Matrix<double> FINCH\_DATA::Rn

Time Coeff Old.

**5.10.2.81** Matrix<double> FINCH\_DATA::Rnp1

Time Coeff New.

**5.10.2.82** Matrix<double> FINCH\_DATA::Fn

Flux Limiter Old.

**5.10.2.83** Matrix<double> FINCH\_DATA::Fnp1

Flux Limiter New.

**5.10.2.84** Matrix<double> FINCH\_DATA::gl

Implicit Side Boundary Conditions.

**5.10.2.85** Matrix<double> FINCH\_DATA::gE

Explicit Side Boundary Conditions.

**5.10.2.86** Matrix<double> FINCH\_DATA::res

Current residual.

**5.10.2.87** Matrix<double> FINCH\_DATA::pres

Current search direction.

**5.10.2.88** int(\* FINCH\_DATA::callroutine)(const void \*user\_data)

Function pointer to executioner (DEFAULT = default\_execution)

**5.10.2.89** int(\* FINCH\_DATA::setic)(const void \*user\_data)

Function pointer to initial conditions (DEFAULT = default\_ic)

**5.10.2.90** int(\* FINCH\_DATA::settime)(const void \*user\_data)

Function pointer to set time step (DEFAULT = default\_timestep)

**5.10.2.91** int(\* FINCH\_DATA::setpreprocess)(const void \*user\_data)

Function pointer to preprocesses (DEFAULT = default\_preprocess)

**5.10.2.92** int(\* FINCH\_DATA::solve)(const void \*user\_data)

Function pointer to the solver (DEFAULT = default\_solve)

**5.10.2.93** int(\* FINCH\_DATA::setparams)(const void \*user\_data)

Function pointer to set parameters (DEFAULT = default\_params)

5.10.2.94 `int(* FINCH_DATA::discretize)(const void *user_data)`

Function pointer to discretization (DEFAULT = `ospre_discretization`)

5.10.2.95 `int(* FINCH_DATA::setbcs)(const void *user_data)`

Function pointer to set boundary conditions (DEFAULT = `default_bcs`)

5.10.2.96 `int(* FINCH_DATA::evalres)(const Matrix< double > &x, Matrix< double > &res, const void *user_data)`

Function pointer to the residual function (DEFAULT = `default_res`)

5.10.2.97 `int(* FINCH_DATA::evalprecon)(const Matrix< double > &b, Matrix< double > &p, const void *user_data)`

Function pointer to the preconditioning function (DEFAULT = `default_precon`)

5.10.2.98 `int(* FINCH_DATA::setpostprocess)(const void *user_data)`

Function pointer to the postprocesses (DEFAULT = `default_postprocess`)

5.10.2.99 `int(* FINCH_DATA::resettime)(const void *user_data)`

Function pointer to reset time (DEFAULT = `default_reset`)

5.10.2.100 `PICARD_DATA FINCH_DATA::picard_dat`

Data structure for PICARD method (no need to use this)

5.10.2.101 `PJFNK_DATA FINCH_DATA::pjfnk_dat`

Data structure for PJFNK method (more rigours method)

5.10.2.102 `const void* FINCH_DATA::param_data`

User's data structure used to evaluate the parameter function (Must override if `setparams` is overridden)

The documentation for this struct was generated from the following file:

- [finch.h](#)

## 5.11 GCR\_DATA Struct Reference

Data structure for the implementation of the GCR algorithm for non-symmetric linear systems.

```
#include <lark.h>
```

### Public Attributes

- `int restart = -1`  
*Restart parameter for outer iterations - default = 20.*
- `int maxit = 0`  
*Maximum allowable outer iterations.*
- `int iter_outer = 0`  
*Number of outer iterations taken.*
- `int iter_inner = 0`  
*Number of inner iterations taken.*
- `int total_iter = 0`  
*Total number of iterations taken.*

- bool `breakdown` = false  
*Boolean to determine if a step has failed.*
- double `alpha`  
*Inner iteration step size.*
- double `beta`  
*Outer iteration step size.*
- double `tol_rel` = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double `tol_abs` = 1e-6  
*Absolute tolerance for convergence - default = 1e-6.*
- double `res`  
*Absolute residual norm for linear system.*
- double `relres`  
*Relative residual norm for linear system.*
- double `relres_base`  
*Initial residual norm of the linear system.*
- double `bestres`  
*Best found residual norm of the linear system.*
- bool `Output` = true  
*True = print messages to the console.*
- `Matrix< double > x`  
*Current solution to the linear system.*
- `Matrix< double > bestx`  
*Best found solution to the linear system.*
- `Matrix< double > r`  
*Residual Vector.*
- `Matrix< double > c_temp`  
*Temporary c vector to be updated.*
- `Matrix< double > u_temp`  
*Temporary u vector to be updated.*
- `std::vector< Matrix< double > > u`  
*Vector span for updating x.*
- `std::vector< Matrix< double > > c`  
*Vector span for updating r.*
- `OPTRANS_DATA transpose_dat`  
*Data structure for Operator Transposition.*

### 5.11.1 Detailed Description

Data structure for the implementation of the GCR algorithm for non-symmetric linear systems.

C-style object used in conjunction with the Generalized Conjugate Residual (GCR) algorithm for solving a non-symmetric linear system of equations. When the linear system in question has a positive-definite-symmetric component to it, then this algorithm is equivalent to GMRESRP. However, it is generally less efficient than GMRESRP and can suffer breakdowns.

### 5.11.2 Member Data Documentation

#### 5.11.2.1 int GCR\_DATA::restart = -1

Restart parameter for outer iterations - default = 20.

5.11.2.2 `int GCR_DATA::maxit = 0`

Maximum allowable outer iterations.

5.11.2.3 `int GCR_DATA::iter_outer = 0`

Number of outer iterations taken.

5.11.2.4 `int GCR_DATA::iter_inner = 0`

Number of inner iterations taken.

5.11.2.5 `int GCR_DATA::total_iter = 0`

Total number of iterations taken.

5.11.2.6 `bool GCR_DATA::breakdown = false`

Boolean to determine if a step has failed.

5.11.2.7 `double GCR_DATA::alpha`

Inner iteration step size.

5.11.2.8 `double GCR_DATA::beta`

Outer iteration step size.

5.11.2.9 `double GCR_DATA::tol_rel = 1e-6`

Relative tolerance for convergence - default = 1e-6.

5.11.2.10 `double GCR_DATA::tol_abs = 1e-6`

Absolute tolerance for convergence - default = 1e-6.

5.11.2.11 `double GCR_DATA::res`

Absolute residual norm for linear system.

5.11.2.12 `double GCR_DATA::relres`

Relative residual norm for linear system.

5.11.2.13 `double GCR_DATA::relres_base`

Initial residual norm of the linear system.

5.11.2.14 `double GCR_DATA::bestres`

Best found residual norm of the linear system.

5.11.2.15 `bool GCR_DATA::Output = true`

True = print messages to the console.

5.11.2.16 `Matrix<double> GCR_DATA::x`

Current solution to the linear system.

**5.11.2.17** Matrix<double> GCR\_DATA::bestx

Best found solution to the linear system.

**5.11.2.18** Matrix<double> GCR\_DATA::r

Residual Vector.

**5.11.2.19** Matrix<double> GCR\_DATA::c\_temp

Temporary c vector to be updated.

**5.11.2.20** Matrix<double> GCR\_DATA::u\_temp

Temporary u vector to be updated.

**5.11.2.21** std::vector<Matrix<double> > GCR\_DATA::u

Vector span for updating x.

**5.11.2.22** std::vector<Matrix<double> > GCR\_DATA::c

Vector span for updating r.

**5.11.2.23** OPTRANS\_DATA GCR\_DATA::transpose\_dat

Data structure for Operator Transposition.

The documentation for this struct was generated from the following file:

- [lark.h](#)

**5.12** GMRESLP\_DATA Struct Reference

Data structure for implementation of the Restarted GMRES algorithm with Left Preconditioning.

```
#include <lark.h>
```

**Public Attributes**

- int [restart](#) = -1  
*Restart parameter - default = min(vector\_size,20)*
- int [maxit](#) = 0  
*Maximum allowable iterations - default = min(vector\_size,1000)*
- int [iter](#) = 0  
*Number of iterations needed for convergence.*
- int [steps](#) = 0  
*Total number of gmres iterations and krylov iterations.*
- double [tol\\_rel](#) = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double [tol\\_abs](#) = 1e-6  
*Absolution tolerance for convergence - default = 1e-6.*
- double [res](#)  
*Absolution redisual norm of the linear system.*
- double [relres](#)  
*Relative residual norm of the linear system.*
- double [relres\\_base](#)

- Initial residual norm of the linear system.*
- double `bestres`
- Best found residual norm of the linear system.*
- bool `Output` = true
- True = print messages to console.*
- `Matrix`< double > `x`
- Current solution to the linear system.*
- `Matrix`< double > `bestx`
- Best found solution to the linear system.*
- `Matrix`< double > `r`
- Residual vector for the linear system.*
- `ARNOLDI_DATA` `arnoldi_dat`
- Data structure for the kyrlov subspace.*

### 5.12.1 Detailed Description

Data structure for implementation of the Restarted GMRES algorithm with Left Preconditioning.

C-style object used in conjunction with Generalized Minimum RESidual Left-Preconditioned (GMRESLP) and Full Orthogonalization Method (FOM) algorithms to iteratively or directly solve a linear system of equations. When using with GMRESLP, you can only check/observe the linear residuals before a restart or after the Arnoldi space is constructed. This is because this object uses Left-side Preconditioning. A faster routine may be GMRESRP, which is able to construct residuals after each Arnoldi iteration.

### 5.12.2 Member Data Documentation

#### 5.12.2.1 int GMRESLP\_DATA::restart = -1

Restart parameter - default = min(vector\_size,20)

#### 5.12.2.2 int GMRESLP\_DATA::maxit = 0

Maximum allowable iterations - default = min(vector\_size,1000)

#### 5.12.2.3 int GMRESLP\_DATA::iter = 0

Number of iterations needed for convergence.

#### 5.12.2.4 int GMRESLP\_DATA::steps = 0

Total number of gmres iterations and krylov iterations.

#### 5.12.2.5 double GMRESLP\_DATA::tol\_rel = 1e-6

Relative tolerance for convergence - default = 1e-6.

#### 5.12.2.6 double GMRESLP\_DATA::tol\_abs = 1e-6

Absolution tolerance for convergence - default = 1e-6.

#### 5.12.2.7 double GMRESLP\_DATA::res

Absolution redisual norm of the linear system.

#### 5.12.2.8 double GMRESLP\_DATA::relres

Relative residual norm of the linear system.

## 5.12.2.9 double GMRESLP\_DATA::relres\_base

Initial residual norm of the linear system.

## 5.12.2.10 double GMRESLP\_DATA::bestres

Best found residual norm of the linear system.

## 5.12.2.11 bool GMRESLP\_DATA::Output = true

True = print messages to console.

## 5.12.2.12 Matrix&lt;double&gt; GMRESLP\_DATA::x

Current solution to the linear system.

## 5.12.2.13 Matrix&lt;double&gt; GMRESLP\_DATA::bestx

Best found solution to the linear system.

## 5.12.2.14 Matrix&lt;double&gt; GMRESLP\_DATA::r

Residual vector for the linear system.

## 5.12.2.15 ARNOLDI\_DATA GMRESLP\_DATA::arnoldi\_dat

Data structure for the kyrlov subspace.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.13 GMRESR\_DATA Struct Reference

Data structure for the implementation of GCR with Nested GMRES preconditioning (i.e., GMRESR)

```
#include <lark.h>
```

## Public Attributes

- int [gcr\\_restart](#) = -1  
*Number of GCR restarts (default = 20, max = N)*
- int [gcr\\_maxit](#) = 0  
*Number of GCR iterations.*
- int [gmres\\_restart](#) = -1  
*Number of GMRES restarts (max = 20)*
- int [gmres\\_maxit](#) = 1  
*Number of GMRES iterations (max = 5, default = 1)*
- int [N](#)  
*Dimension of the linear system.*
- int [total\\_iter](#)  
*Total GMRES and GCR iterations.*
- int [iter\\_outer](#)  
*Total GCR iterations.*
- int [iter\\_inner](#)  
*Total GMRES iterations.*
- bool [GCR\\_Output](#) = true



- True = print GCR messages.*
- bool `GMRES_Output` = false
- True = print GMRES messages.*
- double `gmres_tol` = 0.1
- Tolerance relative to GCR iterations.*
- double `gcr_rel_tol` = 1e-6
- Relative outer residual tolerance.*
- double `gcr_abs_tol` = 1e-6
- Absolute outer residual tolerance.*
- `Matrix`< double > `arg`
- Argument matrix passed between preconditioner and iterator.*
- `GCR_DATA gcr_dat`
- Data structure for the outer GCR steps.*
- `GMRESR_DATA gmres_dat`
- Data structure for the inner GMRES steps.*
- `int(* matvec)(const Matrix< double > &x, Matrix< double > &Ax, const void *matvec_data)`
- User supplied matrix-vector product function.*
- `int(* terminal_precon)(const Matrix< double > &r, Matrix< double > &p, const void *precon_data)`
- Optional user supplied terminal preconditioner.*
- const void \* `matvec_data`
- Data structure for the user's matvec function.*
- const void \* `term_precon`
- Data structure for the user's terminal preconditioner.*

#### 5.13.1 Detailed Description

Data structure for the implementation of GCR with Nested GMRES preconditioning (i.e., GMRESR)

C-style object to be used in conjunction with the Generalized Minimum RESidual Recurive (GMRESR) algorithm. Although the name suggests that this method used GMRES recursively, what it is actually doing is nesting GMRESR iterations inside the GCR method to form a preconditioner for GCR. The name GMRESR came from literature (Vorst and Vuik, "GMRESR: A family of nested GMRES methods", 1991).

#### 5.13.2 Member Data Documentation

##### 5.13.2.1 int GMRESR\_DATA::gcr\_restart = -1

Number of GCR restarts (default = 20, max = N)

##### 5.13.2.2 int GMRESR\_DATA::gcr\_maxit = 0

Number of GCR iterations.

##### 5.13.2.3 int GMRESR\_DATA::gmres\_restart = -1

Number of GMRES restarts (max = 20)

##### 5.13.2.4 int GMRESR\_DATA::gmres\_maxit = 1

Number of GMRES iterations (max = 5, default = 1)

##### 5.13.2.5 int GMRESR\_DATA::N

Dimension of the linear system.

**5.13.2.6** int GMRESR\_DATA::total\_iter

Total GMRES and GCR iterations.

**5.13.2.7** int GMRESR\_DATA::iter\_outer

Total GCR iterations.

**5.13.2.8** int GMRESR\_DATA::iter\_inner

Total GMRES iterations.

**5.13.2.9** bool GMRESR\_DATA::GCR\_Output = true

True = print GCR messages.

**5.13.2.10** bool GMRESR\_DATA::GMRES\_Output = false

True = print GMRES messages.

**5.13.2.11** double GMRESR\_DATA::gmres\_tol = 0.1

Tolerance relative to GCR iterations.

**5.13.2.12** double GMRESR\_DATA::gcr\_rel\_tol = 1e-6

Relative outer residual tolerance.

**5.13.2.13** double GMRESR\_DATA::gcr\_abs\_tol = 1e-6

Absolute outer residual tolerance.

**5.13.2.14** Matrix<double> GMRESR\_DATA::arg

Argument matrix passed between preconditioner and iterator.

**5.13.2.15** GCR\_DATA GMRESR\_DATA::gcr\_dat

Data structure for the outer GCR steps.

**5.13.2.16** GMRESRP\_DATA GMRESR\_DATA::gmres\_dat

Data structure for the inner GMRES steps.

**5.13.2.17** int(\* GMRESR\_DATA::matvec)(const Matrix< double > &x, Matrix< double > &Ax, const void \*matvec\_data)

User supplied matrix-vector product function.

**5.13.2.18** int(\* GMRESR\_DATA::terminal\_precon)(const Matrix< double > &r, Matrix< double > &p, const void \*precon\_data)

Optional user supplied terminal preconditioner.

**5.13.2.19** const void\* GMRESR\_DATA::matvec\_data

Data structure for the user's matvec function.

**5.13.2.20** const void\* GMRESR\_DATA::term\_precon

Data structure for the user's terminal preconditioner.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.14 GMRESRP\_DATA Struct Reference

Data structure for the Restarted GMRES algorithm with Right Preconditioning.

```
#include <lark.h>
```

### Public Attributes

- int [restart](#) = -1  
*Restart parameter - default = min(20,vector\_size)*
- int [maxit](#) = 0  
*Maximum allowable outer iterations.*
- int [iter\\_outer](#) = 0  
*Total number of outer iterations.*
- int [iter\\_inner](#) = 0  
*Total number of inner iterations.*
- int [iter\\_total](#) = 0  
*Total number of overall iterations.*
- double [tol\\_rel](#) = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double [tol\\_abs](#) = 1e-6  
*Absolute tolerance for convergence - default = 1e-6.*
- double [res](#)  
*Absolute residual norm for linear system.*
- double [relres](#)  
*Relative residual norm for linear system.*
- double [relres\\_base](#)  
*Initial residual norm of the linear system.*
- double [bestres](#)  
*Best found residual norm of the linear system.*
- bool [Output](#) = true  
*True = print messages to console.*
- [Matrix](#)< double > [x](#)  
*Current solution to the linear system.*
- [Matrix](#)< double > [bestx](#)  
*Best found solution to the linear system.*
- [Matrix](#)< double > [r](#)  
*Residual vector for the linear system.*
- std::vector< [Matrix](#)< double > > [Vk](#)  
*(N x k) orthonormal vector basis*
- std::vector< [Matrix](#)< double > > [Zk](#)  
*(N x k) preconditioned vector set*
- std::vector< std::vector< double > > [H](#)  
*(k+1 x k) upper Hessenberg storage matrix*
- std::vector< std::vector< double > > [H\\_bar](#)  
*(k+1 x k) Factorized matrix*
- std::vector< double > [y](#)

- (k x 1) Vector search direction*
- `std::vector< double > e0`
- (k+1 x 1) Normalized vector with residual info*
- `std::vector< double > e0_bar`
- (k+1 x 1) Factorized normal vector*
- `Matrix< double > w`
- (N) x (1) interim result of the matrix\_vector multiplication*
- `Matrix< double > v`
- (N) x (1) holding cell for the column entries of  $V_k$  and other interims*
- `Matrix< double > sum`
- (N) x (1) running sum of subspace vectors for use in altering  $w$*

#### 5.14.1 Detailed Description

Data structure for the Restarted GMRES algorithm with Right Preconditioning.

C-style object used in conjunction with Generalized Minimum RESidual Right Preconditioned (GMRESRP) algorithm to iteratively solve a linear system of equations. Unlike GMRESLP, the GMRESRP method is capable of checking linear residuals at both the inner and outer steps. As a result, this algorithm may terminate earlier than GMRESLP if it has found a suitable solution during one of the inner steps.

#### 5.14.2 Member Data Documentation

##### 5.14.2.1 `int GMRESRP_DATA::restart = -1`

Restart parameter - default =  $\min(20, \text{vector\_size})$

##### 5.14.2.2 `int GMRESRP_DATA::maxit = 0`

Maximum allowable outer iterations.

##### 5.14.2.3 `int GMRESRP_DATA::iter_outer = 0`

Total number of outer iterations.

##### 5.14.2.4 `int GMRESRP_DATA::iter_inner = 0`

Total number of inner iterations.

##### 5.14.2.5 `int GMRESRP_DATA::iter_total = 0`

Total number of overall iterations.

##### 5.14.2.6 `double GMRESRP_DATA::tol_rel = 1e-6`

Relative tolerance for convergence - default =  $1e-6$ .

##### 5.14.2.7 `double GMRESRP_DATA::tol_abs = 1e-6`

Absolute tolerance for convergence - default =  $1e-6$ .

##### 5.14.2.8 `double GMRESRP_DATA::res`

Absolute residual norm for linear system.

##### 5.14.2.9 `double GMRESRP_DATA::relres`

Relative residual norm for linear system.

5.14.2.10 `double GMRESRP_DATA::relres_base`

Initial residual norm of the linear system.

5.14.2.11 `double GMRESRP_DATA::bestres`

Best found residual norm of the linear system.

5.14.2.12 `bool GMRESRP_DATA::Output = true`

True = print messages to console.

5.14.2.13 `Matrix<double> GMRESRP_DATA::x`

Current solution to the linear system.

5.14.2.14 `Matrix<double> GMRESRP_DATA::bestx`

Best found solution to the linear system.

5.14.2.15 `Matrix<double> GMRESRP_DATA::r`

Residual vector for the linear system.

5.14.2.16 `std::vector< Matrix<double> > GMRESRP_DATA::Vk`

(N x k) orthonormal vector basis

5.14.2.17 `std::vector< Matrix<double> > GMRESRP_DATA::Zk`

(N x k) preconditioned vector set

5.14.2.18 `std::vector< std::vector< double > > GMRESRP_DATA::H`

(k+1 x k) upper Hessenberg storage matrix

5.14.2.19 `std::vector< std::vector< double > > GMRESRP_DATA::H_bar`

(k+1 x k) Factorized matrix

5.14.2.20 `std::vector< double > GMRESRP_DATA::y`

(k x 1) Vector search direction

5.14.2.21 `std::vector< double > GMRESRP_DATA::e0`

(k+1 x 1) Normalized vector with residual info

5.14.2.22 `std::vector< double > GMRESRP_DATA::e0_bar`

(k+1 x 1) Factorized normal vector

5.14.2.23 `Matrix<double> GMRESRP_DATA::w`

(N) x (1) interim result of the matrix\_vector multiplication

5.14.2.24 `Matrix<double> GMRESRP_DATA::v`

(N) x (1) holding cell for the column entries of Vk and other interims

## 5.14.2.25 Matrix&lt;double&gt; GMRESRP\_DATA::sum

(N) x (1) running sum of subspace vectors for use in altering w

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.15 GPAST\_DATA Struct Reference

GPAST Data Structure.

```
#include <magpie.h>
```

## Public Attributes

- double [x](#)  
*Adsorbed mole fraction.*
- double [y](#)  
*Gas phase mole fraction.*
- double [He](#)  
*Henry's Coefficient (mol/kg/kPa)*
- double [q](#)  
*Amount adsorbed for each component (mol/kg)*
- std::vector< double > [gama\\_inf](#)  
*Infinite dilution activities.*
- double [qo](#)  
*Pure component capacities (mol/kg)*
- double [Plo](#)  
*Pure component spreading pressures (mol/kg)*
- std::vector< double > [po](#)  
*Pure component reference state pressures (kPa)*
- double [poi](#)  
*Reference state pressures solved for using Recover eval GPAST.*
- bool [present](#)  
*If true, then the component is present; if false, then the component is not present.*

## 5.15.1 Detailed Description

GPAST Data Structure.

C-style object holding all parameter information associated with the Generalized Predictive Adsorbed Solution Theory (GPAST) system of equations. Each species in the gas phase will have one of these objects.

## 5.15.2 Member Data Documentation

## 5.15.2.1 double GPAST\_DATA::x

Adsorbed mole fraction.

## 5.15.2.2 double GPAST\_DATA::y

Gas phase mole fraction.

## 5.15.2.3 double GPAST\_DATA::He

Henry's Coefficient (mol/kg/kPa)

## 5.15.2.4 double GPAST\_DATA::q

Amount adsorbed for each component (mol/kg)

## 5.15.2.5 std::vector&lt;double&gt; GPAST\_DATA::gama\_inf

Infinite dilution activities.

## 5.15.2.6 double GPAST\_DATA::qo

Pure component capacities (mol/kg)

## 5.15.2.7 double GPAST\_DATA::Plo

Pure component spreading pressures (mol/kg)

## 5.15.2.8 std::vector&lt;double&gt; GPAST\_DATA::po

Pure component reference state pressures (kPa)

## 5.15.2.9 double GPAST\_DATA::poi

Reference state pressures solved for using Recover eval GPAST.

## 5.15.2.10 bool GPAST\_DATA::present

If true, then the component is present; if false, then the component is not present.

The documentation for this struct was generated from the following file:

- [magpie.h](#)

## 5.16 GSTA\_DATA Struct Reference

GSTA Data Structure.

```
#include <magpie.h>
```

## Public Attributes

- double [qmax](#)  
*Theoretical maximum capacity of adsorbate-adsorbent pair (mol/kg)*
- int [m](#)  
*Number of parameters in the GSTA isotherm.*
- std::vector< double > [dHo](#)  
*Enthalpies for each site (J/mol)*
- std::vector< double > [dSo](#)  
*Entropies for each site (J/(K\*mol))*

## 5.16.1 Detailed Description

GSTA Data Structure.

C-style object holding all parameter information associated with the Generalized Statistical Thermodynamic Adsorption (GSTA) isotherm model. Each species in the gas phase will have one of these objects.

## 5.16.2 Member Data Documentation

## 5.16.2.1 double GSTA\_DATA::qmax

Theoretical maximum capacity of adsorbate-adsorbent pair (mol/kg)

## 5.16.2.2 int GSTA\_DATA::m

Number of parameters in the GSTA isotherm.

## 5.16.2.3 std::vector&lt;double&gt; GSTA\_DATA::dHo

Enthalpies for each site (J/mol)

## 5.16.2.4 std::vector&lt;double&gt; GSTA\_DATA::dSo

Entropies for each site (J/(K\*mol))

The documentation for this struct was generated from the following file:

- [magpie.h](#)

## 5.17 GSTA\_OPT\_DATA Struct Reference

Data structure used in the GSTA optimization routines.

```
#include <gsta_opt.h>
```

## Public Attributes

- int [total\\_eval](#)  
*Keeps track of the total number of function evaluations.*
- int [n\\_par](#)  
*Number of parameters being optimized for.*
- double [qmax](#)  
*Maximum theoretical adsorption capacity (M/M) (0 if unknown)*
- int [iso](#)  
*Keeps isotherm that is currently being optimized.*
- std::vector< std::vector  
< double > > [Fobj](#)  
*Creates a dynamic array to store all Fobj values.*
- std::vector< std::vector  
< double > > [q](#)
- std::vector< std::vector  
< double > > [P](#)  
*Creates a dynamic array for q and P data pairs.*
- std::vector< std::vector  
< double > > [best\\_par](#)  
*Used to store the values of the parameters of best fit.*
- std::vector< std::vector  
< double > > [Kno](#)  
*Dimensionless parameters determined from best\_par.*
- std::vector< std::vector  
< std::vector< double > > > [all\\_pars](#)  
*Used to create a ragged array of all parameters.*



- `std::vector< std::vector< double > > norms`  
Used to store the values of all the calculated norms.
- `std::vector< double > opt_qmax`  
If *qmax* is unknown, this vector holds it's optimized values.

### 5.17.1 Detailed Description

Data structure used in the GSTA optimization routines.

C-style structure that keeps track of all information during the optimization routine. All solutions and parameters to the GSTA isotherm are held in order to find the best solution with the fewest parameters.

### 5.17.2 Member Data Documentation

#### 5.17.2.1 `int GSTA_OPT_DATA::total_eval`

Keeps track of the total number of function evaluations.

#### 5.17.2.2 `int GSTA_OPT_DATA::n_par`

Number of parameters being optimized for.

#### 5.17.2.3 `double GSTA_OPT_DATA::qmax`

Maximum theoretical adsorption capacity (M/M) (0 if unknown)

#### 5.17.2.4 `int GSTA_OPT_DATA::iso`

Keeps isotherm that is currently being optimized.

#### 5.17.2.5 `std::vector<std::vector<double> > GSTA_OPT_DATA::Fobj`

Creates a dynamic array to store all Fobj values.

#### 5.17.2.6 `std::vector<std::vector<double> > GSTA_OPT_DATA::q`

#### 5.17.2.7 `std::vector<std::vector<double> > GSTA_OPT_DATA::P`

Creates a dynamic array for q and P data pairs.

#### 5.17.2.8 `std::vector<std::vector<double> > GSTA_OPT_DATA::best_par`

Used to store the values of the parameters of best fit.

#### 5.17.2.9 `std::vector<std::vector<double> > GSTA_OPT_DATA::Kno`

Dimensionless parameters determined from best\_par.

#### 5.17.2.10 `std::vector<std::vector<std::vector<double> > > GSTA_OPT_DATA::all_pars`

Used to create a ragged array of all parameters.

#### 5.17.2.11 `std::vector<std::vector<double> > GSTA_OPT_DATA::norms`

Used to store the values of all the calculated norms.

#### 5.17.2.12 `std::vector<double> GSTA_OPT_DATA::opt_qmax`

If *qmax* is unknown, this vector holds it's optimized values.

The documentation for this struct was generated from the following file:

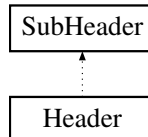
- [gsta\\_opt.h](#)

## 5.18 Header Class Reference

Object for headers in a yaml document (inherits from [SubHeader](#))

```
#include <yaml_wrapper.h>
```

Inheritance diagram for Header:



### Public Member Functions

- [Header](#) ()  
*Default Constructor.*
- [~Header](#) ()  
*Default Destructor.*
- [Header](#) (const [Header](#) &head)  
*Copy constructor.*
- [Header](#) (std::string name)  
*Constructor by header name.*
- [Header](#) (const [KeyValueMap](#) &map)  
*Constructor by existing map.*
- [Header](#) (std::string name, const [KeyValueMap](#) &map)  
*Constructor by name and map.*
- [Header](#) (std::string key, const [SubHeader](#) &sub)  
*Constructor by single subheader object.*
- [Header](#) & operator= (const [Header](#) &head)  
*Equals overload.*
- [ValueTypePair](#) & operator[] (const std::string key)  
*Return the ValueType reference at the given key.*
- [ValueTypePair](#) operator[] (const std::string key) const  
*Return the ValueType at the given key.*
- [SubHeader](#) & operator() (const std::string key)  
*Return the SubHeader reference at the given key.*
- [SubHeader](#) operator() (const std::string key) const  
*Return the SubHeader at the given key.*
- std::map< std::string, [SubHeader](#) > & getSubMap ()  
*Return the reference to the SubHeader Map.*
- [KeyValueMap](#) & getDataMap ()  
*Return the reference to the KeyValueMap.*
- [SubHeader](#) & getSubHeader (std::string key)  
*Return the subheader at the given key.*

- `std::map< std::string, SubHeader >::const_iterator end () const`  
Returns a const iterator pointing to the end of the list.
- `std::map< std::string, SubHeader >::iterator end ()`  
Returns an iterator pointing to the end of the list.
- `std::map< std::string, SubHeader >::const_iterator begin () const`  
Returns a const iterator pointing to the beginning of the list.
- `std::map< std::string, SubHeader >::iterator begin ()`  
Returns an iterator pointing to the beginning of the list.
- `void clear ()`  
Clear out the SubMap, KeyValueMap, and other info.
- `void resetKeys ()`  
Reset the keys of the SubMap to the names of each SubHeader.
- `void changeKey (std::string oldKey, std::string newKey)`  
Change one of the keys in the map.
- `void addPair (std::string key, std::string val)`  
Adds a pair object to the map (with only strings)
- `void addPair (std::string key, std::string val, int t)`  
Adds a pair object and asserts a type.
- `void setName (std::string name)`  
Set the name of the Header.
- `void setAlias (std::string alias)`  
Set the alias of the header, if any.
- `void setNameAliasPair (std::string n, std::string a, int s)`  
Set the name, alias, and state for the header.
- `void setState (int state)`  
Set the state of the header, if any.
- `void DisplayContents ()`  
Display the contents of the header object.
- `void addSubKey (std::string key)`  
Adds a key to the SubHeader Map.
- `void copyAnchor2Alias (std::string alias, SubHeader &ref)`  
Find the anchor in the map, and copy to the Header reference given.
- `int size ()`  
Return the size of the Sub\_Map.
- `std::string getName ()`  
Return the name of the header.
- `std::string getAlias ()`  
Return the alias of the header.
- `int getState ()`  
Return the state of the header.
- `bool isAlias ()`  
Returns true if the header is an alias.
- `bool isAnchor ()`  
Returns true if the header is an anchor.
- `SubHeader & getAnchoredSub (std::string alias)`  
Returns reference to the anchored subheader, if any.

## Private Attributes

- `std::map< std::string, SubHeader > Sub_Map`  
*Map of the contained subheaders in the main header.*

## Additional Inherited Members

## 5.18.1 Detailed Description

Object for headers in a yaml document (inherits from [SubHeader](#))

C++ Object for headers in a yaml document that is built from the [SubHeader](#) object already created. The chain of inheritance works in this direction because a [Header](#) can have both a map of SubHeaders and a map of Key-Value-Pairs. Therefore, the [SubHeader](#) object is actually the more generic form of a header.

Since this object inherits from [SubHeader](#), it has access to all its protected members, including the alias, state, name, and [KeyValueMap](#). Operator overloads and other functions are provided to allow the user to query both the [KeyValueMap](#) and [SubHeader](#) for specific information. The names of the SubHeaders are also used as its keys. Make sure all [SubHeader](#) keys are unique to this header.

## 5.18.2 Constructor &amp; Destructor Documentation

5.18.2.1 `Header::Header ( )`

Default Constructor.

5.18.2.2 `Header::~Header ( )`

Default Destructor.

5.18.2.3 `Header::Header ( const Header & head )`

Copy constructor.

5.18.2.4 `Header::Header ( std::string name )`

Constructor by header name.

5.18.2.5 `Header::Header ( const KeyValueMap & map )`

Constructor by existing map.

5.18.2.6 `Header::Header ( std::string name, const KeyValueMap & map )`

Constructor by name and map.

5.18.2.7 `Header::Header ( std::string key, const SubHeader & sub )`

Constructor by single subheader object.

## 5.18.3 Member Function Documentation

5.18.3.1 `Header& Header::operator= ( const Header & head )`

Equals overload.

5.18.3.2 `ValueTypePair& Header::operator[] ( const std::string key )`

Return the ValueType reference at the given key.

**5.18.3.3** `ValueTypePair Header::operator[] ( const std::string key ) const`

Return the `ValueType` at the given key.

**5.18.3.4** `SubHeader& Header::operator() ( const std::string key )`

Return the `SubHeader` reference at the given key.

**5.18.3.5** `SubHeader Header::operator() ( const std::string key ) const`

Return the `SubHeader` at the given key.

**5.18.3.6** `std::map<std::string, SubHeader>& Header::getSubMap ( )`

Return the reference to the `SubHeader` Map.

**5.18.3.7** `KeyValueMap& Header::getDataMap ( )`

Return the reference to the `KeyValueMap`.

**5.18.3.8** `SubHeader& Header::getSubHeader ( std::string key )`

Return the subheader at the given key.

**5.18.3.9** `std::map<std::string, SubHeader>::const_iterator Header::end ( ) const`

Returns a const iterator pointing to the end of the list.

**5.18.3.10** `std::map<std::string, SubHeader>::iterator Header::end ( )`

Returns an iterator pointing to the end of the list.

**5.18.3.11** `std::map<std::string, SubHeader>::const_iterator Header::begin ( ) const`

Returns a const iterator pointing to the beginning of the list.

**5.18.3.12** `std::map<std::string, SubHeader>::iterator Header::begin ( )`

Returns an iterator pointing to the beginning of the list.

**5.18.3.13** `void Header::clear ( )`

Clear out the SubMap, `KeyValueMap`, and other info.

**5.18.3.14** `void Header::resetKeys ( )`

Reset the keys of the SubMap to the names of each `SubHeader`.

**5.18.3.15** `void Header::changeKey ( std::string oldKey, std::string newKey )`

Change one of the keys in the map.

**5.18.3.16** `void Header::addPair ( std::string key, std::string val )`

Adds a pair object to the map (with only strings)

**5.18.3.17** `void Header::addPair ( std::string key, std::string val, int t )`

Adds a pair object and asserts a type.

5.18.3.18 void Header::setName ( std::string *name* )

Set the name of the [Header](#).

5.18.3.19 void Header::setAlias ( std::string *alias* )

Set the alias of the header, if any.

5.18.3.20 void Header::setNameAliasPair ( std::string *n*, std::string *a*, int *s* )

Set the name, alias, and state for the header.

5.18.3.21 void Header::setState ( int *state* )

Set the state of the header, if any.

5.18.3.22 void Header::DisplayContents ( )

Display the contents of the header object.

5.18.3.23 void Header::addSubKey ( std::string *key* )

Adds a key to the [SubHeader](#) Map.

5.18.3.24 void Header::copyAnchor2Alias ( std::string *alias*, SubHeader & *ref* )

Find the anchor in the map, and copy to the [Header](#) reference given.

5.18.3.25 int Header::size ( )

Return the size of the Sub\_Map.

5.18.3.26 std::string Header::getName ( )

Return the name of the header.

5.18.3.27 std::string Header::getAlias ( )

Return the alias of the header.

5.18.3.28 int Header::getState ( )

Return the state of the header.

5.18.3.29 bool Header::isAlias ( )

Returns true if the header is an alias.

5.18.3.30 bool Header::isAnchor ( )

Returns true if the header is an anchor.

5.18.3.31 SubHeader& Header::getAnchoredSub ( std::string *alias* )

Returns reference to the anchored subheader, if any.

## 5.18.4 Member Data Documentation

5.18.4.1 std::map<std::string, SubHeader> Header::Sub\_Map [private]

Map of the contained subheaders in the main header.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 5.19 KeyValueTypeMap Class Reference

Key-Value-Type Map object creating a map of the KeyValueType objects.

```
#include <yaml_wrapper.h>
```

### Public Member Functions

- [KeyValueTypeMap](#) ()  
*Default constructor.*
- [~KeyValueTypeMap](#) ()  
*Default destructor.*
- [KeyValueTypeMap](#) (const std::map< std::string, std::string > &map)  
*Construct from a map of strings.*
- [KeyValueTypeMap](#) (std::string key, std::string value)  
*Construct one element in the map.*
- [KeyValueTypeMap](#) (const [KeyValueTypeMap](#) &map)  
*Copy constructor.*
- [KeyValueTypeMap](#) & [operator=](#) (const [KeyValueTypeMap](#) &map)  
*Equals overload.*
- [ValueTypePair](#) & [operator\[\]](#) (const std::string key)  
*Return the ValueType reference at the given key.*
- [ValueTypePair](#) [operator\[\]](#) (const std::string key) const  
*Return the ValueType at the give key.*
- std::map< std::string, [ValueTypePair](#) > & [getMap](#) ()  
*Return a reference to the Key\_Value map object.*
- std::map< std::string, [ValueTypePair](#) > ::const\_iterator [end](#) () const  
*Returns a const iterator pointing to the end of the list.*
- std::map< std::string, [ValueTypePair](#) > ::iterator [end](#) ()  
*Returns an iterator pointing to the end of the list.*
- std::map< std::string, [ValueTypePair](#) > ::const\_iterator [begin](#) () const  
*Returns a const iterator pointing to the beginning of the list.*
- std::map< std::string, [ValueTypePair](#) > ::iterator [begin](#) ()  
*Returns an iterator pointing to the beginning of the list.*
- void [clear](#) ()  
*Clears the map.*
- void [addKey](#) (std::string key)  
*Adds a key to the object with a default value.*
- void [editValue4Key](#) (std::string val, std::string key)  
*Edits a given value for a pre-existing key.*
- void [editValue4Key](#) (std::string val, int type, std::string key)

- Edits a value for a pre-existing key and asserts type.*
- void `addPair` (std::string key, `ValueTypePair` val)
  - Adds a pair object to the map.*
- void `addPair` (std::string key, std::string val)
  - Adds a pair object to the map (with only strings)*
- void `addPair` (std::string key, std::string val, int type)
  - Adds a pair object and asserts a type.*
- void `findType` (std::string key)
  - Find what data type the value at the key is.*
- void `assertType` (std::string key, int type)
  - Assert the given type at the given key.*
- void `findAllTypes` ()
  - Find all types for all data in map.*
- void `DisplayMap` ()
  - Print out the map to console.*
- int `size` ()
  - Returns the size of the map.*
- std::string `getString` (std::string key)
  - Retrieve the string at the key.*
- bool `getBool` (std::string key)
  - Retrieve the boolean at the key.*
- double `getDouble` (std::string key)
  - Retrieve the double at the key.*
- int `getInt` (std::string key)
  - Retrieve the int at the key.*
- std::string `getValue` (std::string key)
  - Retrieve the value at the key.*
- int `getType` (std::string key)
  - Retrieve the type at the key.*
- `ValueTypePair` & `getPair` (std::string key)
  - Retrieve the pair at the key.*

#### Private Attributes

- std::map< std::string,  
`ValueTypePair` > `Key_Value`
  - Map of Keys and Values paired with types.*

#### 5.19.1 Detailed Description

Key-Value-Type Map object creating a map of the KeyValueType objects.

C++ Object that creates a map of the KeyValueType objects. Functions defined here allow the user to iterate through this map, access specific keys in the map, edit values associated with those keys, find the data types for the values in those keys, ect. The keys are used as an access operator for their corresponding value. As such, each key in the map is required to be unique, but the values are allowed to be duplicated.

#### 5.19.2 Constructor & Destructor Documentation

##### 5.19.2.1 KeyValueType::KeyValueType ( )

Default constructor.



#### 5.19.2.2 KeyValueType::~~KeyValueType ( )

Default destructor.

#### 5.19.2.3 KeyValueType::KeyValueType ( const std::map< std::string, std::string > & map )

Construct from a map of strings.

#### 5.19.2.4 KeyValueType::KeyValueType ( std::string key, std::string value )

Construct one element in the map.

#### 5.19.2.5 KeyValueType::KeyValueType ( const KeyValueType & map )

Copy constructor.

### 5.19.3 Member Function Documentation

#### 5.19.3.1 KeyValueType& KeyValueType::operator= ( const KeyValueType & map )

Equals overload.

#### 5.19.3.2 ValueTypePair& KeyValueType::operator[] ( const std::string key )

Return the ValueType reference at the given key.

#### 5.19.3.3 ValueTypePair KeyValueType::operator[] ( const std::string key ) const

Return the ValueType at the give key.

#### 5.19.3.4 std::map<std::string, ValueTypePair> & KeyValueType::getMap ( )

Return a reference to the Key\_Value map object.

#### 5.19.3.5 std::map<std::string, ValueTypePair>::const\_iterator KeyValueType::end ( ) const

Returns a const iterator pointing to the end of the list.

#### 5.19.3.6 std::map<std::string, ValueTypePair>::iterator KeyValueType::end ( )

Returns an iterator pointing to the end of the list.

#### 5.19.3.7 std::map<std::string, ValueTypePair>::const\_iterator KeyValueType::begin ( ) const

Returns a const iterator pointing to the beginning of the list.

#### 5.19.3.8 std::map<std::string, ValueTypePair>::iterator KeyValueType::begin ( )

Returns an iterator pointing to the beginning of the list.

#### 5.19.3.9 void KeyValueType::clear ( )

Clears the map.

#### 5.19.3.10 void KeyValueType::addKey ( std::string key )

Adds a key to the object with a default value.

#### 5.19.3.11 void KeyValueType::editValue4Key ( std::string val, std::string key )

Edits a given value for a pre-existing key.

5.19.3.12 void KeyValueType::editValue4Key ( std::string val, int type, std::string key )

Edits a value for a pre-existing key and asserts type.

5.19.3.13 void KeyValueType::addPair ( std::string key, ValueTypePair val )

Adds a pair object to the map.

5.19.3.14 void KeyValueType::addPair ( std::string key, std::string val )

Adds a pair object to the map (with only strings)

5.19.3.15 void KeyValueType::addPair ( std::string key, std::string val, int type )

Adds a pair object and asserts a type.

5.19.3.16 void KeyValueType::findType ( std::string key )

Find what data type the value at the key is.

5.19.3.17 void KeyValueType::assertType ( std::string key, int type )

Assert the given type at the given key.

5.19.3.18 void KeyValueType::findAllTypes ( )

Find all types for all data in map.

5.19.3.19 void KeyValueType::DisplayMap ( )

Print out the map to console.

5.19.3.20 int KeyValueType::size ( )

Returns the size of the map.

5.19.3.21 std::string KeyValueType::getString ( std::string key )

Retrieve the string at the key.

5.19.3.22 bool KeyValueType::getBool ( std::string key )

Retrieve the boolean at the key.

5.19.3.23 double KeyValueType::getDouble ( std::string key )

Retrieve the double at the key.

5.19.3.24 int KeyValueType::getInt ( std::string key )

Retrieve the int at the key.

5.19.3.25 std::string KeyValueType::getValue ( std::string key )

Retrieve the value at the key.

5.19.3.26 int KeyValueType::getType ( std::string key )

Retrieve the type at the key.

## 5.19.3.27 ValueTypePair&amp; KeyValueMap::getPair ( std::string key )

Retrieve the pair at the key.

## 5.19.4 Member Data Documentation

## 5.19.4.1 std::map&lt;std::string, ValueTypePair &gt; KeyValueMap::Key\_Value [private]

Map of Keys and Values paired with types.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 5.20 KMS\_DATA Struct Reference

Data structure for the implemenation of the Krylov Multi-Space (KMS) Method.

```
#include <lark.h>
```

## Public Attributes

- int [level](#) = 0  
*Current level in the recursion.*
- int [max\\_level](#) = 0  
*Maximum allowable recursion levels (Default = 0 -> GMRES, Max = 5)*
- int [restart](#) = -1  
*Restart parameter for the outer iterates (Default = 20, Max = N)*
- int [maxit](#) = 0  
*Maximum allowable iterations for the outer steps.*
- int [inner\\_iter](#) = 0  
*Number of inner steps taken.*
- int [outer\\_iter](#) = 0  
*Number of outer steps taken.*
- int [total\\_iter](#) = 0  
*Total number of iterations in all steps.*
- double [outer\\_reltol](#) = 1e-6  
*Relative residual tolerance for outer steps (Default = 1e-6)*
- double [outer\\_abstol](#) = 1e-6  
*Absolute residual tolerance for outer steps (Default = 1e-6)*
- double [inner\\_reltol](#) = 0.1  
*Residual tolerance for inner steps made relative to outer steps (Default = 0.1)*
- bool [Output\\_outer](#) = true  
*True = Print the outer steps residuals.*
- bool [Output\\_inner](#) = false  
*True = Print the inner steps residuals.*
- [GMRESRP\\_DATA](#) [gmres\\_out](#)  
*Data structure for the outer steps.*
- std::vector< [GMRESRP\\_DATA](#) > [gmres\\_in](#)  
*Data structures for each recursion level.*
- int(\* [matvec](#))(const [Matrix](#)< double > &x, [Matrix](#)< double > &Ax, const void \*[matvec\\_data](#))  
*User supplied matrix-vector product function.*

- `int(* terminal_precon)(const Matrix< double > &r, Matrix< double > &p, const void *precon_data)`  
*Optional user supplied terminal preconditioner.*
- `const void * matvec_data`  
*Data structure for the user's matvec function.*
- `const void * term_precon`  
*Data structure for the user's terminal preconditioner.*

### 5.20.1 Detailed Description

Data structure for the implementation of the Krylov Multi-Space (KMS) Method.

C-style object to be used in conjunction with the Krylov Multi-Space (KMS) Algorithm to iteratively solve non-symmetric, indefinite linear systems. This method was inspired by the Flexible GMRES (FGMRES) and Recursive GMRES (GMRESR) methods proposed by Saad (1993) and Vorst and Vuik (1991), respectively. The idea behind this method is to recursively call FGMRES to solve a linear system with progressively smaller Krylov Subspaces built by a Right-Preconditioned GMRES algorithm. Thus creating a "V-cycle" of iteration similar to that seen in Multi-Grid algorithms.

### 5.20.2 Member Data Documentation

#### 5.20.2.1 `int KMS_DATA::level = 0`

Current level in the recursion.

#### 5.20.2.2 `int KMS_DATA::max_level = 0`

Maximum allowable recursion levels (Default = 0 -> GMRES, Max = 5)

#### 5.20.2.3 `int KMS_DATA::restart = -1`

Restart parameter for the outer iterates (Default = 20, Max = N)

#### 5.20.2.4 `int KMS_DATA::maxit = 0`

Maximum allowable iterations for the outer steps.

#### 5.20.2.5 `int KMS_DATA::inner_iter = 0`

Number of inner steps taken.

#### 5.20.2.6 `int KMS_DATA::outer_iter = 0`

Number of outer steps taken.

#### 5.20.2.7 `int KMS_DATA::total_iter = 0`

Total number of iterations in all steps.

#### 5.20.2.8 `double KMS_DATA::outer_reltol = 1e-6`

Relative residual tolerance for outer steps (Default = 1e-6)

#### 5.20.2.9 `double KMS_DATA::outer_abstol = 1e-6`

Absolute residual tolerance for outer steps (Default = 1e-6)

#### 5.20.2.10 `double KMS_DATA::inner_reltol = 0.1`

Residual tolerance for inner steps made relative to outer steps (Default = 0.1)

5.20.2.11 `bool KMS_DATA::Output_outer = true`

True = Print the outer steps residuals.

5.20.2.12 `bool KMS_DATA::Output_inner = false`

True = Print the inner steps residuals.

5.20.2.13 `GMRESRP_DATA KMS_DATA::gmres_out`

Data structure for the outer steps.

5.20.2.14 `std::vector<GMRESRP_DATA> KMS_DATA::gmres_in`

Data structures for each recursion level.

5.20.2.15 `int(* KMS_DATA::matvec)(const Matrix< double > &x, Matrix< double > &Ax, const void *matvec_data)`

User supplied matrix-vector product function.

5.20.2.16 `int(* KMS_DATA::terminal_precon)(const Matrix< double > &r, Matrix< double > &p, const void *precon_data)`

Optional user supplied terminal preconditioner.

5.20.2.17 `const void* KMS_DATA::matvec_data`

Data structure for the user's matvec function.

5.20.2.18 `const void* KMS_DATA::term_precon`

Data structure for the user's terminal preconditioner.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.21 MAGPIE\_DATA Struct Reference

MAGPIE Data Structure.

```
#include <magpie.h>
```

### Public Attributes

- `std::vector< GSTA_DATA > gsta_dat`
- `std::vector< mSPD_DATA > mspd_dat`
- `std::vector< GPAST_DATA > gpast_dat`
- `SYSTEM_DATA sys_dat`

### 5.21.1 Detailed Description

MAGPIE Data Structure.

C-style object holding all information necessary to run a MAGPIE simulation. This is the data structure that will be used in other sub-routines when a mixed gas adsorption simulation needs to be run.

### 5.21.2 Member Data Documentation

5.21.2.1 `std::vector<GSTA_DATA> MAGPIE_DATA::gsta_dat`

5.21.2.2 `std::vector<mSPD_DATA> MAGPIE_DATA::mspd_dat`

5.21.2.3 `std::vector<GPAST_DATA> MAGPIE_DATA::gpast_dat`

5.21.2.4 `SYSTEM_DATA MAGPIE_DATA::sys_dat`

The documentation for this struct was generated from the following file:

- [magpie.h](#)

## 5.22 MassBalance Class Reference

Mass Balance Object.

```
#include <shark.h>
```

### Public Member Functions

- [MassBalance](#) ()  
*Default Constructor.*
- [~MassBalance](#) ()  
*Default Destructor.*
- void [Initialize\\_Object](#) ([MasterSpeciesList](#) &[List](#))  
*Function to initialize the [MassBalance](#) object from the [MasterSpeciesList](#).*
- void [Display\\_Info](#) ()  
*Display the mass balance information.*
- void [Set\\_Delta](#) (int i, double v)  
*Function to set the ith weight (delta) for the mass balance.*
- void [Set\\_TotalConcentration](#) (double v)  
*Set the total concentration of the mass balance to v (mol/L)*
- void [Set\\_Name](#) (std::string name)  
*Set the name of the mass balance (i.e., Uranium, Carbonate, etc.)*
- double [Get\\_Delta](#) (int i)  
*Fetch the ith weight (i.e., delta) value.*
- double [Sum\\_Delta](#) ()  
*Sums up the delta values and returns the total (should never be zero)*
- double [Get\\_TotalConcentration](#) ()  
*Fetch the total concentration (mol/L)*
- std::string [Get\\_Name](#) ()  
*Return name of mass balance object.*
- double [Eval\\_Residual](#) (const [Matrix](#)< double > &x)  
*Evaluate the residual for the mass balance object given the log(C) concentrations.*

### Protected Attributes

- [MasterSpeciesList](#) \* [List](#)  
*Pointer to a master species object.*
- std::vector< double > [Delta](#)  
*Vector of weights (i.e., deltas) used in the mass balance.*
- double [TotalConcentration](#)  
*Total concentration of specific object (mol/L)*

## Private Attributes

- `std::string` [Name](#)  
*Name designation used in mass balance.*

## 5.22.1 Detailed Description

Mass Balance Object.

C++ style object that holds data and functions associated with mass balances of primary species in a system. The mass balances involve a total concentration (in mol/L) and a vector of weighted contributions to that total concentration from each species in the [MasterSpeciesList](#). This object only considers mass balances in a batch type of system (i.e., not input or output of mass). However, one could inherit from this object to create mass balances for flow systems as well.

## 5.22.2 Constructor &amp; Destructor Documentation

5.22.2.1 `MassBalance::MassBalance ( )`

Default Constructor.

5.22.2.2 `MassBalance::~~MassBalance ( )`

Default Destructor.

## 5.22.3 Member Function Documentation

5.22.3.1 `void MassBalance::Initialize_Object ( MasterSpeciesList & List )`

Function to initialize the [MassBalance](#) object from the [MasterSpeciesList](#).

5.22.3.2 `void MassBalance::Display_Info ( )`

Display the mass balance information.

5.22.3.3 `void MassBalance::Set_Delta ( int i, double v )`

Function to set the ith weight (delta) for the mass balance.

This function sets the weight (i.e., delta value) of the ith species in the list to the value of v. That value represents the weighting of that species in the determination of the total mass for the primary species set.

## Parameters

<i>i</i>	index of the species in the <a href="#">MasterSpeciesList</a>
<i>v</i>	value of the weighth (or delta) applied to the mass balance

5.22.3.4 `void MassBalance::Set_TotalConcentration ( double v )`

Set the total concentration of the mass balance to v (mol/L)

5.22.3.5 `void MassBalance::Set_Name ( std::string name )`

Set the name of the mass balance (i.e., Uranium, Carbonate, etc.)

5.22.3.6 `double MassBalance::Get_Delta ( int i )`

Fetch the ith weight (i.e., delta) value.

**5.22.3.7** `double MassBalance::Sum_Delta ( )`

Sums up the delta values and returns the total (should never be zero)

**5.22.3.8** `double MassBalance::Get_TotalConcentration ( )`

Fetch the total concentration (mol/L)

**5.22.3.9** `std::string MassBalance::Get_Name ( )`

Return name of mass balance object.

**5.22.3.10** `double MassBalance::Eval_Residual ( const Matrix< double > & x )`

Evaluate the residual for the mass balance object given the log(C) concentrations.

This function calculates and provides the residual for this mass balance object based on the total concentration in the system and the weighted contributions from each species. Concentrations are given as the log(C) values.

**Parameters**

<code>x</code>	matrix of the log(C) concentration values at the current non-linear step
----------------	--

**5.22.4** Member Data Documentation**5.22.4.1** `MasterSpeciesList* MassBalance::List` [protected]

Pointer to a master species object.

**5.22.4.2** `std::vector<double> MassBalance::Delta` [protected]

Vector of weights (i.e., deltas) used in the mass balance.

**5.22.4.3** `double MassBalance::TotalConcentration` [protected]

Total concentration of specific object (mol/L)

**5.22.4.4** `std::string MassBalance::Name` [private]

Name designation used in mass balance.

The documentation for this class was generated from the following file:

- [shark.h](#)

**5.23** MasterSpeciesList Class Reference

Master Species List Object.

```
#include <shark.h>
```

**Public Member Functions**

- [MasterSpeciesList](#) ()  
*Default constructor.*
- [~MasterSpeciesList](#) ()  
*Default destructor.*
- [MasterSpeciesList](#) (const [MasterSpeciesList](#) &msl)  
*Copy Constructor.*



- [MasterSpeciesList](#) & [operator=](#) (const [MasterSpeciesList](#) &mssl)  
*Equals operator.*
- void [set\\_list\\_size](#) (int i)  
*Function to initialize the size of the list.*
- void [set\\_species](#) (int i, std::string formula)  
*Function to register the ith species in the list based on a registered molecular formula (see [mola.h](#))*
- void [set\\_species](#) (int i, int [charge](#), double enthalpy, double entropy, double energy, bool HS, bool G, std::string Phase, std::string Name, std::string Formula, std::string lin\_formula)  
*Function to register the ith species in the list based on custom molecule information (see [mola.h](#))*
- void [DisplayInfo](#) (int i)  
*Function to display information of ith object.*
- void [DisplayAll](#) ()  
*Function to display all information of list.*
- void [DisplayConcentrations](#) ([Matrix](#)< double > &C)  
*Function to display the concentrations of species in list.*
- void [set\\_alkalinity](#) (double alk)  
*Set the alkalinity of the solution (Default = 0 M)*
- int [list\\_size](#) ()  
*Returns size of list.*
- [Molecule](#) & [get\\_species](#) (int i)  
*Returns a reference to the ith species in master list.*
- int [get\\_index](#) (std::string name)  
*Returns an integer representing location of the named species in the list.*
- double [charge](#) (int i)  
*Fetch and return charge of ith species in list.*
- double [alkalinity](#) ()  
*Fetch the value of alkalinity of the solution (mol/L)*
- std::string [speciesName](#) (int i)  
*Function to return the name of the ith species.*
- double [Eval\\_ChargeResidual](#) (const [Matrix](#)< double > &x)  
*Calculate charge balance residual for the electroneutrality constraint.*

#### Protected Attributes

- int [size](#)  
*Size of the list.*
- std::vector< [Molecule](#) > [species](#)  
*List of [Molecule](#) Objects.*
- double [residual\\_alkalinity](#)  
*Conc of strong base - conc of strong acid in solution (mol/L)*

#### 5.23.1 Detailed Description

##### Master Species List Object.

C++ style object that holds data and function associated with solving multi-species problems. This object contains a vector of [Molecule](#) objects from [mola.h](#) and uses those objects to help setup speciation problems that need to be solved. One of the primary functions in this object is the contribution of electroneutrality ([Eval\\_ChargeResidual](#)). However, we only need this constraint if the pH of our aqueous system is unknown.

## 5.23.2 Constructor &amp; Destructor Documentation

## 5.23.2.1 MasterSpeciesList::MasterSpeciesList ( )

Default constructor.

## 5.23.2.2 MasterSpeciesList::~MasterSpeciesList ( )

Default destructor.

## 5.23.2.3 MasterSpeciesList::MasterSpeciesList ( const MasterSpeciesList &amp; msl )

Copy Constructor.

## 5.23.3 Member Function Documentation

## 5.23.3.1 MasterSpeciesList&amp; MasterSpeciesList::operator= ( const MasterSpeciesList &amp; msl )

Equals operator.

## 5.23.3.2 void MasterSpeciesList::set\_list\_size ( int i )

Function to initialize the size of the list.

## 5.23.3.3 void MasterSpeciesList::set\_species ( int i, std::string formula )

Function to register the ith species in the list based on a registered molecular formula (see [mola.h](#))

## 5.23.3.4 void MasterSpeciesList::set\_species ( int i, int charge, double enthalpy, double entropy, double energy, bool HS, bool G, std::string Phase, std::string Name, std::string Formula, std::string lin\_formula )

Function to register the ith species in the list based on custom molecule information (see [mola.h](#))

## 5.23.3.5 void MasterSpeciesList::DisplayInfo ( int i )

Function to display information of ith object.

## 5.23.3.6 void MasterSpeciesList::DisplayAll ( )

Function to display all information of list.

## 5.23.3.7 void MasterSpeciesList::DisplayConcentrations ( Matrix&lt; double &gt; &amp; C )

Function to display the concentrations of species in list.

This function will print to the console the species list in order with each species associated concentration from the matrix C. The concentrations and species list MUST be in the same order and the units of C are assumed to be mol/L.

## Parameters

C	matrix of concentrations of species in the list in mol/L
---	--

## 5.23.3.8 void MasterSpeciesList::set\_alkalinity ( double alk )

Set the alkalinity of the solution (Default = 0 M)

This function is used to set the value of residual alkalinity used in the electroneutrality calculations. Typically, this value will be 0 M (mol/L) if all species in the system are present as variables. However, occasionally, one may want to set the alkalinity of the solution to a constant in order to restrict the pH of the solution.

## Parameters

<i>alk</i>	Residual alkalinity in M (mol/L)
------------	----------------------------------

## 5.23.3.9 int MasterSpeciesList::list\_size ( )

Returns size of list.

## 5.23.3.10 Molecule&amp; MasterSpeciesList::get\_species ( int i )

Returns a reference to the ith species in master list.

This function will return a [Molecule](#) object for the ith species in the list of molecules. Once returned, the user then can operate on that molecule using the functions define in [mola.h](#).

## 5.23.3.11 int MasterSpeciesList::get\_index ( std::string name )

Returns an integer representing location of the named species in the list.

## 5.23.3.12 double MasterSpeciesList::charge ( int i )

Fetch and return charge of ith species in list.

## 5.23.3.13 double MasterSpeciesList::alkalinity ( )

Fetch the value of alkalinity of the solution (mol/L)

## 5.23.3.14 std::string MasterSpeciesList::speciesName ( int i )

Function to return the name of the ith species.

## 5.23.3.15 double MasterSpeciesList::Eval\_ChargeResidual ( const Matrix&lt; double &gt; &amp; x )

Calculate charge balance residual for the electroneutrality constraint.

This function returns the value of the residual for the electroneutrality equation in the system. Electroneutrality is based on the concentrations and charges of each species in the system so the charges of each molecule must be appropriately set. Concentrations of those species are fed into this function via the argument x, but come in as the log(C) values (i.e.,  $x = \log(C)$ ).

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
----------	--

## 5.23.4 Member Data Documentation

## 5.23.4.1 int MasterSpeciesList::size [protected]

Size of the list.

## 5.23.4.2 std::vector&lt;Molecule&gt; MasterSpeciesList::species [protected]

List of [Molecule](#) Objects.

## 5.23.4.3 double MasterSpeciesList::residual\_alkalinity [protected]

Conc of strong base - conc of strong acid in solution (mol/L)

The documentation for this class was generated from the following file:

- [shark.h](#)

**5.24 Matrix< T > Class Template Reference**

Templated C++ [Matrix](#) Class Object (click [Matrix](#) to go to function definitions)

```
#include <macaw.h>
```

**Public Member Functions**

- [Matrix](#) (int [rows](#), int [columns](#))  
*Constructor for matrix with given number of rows and columns.*
- T & [operator\(\)](#) (int i, int j)  
*Access operator for the matrix element at row i and column j (e.g.,  $a_{ij} = A(i,j)$ )*
- T [operator\(\)](#) (int i, int j) const  
*Constant access operator for the the matrix element at row i and column j.*
- [Matrix](#) (const [Matrix](#) &M)  
*Copy constructor for constructing a matrix as a copy of another matrix.*
- [Matrix](#) & [operator=](#) (const [Matrix](#) &M)  
*Equals operator for setting one matrix equal to another matrix.*
- [Matrix](#) ()  
*Default constructor for creating an empty matrix.*
- [~Matrix](#) ()  
*Default destructor for clearing out memory.*
- void [set\\_size](#) (int i, int j)  
*Function to set/change the size of a matrix to i rows and j columns.*
- void [zeros](#) ()  
*Function to set/change all values in a matrix to zeros.*
- void [edit](#) (int i, int j, T value)  
*Function to set/change the element of a matrix at row i and column j to given value.*
- int [rows](#) ()  
*Function to return the number of rows in a given matrix.*
- int [columns](#) ()  
*Function to return the number of columns in a matrix.*
- T [determinate](#) ()  
*Function to compute the determinate of a matrix and return that value.*
- T [norm](#) ()  
*Function to compute the L2-norm of a matrix and return that value.*
- T [sum](#) ()  
*Function to compute the sum of all elements in a matrix and return that value.*
- T [inner\\_product](#) (const [Matrix](#) &x)  
*Function to compute the inner product between this matrix and matrix x.*
- [Matrix](#) & [cofactor](#) (const [Matrix](#) &M)  
*Function to convert this matrix to a cofactor matrix of the given matrix M.*
- [Matrix](#) [operator+](#) (const [Matrix](#) &M)  
*Operator to add this matrix and matrix M and return the new matrix result.*
- [Matrix](#) [operator-](#) (const [Matrix](#) &M)  
*Operator to subtract this matrix and matrix M and return the new matrix result.*
- [Matrix](#) [operator\\*](#) (const T)  
*Operator to multiply this matrix by a scalar T return the new matrix result.*
- [Matrix](#) [operator/](#) (const T)  
*Operator to divide this matrix by a scalar T and return the new matrix result.*
- [Matrix](#) [operator\\*](#) (const [Matrix](#) &M)

*Operator to multiply this matrix and matrix M and return the new matrix result.*

- [Matrix & transpose](#) (const [Matrix](#) &M)

*Function to convert this matrix to the transpose of the given matrix M.*

- [Matrix & transpose\\_multiply](#) (const [Matrix](#) &MT, const [Matrix](#) &v)

*Function to convert this matrix into the result of the given matrix M transposed and multiplied by the other given matrix v.*

- [Matrix & adjoint](#) (const [Matrix](#) &M)

*Function to convert this matrix to the adjoint of the given matrix.*

- [Matrix & inverse](#) (const [Matrix](#) &M)

*Function to convert this matrix to the inverse of the given matrix.*

- void [Display](#) (const std::string Name)

*Function to display the contents of this matrix given a Name for the matrix.*

- [Matrix & tridiagonalSolve](#) (const [Matrix](#) &A, const [Matrix](#) &b)

*Function to solve  $Ax=b$  for x if A is symmetric, tridiagonal (this->x)*

- [Matrix & ladshawSolve](#) (const [Matrix](#) &A, const [Matrix](#) &d)

*Function to solve  $Ax=d$  for x if A is non-symmetric, tridiagonal (this->x)*

- [Matrix & tridiagonalFill](#) (const T A, const T B, const T C, bool [Spherical](#))

*Function to fill in this matrix with coefficients A, B, and C to form a tridiagonal matrix.*

- [Matrix & naturalLaplacian3D](#) (int m)

*Function to fill out this matrix with coefficients from a 3D Laplacian function.*

- [Matrix & sphericalBCFill](#) (int node, const T coeff, T variable)

*Function to fill out a column matrix with spherical specific boundary conditions.*

- [Matrix & ConstantICFill](#) (const T IC)

*Function to set all values in a column matrix to a given constant.*

- [Matrix & SolnTransform](#) (const [Matrix](#) &A, bool Forward)

*Function to transform the values in a column matrix from cartesian to spherical coordinates.*

- T [sphericalAvg](#) (double radius, double dr, double bound, bool Dirichlet)

*Function to compute a spatial average of this column matrix in spherical coordinates.*

- T [IntegralAvg](#) (double radius, double dr, double bound, bool Dirichlet)

*Function to compute a spatial average of this column matrix in spherical coordinates.*

- T [IntegralTotal](#) (double dr, double bound, bool Dirichlet)

*Function to compute a spatial total of this column matrix in spherical coordinates.*

- [Matrix & tridiagonalVectorFill](#) (const std::vector< T > &A, const std::vector< T > &B, const std::vector< T > &C)

*Function to fill in this matrix, in tridiagonal fashion, using the vectors of coefficients.*

- [Matrix & columnVectorFill](#) (const std::vector< T > &A)

*Function to fill in a column matrix with the values of the given vector object.*

- [Matrix & columnProjection](#) (const [Matrix](#) &b, const [Matrix](#) &b\_old, const double dt, const double dt\_old)

*Function to project a column matrix solution in time based on older state vectors.*

- [Matrix & dirichletBCFill](#) (int node, const T coeff, T variable)

*Function to fill in a column matrix with all zeros except at the given node.*

- [Matrix & diagonalSolve](#) (const [Matrix](#) &D, const [Matrix](#) &v)

*Function to solve the system  $Dx=v$  for x given that D is diagonal (this->x)*

- [Matrix & upperTriangularSolve](#) (const [Matrix](#) &U, const [Matrix](#) &v)

*Function to solve the system  $Ux=v$  for x given that U is upper Triangular (this->x)*

- [Matrix & lowerTriangularSolve](#) (const [Matrix](#) &L, const [Matrix](#) &v)

*Function to solve the system  $Lx=v$  for x given that L is lower Triangular (this->x)*

- [Matrix & upperHessenberg2Triangular](#) ([Matrix](#) &b)

*Function to convert this square matrix to upper Triangular (assuming this is upper Hessenberg)*

- [Matrix & lowerHessenberg2Triangular](#) ([Matrix](#) &b)

*Function to convert this square matrix to lower Triangular (assuming this is lower Hessenberg)*

- [Matrix & upperHessenbergSolve](#) (const [Matrix](#) &H, const [Matrix](#) &v)  
*Function to solve the system  $Hx=v$  for  $x$  given that  $H$  is upper Hessenberg (this->x)*
- [Matrix & lowerHessenbergSolve](#) (const [Matrix](#) &H, const [Matrix](#) &v)  
*Function to solve the system  $Hx=v$  for  $x$  given that  $H$  is lower Hessenberg (this->x)*
- [Matrix & columnExtract](#) (int j, const [Matrix](#) &M)  
*Function to set this column matrix to the jth column of the given matrix M.*
- [Matrix & rowExtract](#) (int i, const [Matrix](#) &M)  
*Function to set this row matrix to the ith row of the given matrix M.*
- [Matrix & columnReplace](#) (int j, const [Matrix](#) &v)  
*Function to this matrices' jth column with the given column matrix v.*
- [Matrix & rowReplace](#) (int i, const [Matrix](#) &v)  
*Function to this matrices' ith row with the given row matrix v.*
- void [rowShrink](#) ()  
*Function to delete the last row of this matrix.*
- void [columnShrink](#) ()  
*Function to delete the last column of this matrix.*
- void [rowExtend](#) (const [Matrix](#) &v)  
*Function to add the row matrix v to the end of this matrix.*
- void [columnExtend](#) (const [Matrix](#) &v)  
*Function to add the column matrix v to the end of this matrix.*

**Protected Attributes**

- int [num\\_rows](#)  
*Number of rows of the matrix.*
- int [num\\_cols](#)  
*Number of columns of the matrix.*
- std::vector< T > [Data](#)  
*Storage vector for the elements of the matrix.*

**5.24.1 Detailed Description**

template<class T>class [Matrix](#)< T >

Templated C++ [Matrix](#) Class Object (click [Matrix](#) to go to function definitions)

C++ templated class object containing many different functions, actions, and solver routines associated with Dense Matrices. Operator overloads are also provided to give the user a more natural way of operating matrices on other matrices or scalars. These operator overloads are especially useful for reducing the amount of code needed to be written when working with matrix-based problems.

**5.24.2 Constructor & Destructor Documentation****5.24.2.1 template<class T > [Matrix](#)< T >::Matrix ( int rows, int columns )**

Constructor for matrix with given number of rows and columns.

**5.24.2.2 template<class T > [Matrix](#)< T >::Matrix ( const [Matrix](#)< T > & M )**

Copy constructor for constructing a matrix as a copy of another matrix.

**5.24.2.3 template<class T > [Matrix](#)< T >::Matrix ( )**

Default constructor for creating an empty matrix.

**5.24.2.4    template<class T > Matrix< T >::~~Matrix (    )**

Default destructor for clearing out memory.

**5.24.3    Member Function Documentation****5.24.3.1    template<class T > T & Matrix< T >::operator() ( int *i*, int *j* )**

Access operator for the matrix element at row *i* and column *j* (e.g.,  $a_{ij} = A(i,j)$ )

**5.24.3.2    template<class T > T Matrix< T >::operator() ( int *i*, int *j* ) const**

Constant access operator for the the matrix element at row *i* and column *j*.

**5.24.3.3    template<class T > Matrix< T > & Matrix< T >::operator= ( const Matrix< T > & *M* )**

Equals operator for setting one matrix equal to another matrix.

**5.24.3.4    template<class T > void Matrix< T >::set\_size ( int *i*, int *j* )**

Function to set/change the size of a matrix to *i* rows and *j* columns.

**5.24.3.5    template<class T > void Matrix< T >::zeros (    )**

Function to set/change all values in a matrix to zeros.

**5.24.3.6    template<class T> void Matrix< T >::edit ( int *i*, int *j*, T *value* )**

Function to set/change the element of a matrix at row *i* and column *j* to given value.

**5.24.3.7    template<class T > int Matrix< T >::rows (    )**

Function to return the number of rows in a given matrix.

**5.24.3.8    template<class T > int Matrix< T >::columns (    )**

Function to return the number of columns in a matrix.

**5.24.3.9    template<class T > T Matrix< T >::determinate (    )**

Function to compute the determinate of a matrix and return that value.

**5.24.3.10    template<class T > T Matrix< T >::norm (    )**

Function to compute the L2-norm of a matrix and return that value.

**5.24.3.11    template<class T > T Matrix< T >::sum (    )**

Function to compute the sum of all elements in a matrix and return that value.

**5.24.3.12    template<class T > T Matrix< T >::inner\_product ( const Matrix< T > & *x* )**

Function to compute the inner product between this matrix and matrix *x*.

**5.24.3.13    template<class T > Matrix< T > & Matrix< T >::cofactor ( const Matrix< T > & *M* )**

Function to convert this matrix to a cofactor matrix of the given matrix *M*.

**5.24.3.14    template<class T > Matrix< T > Matrix< T >::operator+ ( const Matrix< T > & *M* )**

Operator to add this matrix and matrix *M* and return the new matrix result.

**5.24.3.15** `template<class T> Matrix< T > Matrix< T >::operator- ( const Matrix< T > & M )`

Operator to subtract this matrix and matrix M and return the new matrix result.

**5.24.3.16** `template<class T> Matrix< T > Matrix< T >::operator* ( const T a )`

Operator to multiply this matrix by a scalar T return the new matrix result.

**5.24.3.17** `template<class T> Matrix< T > Matrix< T >::operator/ ( const T a )`

Operator to divide this matrix by a scalar T and return the new matrix result.

**5.24.3.18** `template<class T> Matrix< T > Matrix< T >::operator* ( const Matrix< T > & M )`

Operator to multiply this matrix and matrix M and return the new matrix result.

**5.24.3.19** `template<class T> Matrix< T > & Matrix< T >::transpose ( const Matrix< T > & M )`

Function to convert this matrix to the transpose of the given matrix M.

**5.24.3.20** `template<class T> Matrix< T > & Matrix< T >::transpose_multiply ( const Matrix< T > & MT, const Matrix< T > & v )`

Function to convert this matrix into the result of the given matrix M transposed and multiplied by the other given matrix v.

**5.24.3.21** `template<class T> Matrix< T > & Matrix< T >::adjoint ( const Matrix< T > & M )`

Function to convert this matrix to the adjoint of the given matrix.

**5.24.3.22** `template<class T> Matrix< T > & Matrix< T >::inverse ( const Matrix< T > & M )`

Function to convert this matrix to the inverse of the given matrix.

**5.24.3.23** `template<class T> void Matrix< T >::Display ( const std::string Name )`

Function to display the contents of this matrix given a Name for the matrix.

**5.24.3.24** `template<class T> Matrix< T > & Matrix< T >::tridiagonalSolve ( const Matrix< T > & A, const Matrix< T > & b )`

Function to solve  $Ax=b$  for x if A is symmetric, tridiagonal (this->x)

**5.24.3.25** `template<class T> Matrix< T > & Matrix< T >::ladshawSolve ( const Matrix< T > & A, const Matrix< T > & d )`

Function to solve  $Ax=d$  for x if A is non-symmetric, tridiagonal (this->x)

**5.24.3.26** `template<class T> Matrix< T > & Matrix< T >::tridiagonalFill ( const T A, const T B, const T C, bool Spherical )`

Function to fill in this matrix with coefficients A, B, and C to form a tridiagonal matrix.

This function fills in the diagonal elements of a square matrix with coefficient B, upper diagonal with C, and lower diagonal with A. The boolean will apply a transformation to those coefficients, if the problem happens to stem from 1-D diffusion in spherical coordinates.

**5.24.3.27** `template<class T> Matrix< T > & Matrix< T >::naturalLaplacian3D ( int m )`

Function to fill out this matrix with coefficients from a 3D Laplacian function.

This function will fill out the coefficients of the matrix with the coefficients that stem from discretizing a 3D Laplacian on a natural grid with 2nd order finite differences.



5.24.3.28 `template<class T> Matrix< T > & Matrix< T >::sphericalBCFill ( int node, const T coeff, T variable )`

Function to fill out a column matrix with spherical specific boundary conditions.

This function will fill out a column matrix with zeros at all nodes except for the node indicated. That node's value will be the product of the node id with the coeff and variable values given.

5.24.3.29 `template<class T> Matrix< T > & Matrix< T >::ConstantICFill ( const T IC )`

Function to set all values in a column matrix to a given constant.

5.24.3.30 `template<class T> Matrix< T > & Matrix< T >::SolnTransform ( const Matrix< T > & A, bool Forward )`

Function to transform the values in a column matrix from cartesian to spherical coordinates.

5.24.3.31 `template<class T> T Matrix< T >::sphericalAvg ( double radius, double dr, double bound, bool Dirichlet )`

Function to compute a spatial average of this column matrix in spherical coordinates.

This function is used to compute an average value of a variable, represented in this column matrix, by integrating over the domain of the sphere. (Assumes you have variable value at center node)

#### Parameters

<i>radius</i>	radius of the sphere
<i>dr</i>	space between each node
<i>bound</i>	value of the variable at the boundary
<i>Dirichlet</i>	True if problem has a Dirichlet BC, False if Neumann

5.24.3.32 `template<class T> T Matrix< T >::IntegralAvg ( double radius, double dr, double bound, bool Dirichlet )`

Function to compute a spatial average of this column matrix in spherical coordinates.

This function is used to compute an average value of a variable, represented in this column matrix, by integrating over the domain of the sphere. (Assumes you DO NOT have variable value at center node)

#### Parameters

<i>radius</i>	radius of the sphere
<i>dr</i>	space between each node
<i>bound</i>	value of the variable at the boundary
<i>Dirichlet</i>	True if problem has a Dirichlet BC, False if Neumann

5.24.3.33 `template<class T> T Matrix< T >::IntegralTotal ( double dr, double bound, bool Dirichlet )`

Function to compute a spatial total of this column matrix in spherical coordinates.

This function is used to compute an average value of a variable, represented in this column matrix, by integrating over the domain of the sphere. (Assumes you DO NOT have variable value at center node)

#### Parameters

<i>dr</i>	space between each node
<i>bound</i>	value of the variable at the boundary
<i>Dirichlet</i>	True if problem has a Dirichlet BC, False if Neumann

5.24.3.34 `template<class T> Matrix< T > & Matrix< T >::tridiagonalVectorFill ( const std::vector< T > & A, const std::vector< T > & B, const std::vector< T > & C )`

Function to fill in this matrix, in tridiagonal fashion, using the vectors of coefficients.

5.24.3.35 `template<class T> Matrix< T > & Matrix< T >::columnVectorFill ( const std::vector< T > & A )`

Function to fill in a column matrix with the values of the given vector object.

5.24.3.36 `template<class T> Matrix< T > & Matrix< T >::columnProjection ( const Matrix< T > & b, const Matrix< T > & b_old, const double dt, const double dt_old )`

Function to project a column matrix solution in time based on older state vectors.

This function is used in [finch.h](#) to form [Matrix](#) `u_star`. It uses the size of the current step and old step, `dt` and `dt_old` respectively, to form an approximation for the next state. The current state and older state of the variables are passed as `b` and `b_old` respectively.

5.24.3.37 `template<class T> Matrix< T > & Matrix< T >::dirichletBCFill ( int node, const T coeff, T variable )`

Function to fill in a column matrix with all zeros except at the given node.

Similar to `sphericalBCFill`, this function will set the values of all elements in the column matrix to zero except at the given node, where the value is set to the product of `coeff` and `variable`. This is often used to set BCs in [finch.h](#) or other related files/simulations.

5.24.3.38 `template<class T> Matrix< T > & Matrix< T >::diagonalSolve ( const Matrix< T > & D, const Matrix< T > & v )`

Function to solve the system  $Dx=v$  for  $x$  given that  $D$  is diagonal (this-> $x$ )

5.24.3.39 `template<class T> Matrix< T > & Matrix< T >::upperTriangularSolve ( const Matrix< T > & U, const Matrix< T > & v )`

Function to solve the system  $Ux=v$  for  $x$  given that  $U$  is upper Triangular (this-> $x$ )

5.24.3.40 `template<class T> Matrix< T > & Matrix< T >::lowerTriangularSolve ( const Matrix< T > & L, const Matrix< T > & v )`

Function to solve the system  $Lx=v$  for  $x$  given that  $L$  is lower Triangular (this-> $x$ )

5.24.3.41 `template<class T> Matrix< T > & Matrix< T >::upperHessenberg2Triangular ( Matrix< T > & b )`

Function to convert this square matrix to upper Triangular (assuming this is upper Hessenberg)

During this transformation, a column vector (`b`) is also being transformed to represent the BCs in a linear system. This algorithm uses Givens Rotations to efficiently convert the upper Hessenberg matrix to an upper triangular matrix.

5.24.3.42 `template<class T> Matrix< T > & Matrix< T >::lowerHessenberg2Triangular ( Matrix< T > & b )`

Function to convert this square matrix to lower Triangular (assuming this is lower Hessenberg)

During this transformation, a column vector (`b`) is also being transformed to represent the BCs in a linear system. This algorithm uses Givens Rotations to efficiently convert the lower Hessenberg matrix to a lower triangular matrix.

5.24.3.43 `template<class T> Matrix< T > & Matrix< T >::upperHessenbergSolve ( const Matrix< T > & H, const Matrix< T > & v )`

Function to solve the system  $Hx=v$  for  $x$  given that  $H$  is upper Hessenberg (this-> $x$ )

5.24.3.44 `template<class T> Matrix< T > & Matrix< T >::lowerHessenbergSolve ( const Matrix< T > & H, const Matrix< T > & v )`

Function to solve the system  $Hx=v$  for  $x$  given that  $H$  is lower Hessenberg (this-> $x$ )

5.24.3.45 `template<class T> Matrix< T> & Matrix< T>::columnExtract ( int j, const Matrix< T> & M )`

Function to set this column matrix to the jth column of the given matrix M.

5.24.3.46 `template<class T> Matrix< T> & Matrix< T>::rowExtract ( int i, const Matrix< T> & M )`

Function to set this row matrix to the ith row of the given matrix M.

5.24.3.47 `template<class T> Matrix< T> & Matrix< T>::columnReplace ( int j, const Matrix< T> & v )`

Function to this matrices' jth column with the given column matrix v.

5.24.3.48 `template<class T> Matrix< T> & Matrix< T>::rowReplace ( int i, const Matrix< T> & v )`

Function to this matrices' ith row with the given row matrix v.

5.24.3.49 `template<class T> void Matrix< T>::rowShrink ( )`

Function to delete the last row of this matrix.

5.24.3.50 `template<class T> void Matrix< T>::columnShrink ( )`

Function to delete the last column of this matrix.

5.24.3.51 `template<class T> void Matrix< T>::rowExtend ( const Matrix< T> & v )`

Function to add the row matrix v to the end of this matrix.

5.24.3.52 `template<class T> void Matrix< T>::columnExtend ( const Matrix< T> & v )`

Function to add the column matrix v to the end of this matrix.

#### 5.24.4 Member Data Documentation

5.24.4.1 `template<class T> int Matrix< T>::num_rows [protected]`

Number of rows of the matrix.

5.24.4.2 `template<class T> int Matrix< T>::num_cols [protected]`

Number of columns of the matrix.

5.24.4.3 `template<class T> std::vector<T> Matrix< T>::Data [protected]`

Storage vector for the elements of the matrix.

The documentation for this class was generated from the following file:

- [macaw.h](#)

## 5.25 MIXED\_GAS Struct Reference

Data structure holding information necessary for computing mixed gas properties.

```
#include <egret.h>
```

#### Public Attributes

- [int N](#)

- Given: Total number of gas species.*

  - bool `CheckMolefractions` = true

*Given: True = Check Molefractions for errors.*
- double `total_pressure`

*Given: Total gas pressure (kPa)*
- double `gas_temperature`

*Given: Gas temperature (K)*
- double `velocity`

*Given: Gas phase velocity (cm/s)*
- double `char_length`

*Given: Characteristic Length (cm)*
- std::vector< double > `molefraction`

*Given: Gas molefractions of each species (-)*
- double `total_density`

*Calculated: Total gas density (g/cm<sup>3</sup>) {use RE3}.*
- double `total_dyn_vis`

*Calculated: Total dynamic viscosity (g/cm/s)*
- double `kinematic_viscosity`

*Calculated: Kinematic viscosity (cm<sup>2</sup>/s)*
- double `total_molecular_weight`

*Calculated: Total molecular weight (g/mol)*
- double `total_specific_heat`

*Calculated: Total specific heat (J/g/K)*
- double `Reynolds`

*Calculated: Value of the Reynold's number (-)*
- Matrix< double > `binary_diffusion`

*Calculated: Tensor matrix of binary gas diffusivities (cm<sup>2</sup>/s)*
- std::vector< `PURE_GAS` > `species_dat`

*Vector of the pure gas info of all species.*

### 5.25.1 Detailed Description

Data structure holding information necessary for computing mixed gas properties.

C-style object holding the mixed gas information necessary for performing gas dynamic simulations. This object works in conjunction with the `calculate_variables` function and uses the kinetic theory of gases to estimate mixed gas properties.

### 5.25.2 Member Data Documentation

#### 5.25.2.1 int MIXED\_GAS::N

Given: Total number of gas species.

#### 5.25.2.2 bool MIXED\_GAS::CheckMolefractions = true

Given: True = Check Molefractions for errors.

#### 5.25.2.3 double MIXED\_GAS::total\_pressure

Given: Total gas pressure (kPa)

#### 5.25.2.4 double MIXED\_GAS::gas\_temperature

Given: Gas temperature (K)

## 5.25.2.5 double MIXED\_GAS::velocity

Given: Gas phase velocity (cm/s)

## 5.25.2.6 double MIXED\_GAS::char\_length

Given: Characteristic Length (cm)

## 5.25.2.7 std::vector&lt;double&gt; MIXED\_GAS::molefraction

Given: Gas molefractions of each species (-)

## 5.25.2.8 double MIXED\_GAS::total\_density

Calculated: Total gas density (g/cm<sup>3</sup>) {use RE3}.

## 5.25.2.9 double MIXED\_GAS::total\_dyn\_vis

Calculated: Total dynamic viscosity (g/cm/s)

## 5.25.2.10 double MIXED\_GAS::kinematic\_viscosity

Calculated: Kinematic viscosity (cm<sup>2</sup>/s)

## 5.25.2.11 double MIXED\_GAS::total\_molecular\_weight

Calculated: Total molecular weight (g/mol)

## 5.25.2.12 double MIXED\_GAS::total\_specific\_heat

Calculated: Total specific heat (J/g/K)

## 5.25.2.13 double MIXED\_GAS::Reynolds

Calculated: Value of the Reynold's number (-)

## 5.25.2.14 Matrix&lt;double&gt; MIXED\_GAS::binary\_diffusion

Calculated: Tensor matrix of binary gas diffusivities (cm<sup>2</sup>/s)

## 5.25.2.15 std::vector&lt;PURE\_GAS&gt; MIXED\_GAS::species\_dat

Vector of the pure gas info of all species.

The documentation for this struct was generated from the following file:

- [egret.h](#)

## 5.26 Molecule Class Reference

C++ [Molecule](#) Object built from [Atom](#) Objects (click [Molecule](#) to go to function definitions)

```
#include <mola.h>
```

## Public Member Functions

- [Molecule](#) ()  
*Default Constructor (builds an empty molecule object)*
- [~Molecule](#) ()  
*Default Destructor (clears out memory)*

- **Molecule** (int **charge**, double enthalpy, double entropy, double energy, bool HS, bool G, std::string **Phase**, std::string **Name**, std::string **Formula**, std::string lin\_formula)  
*Construct any molecule from the available information.*
- void **Register** (int **charge**, double enthalpy, double entropy, double energy, bool HS, bool G, std::string **Phase**, std::string **Name**, std::string **Formula**, std::string lin\_formula)  
*Function to register this molecule from the available information.*
- void **Register** (std::string formula)  
*Function to register this molecule based on the given formula (if formula is in library)*
- void **setFormula** (std::string form)  
*Sets the formula for a molecule.*
- void **recalculateMolarWeight** ()  
*Forces molecule to recalculate its molar weight.*
- void **setMolarWeight** (double mw)  
*Set the molar weight of species to a constant.*
- void **editCharge** (int c)  
*Change the ionic charge of a molecule.*
- void **editOneOxidationState** (int state, std::string Symbol)  
*Change oxidation state of one of the given atoms (always first match found)*
- void **editAllOxidationStates** (int state, std::string Symbol)  
*Change oxidation state of all of the given atoms.*
- void **calculateAvgOxiState** (std::string Symbol)  
*Function to calculate the average oxidation state of the atoms.*
- void **editEnthalpy** (double enthalpy)  
*Edit the molecules formation enthalpy (J/mol)*
- void **editEntropy** (double entropy)  
*Edit the molecules formation entropy (J/K/mol)*
- void **editHS** (double H, double S)  
*Edit both formation enthalpy and entropy.*
- void **editEnergy** (double energy)  
*Edit Gibb's formation energy.*
- void **removeOneAtom** (std::string Symbol)  
*Removes one atom of the symbol given (always the first atom found)*
- void **removeAllAtoms** (std::string Symbol)  
*Removes all atoms of the symbol given.*
- int **Charge** ()  
*Return the charge of the molecule.*
- double **MolarWeight** ()  
*Return the molar weight of the molecule.*
- bool **HaveHS** ()  
*Returns true if enthalpy and entropy are known.*
- bool **HaveEnergy** ()  
*Returns true if the Gibb's energy is known.*
- bool **isRegistered** ()  
*Returns true if the molecule has been registered.*
- double **Enthalpy** ()  
*Return the formation enthalpy of the molecule.*
- double **Entropy** ()  
*Return the formation entropy of the molecule.*
- double **Energy** ()  
*Return the Gibb's formation energy of the molecule.*
- std::string **MoleculeName** ()

- *Return the common name of the molecule.*
- `std::string MolecularFormula ()`  
*Return the molecular formula of the molecule.*
- `std::string MoleculePhase ()`  
*Return the phase of the molecule.*
- `int MoleculePhaseID ()`  
*Return the enum phase ID of the molecule.*
- `void DisplayInfo ()`  
*Function to display molecule information.*

#### Protected Attributes

- `int charge`  
*Ionic charge of the molecule - specified.*
- `double molar_weight`  
*Molar weight of the molecule (g/mol) - determined from atoms or specified.*
- `double formation_enthalpy`  
*Enthalpy of formation of the molecule (J/mol) - constant.*
- `double formation_entropy`  
*Entropy of formation of the molecule (J/K/mol) - constant.*
- `double formation_energy`  
*Gibb's energy of formation (J/mol) - given.*
- `std::string Phase`  
*Phase of the molecule (i.e. Solid, Liquid, Aqueous, Gas...)*
- `int PhaseID`  
*Phase ID of the molecule (from the enum)*
- `std::vector< Atom > atoms`  
*Atoms which make up the molecule - based on Formula.*

#### Private Attributes

- `std::string Name`  
*Name of the Molecule - Common Name (i.e. H2O = Water)*
- `std::string Formula`  
*Formula for the molecule - specified (i.e. H2O)*
- `bool haveG`  
*True = given Gibb's energy of formation.*
- `bool haveHS`  
*True = give enthalpy and entropy of formation.*
- `bool registered`  
*True = the object was registered.*

#### 5.26.1 Detailed Description

C++ [Molecule](#) Object built from [Atom](#) Objects (click [Molecule](#) to go to function definitions)

C++ Class Object that stores information and certain operations associated with molecules. Registered molecules are built up from their respective atoms so that the molecule can keep track of information such as molecular weight and oxidation states. Primarily, this object is used in conjunction with [shark.h](#) to formulate the system of equations necessary for solving speciation type problems in aqueous systems. However, this object is generalized enough to be of use in RedOx calculations, reaction formulation, and molecular transformations.

All information for a molecule should be initialized prior to performing operations with or on the object. There are several molecules already defined for construction by the formulas listed at the top of this section.

## 5.26.2 Constructor &amp; Destructor Documentation

## 5.26.2.1 Molecule::Molecule ( )

Default Constructor (builds an empty molecule object)

## 5.26.2.2 Molecule::~~Molecule ( )

Default Destructor (clears out memory)

5.26.2.3 Molecule::Molecule ( int *charge*, double *enthalpy*, double *entropy*, double *energy*, bool *HS*, bool *G*, std::string *Phase*, std::string *Name*, std::string *Formula*, std::string *lin\_formula* )

Construct any molecule from the available information.

This constructor will build a user defined custom molecule.

## Parameters

<i>charge</i>	the ionic charge of the molecule
<i>enthalpy</i>	the standard formation enthalpy of the molecule (J/mol)
<i>entropy</i>	the standard formation entropy of the molecule (J/K/mol)
<i>energy</i>	the standard Gibb's Free Energy of formation of the molecule (J/mol)
<i>HS</i>	boolean to be set to true if enthalpy and entropy were given
<i>G</i>	boolean to be set to true if the energy was given
<i>Phase</i>	string denoting molecule's phase (i.e., Liquid, Aqueous, Gas, Solid)
<i>Name</i>	string denoting the common name of the molecule (i.e., H <sub>2</sub> O -> Water)
<i>Formula</i>	string denoting the formula by which the molecule is referenced (i.e., Cl - (aq))
<i>lin_formula</i>	string denoting all the atoms in the molecule (i.e., UO <sub>2</sub> (OH) <sub>2</sub> -> UO <sub>4</sub> H <sub>2</sub> )

## 5.26.3 Member Function Documentation

5.26.3.1 void Molecule::Register ( int *charge*, double *enthalpy*, double *entropy*, double *energy*, bool *HS*, bool *G*, std::string *Phase*, std::string *Name*, std::string *Formula*, std::string *lin\_formula* )

Function to register this molecule from the available information.

This function will build a user defined custom molecule.

## Parameters

<i>charge</i>	the ionic charge of the molecule
<i>enthalpy</i>	the standard formation enthalpy of the molecule (J/mol)
<i>entropy</i>	the standard formation entropy of the molecule (J/K/mol)
<i>energy</i>	the standard Gibb's Free Energy of formation of the molecule (J/mol)
<i>HS</i>	boolean to be set to true if enthalpy and entropy were given
<i>G</i>	boolean to be set to true if the energy was given
<i>Phase</i>	string denoting molecule's phase (i.e., Liquid, Aqueous, Gas, Solid)
<i>Name</i>	string denoting the common name of the molecule (i.e., H <sub>2</sub> O -> Water)
<i>Formula</i>	string denoting the formula by which the molecule is referenced (i.e., Cl - (aq))
<i>lin_formula</i>	string denoting all the atoms in the molecule (i.e., UO <sub>2</sub> (OH) <sub>2</sub> -> UO <sub>4</sub> H <sub>2</sub> )

5.26.3.2 void Molecule::Register ( std::string *formula* )

Function to register this molecule based on the given formula (if formula is in library)

This function will create this molecule object from the given formula, but only if that formula is already registered in the library. See the top of this class section for a list of all currently registered formulas.



## Note

The formula is checked against a known set of molecules inside of the registration function. If the formula is unknown, an error will print to the screen. Unknown molecules should be registered using the full registration function from above. The library can only be added to by going in and editing the source code of the mola.cpp file. However, this is a relatively simple task.

5.26.3.3 void Molecule::setFormula ( std::string *form* )

Sets the formula for a molecule.

## 5.26.3.4 void Molecule::recalculateMolarWeight ( )

Forces molecule to recalculate its molar weight.

5.26.3.5 void Molecule::setMolarWeight ( double *mw* )

Set the molar weight of species to a constant.

5.26.3.6 void Molecule::editCharge ( int *c* )

Change the ionic charge of a molecule.

5.26.3.7 void Molecule::editOneOxidationState ( int *state*, std::string *Symbol* )

Change oxidation state of one of the given atoms (always first match found)

This function will search the list of Atoms that make up the [Molecule](#) for the given atomic Symbol. It will change the oxidation state of the first found matching atom with the given state.

5.26.3.8 void Molecule::editAllOxidationStates ( int *state*, std::string *Symbol* )

Change oxidation state of all of the given atoms.

This function will search the list of Atoms that make up the [Molecule](#) for the given atomic Symbol. It will change the oxidation state of all found matching atoms with the given state.

5.26.3.9 void Molecule::calculateAvgOxiState ( std::string *Symbol* )

Function to calculate the average oxidation state of the atoms.

This function search the atoms in the molecule for the matching atomic Symbol. It then looks at all oxidation states of that atom in the molecule and then sets all the oxidation states of that atom to the average value calculated.

5.26.3.10 void Molecule::editEnthalpy ( double *enthalpy* )

Edit the molecules formation enthalpy (J/mol)

5.26.3.11 void Molecule::editEntropy ( double *entropy* )

Edit the molecules formation entropy (J/K/mol)

5.26.3.12 void Molecule::editHS ( double *H*, double *S* )

Edit both formation enthalpy and entropy.

This function will change or set the values for formation enthalpy (J/mol) and formation entropy (J/K/mol) based on the given values.

## Parameters

<i>H</i>	formation enthalpy (J/mol)
<i>S</i>	formation entropy (J/K/mol)

5.26.3.13 void Molecule::editEnergy ( double *energy* )

Edit Gibb's formation energy.

5.26.3.14 void Molecule::removeOneAtom ( std::string *Symbol* )

Removes one atom of the symbol given (always the first atom found)

5.26.3.15 void Molecule::removeAllAtoms ( std::string *Symbol* )

Removes all atoms of the symbol given.

5.26.3.16 int Molecule::Charge ( )

Return the charge of the molecule.

5.26.3.17 double Molecule::MolarWeight ( )

Return the molar weight of the molecule.

5.26.3.18 bool Molecule::HaveHS ( )

Returns true if enthalpy and entropy are known.

5.26.3.19 bool Molecule::HaveEnergy ( )

Returns true if the Gibb's energy is known.

5.26.3.20 bool Molecule::isRegistered ( )

Returns true if the molecule has been registered.

5.26.3.21 double Molecule::Enthalpy ( )

Return the formation enthalpy of the molecule.

5.26.3.22 double Molecule::Entropy ( )

Return the formation entropy of the molecule.

5.26.3.23 double Molecule::Energy ( )

Return the Gibb's formation energy of the molecule.

5.26.3.24 std::string Molecule::MoleculeName ( )

Return the common name of the molecule.

5.26.3.25 std::string Molecule::MolecularFormula ( )

Return the molecular formula of the molecule.

5.26.3.26 std::string Molecule::MoleculePhase ( )

Return the phase of the molecule.

5.26.3.27 int Molecule::MoleculePhaseID ( )

Return the enum phase ID of the molecule.

### 5.26.3.28 void Molecule::DisplayInfo ( )

Function to display molecule information.

## 5.26.4 Member Data Documentation

### 5.26.4.1 int Molecule::charge [protected]

Ionic charge of the molecule - specified.

### 5.26.4.2 double Molecule::molar\_weight [protected]

Molar weight of the molecule (g/mol) - determined from atoms or specified.

### 5.26.4.3 double Molecule::formation\_enthalpy [protected]

Enthalpy of formation of the molecule (J/mol) - constant.

### 5.26.4.4 double Molecule::formation\_entropy [protected]

Entropy of formation of the molecule (J/K/mol) - constant.

### 5.26.4.5 double Molecule::formation\_energy [protected]

Gibb's energy of formation (J/mol) - given.

### 5.26.4.6 std::string Molecule::Phase [protected]

Phase of the molecule (i.e. Solid, Liquid, Aqueous, Gas...)

### 5.26.4.7 int Molecule::PhaseID [protected]

Phase ID of the molecule (from the enum)

### 5.26.4.8 std::vector<Atom> Molecule::atoms [protected]

Atoms which make up the molecule - based on Formula.

### 5.26.4.9 std::string Molecule::Name [private]

Name of the [Molecule](#) - Common Name (i.e. H2O = Water)

### 5.26.4.10 std::string Molecule::Formula [private]

Formula for the molecule - specified (i.e. H2O)

### 5.26.4.11 bool Molecule::haveG [private]

True = given Gibb's energy of formation.

### 5.26.4.12 bool Molecule::haveHS [private]

True = give enthalpy and entropy of formation.

### 5.26.4.13 bool Molecule::registered [private]

True = the object was registered.

The documentation for this class was generated from the following file:

- [mola.h](#)

## 5.27 MONKFISH\_DATA Struct Reference

Primary data structure for running MONKFISH.

```
#include <monkfish.h>
```

### Public Attributes

- unsigned long int **total\_steps** = 0  
*Total number of steps taken by the algorithm (iterations and time steps)*
- double **time\_old** = 0.0  
*Old value of time in the simulation (hrs)*
- double **time** = 0.0  
*Current value of time in the simulation (hrs)*
- bool **Print2File** = true  
*True = results to .txt; False = no printing.*
- bool **Print2Console** = true  
*True = results to console; False = no printing.*
- bool **DirichletBC** = true  
*False = uses film mass transfer for BC, True = Dirichlet BC.*
- bool **NonLinear** = false  
*False = Solve directly, True = Solve iteratively.*
- bool **haveMinMax** = false  
*True = know min and max fiber density, False = only know avg density (Used in ICs)*
- bool **MultiScale** = true  
*True = solve single fiber model at nodes, False = solve equilibrium at nodes.*
- int **level** = 2  
*Level of coupling between multiple scales (default = 2)*
- double **t\_counter** = 0.0  
*Counter for the time output.*
- double **t\_print**  
*Print output at every t\_print time (hrs)*
- int **NumComp**  
*Number of species to track.*
- double **end\_time**  
*Units: hours.*
- double **total\_sorption\_old**  
*Old total adsorption per mass of woven nest (mg/g)*
- double **total\_sorption**  
*Current total adsorption per mass woven nest (mg/g)*
- double **single\_fiber\_density**  
*Units: g/L.*
- double **avg\_fiber\_density**  
*Units: g/L (Used in ICs)*
- double **max\_fiber\_density**  
*Units: g/L (Used in ICs)*
- double **min\_fiber\_density**  
*Units: g/L (Used in ICs)*
- double **max\_porosity**  
*Units: -.*
- double **min\_porosity**

Units: -.

- double `domain_diameter`  
Nominal diameter of the woven fiber ball - Units: cm.
- FILE \* `Output`  
Output file pointer for printing to text file.
- double(\* `eval_eps`)(int i, int l, const void \*`user_data`)  
Function pointer to evaluate the porosity of the woven bundle of fibers.
- double(\* `eval_rho`)(int i, int l, const void \*`user_data`)  
Function pointer to evaluate the fiber density in the domain.
- double(\* `eval_Dex`)(int i, int l, const void \*`user_data`)  
Function pointer to evaluate the interparticle diffusivity.
- double(\* `eval_ads`)(int i, int l, const void \*`user_data`)  
Function pointer to evaluate the adsorption strength for the macro-scale.
- double(\* `eval_Ret`)(int i, int l, const void \*`user_data`)  
Function pointer to evaluate the retardation coefficient for the macro-scale.
- double(\* `eval_Cex`)(int i, const void \*`user_data`)  
Function pointer to evaluate the exterior concentration for the domain.
- double(\* `eval_kf`)(int i, const void \*`user_data`)  
Function pointer to evaluate the film mass transfer coefficient for the macro-scale.
- const void \* `user_data`  
User supplied data function to evaluate the function pointers (Default = `MONKFISH_DATA`)
- std::vector< `FINCH_DATA` > `finch_dat`  
FINCH data structures to solve each species interparticle diffusion equation.
- std::vector< `MONKFISH_PARAM` > `param_dat`  
MONKFISH parameter data structure for each species adsorbing.
- std::vector< `DOGFISH_DATA` > `dog_dat`  
DOGFISH data structures for each node in the macro-scale problem.

### 5.27.1 Detailed Description

Primary data structure for running MONKFISH.

C-style object holding simulation information for MONKFISH as well as common system parameters like fiber density, fiber diameter, fiber length, etc. This object also contains function pointers to different parameter evaluation functions that can be changed to suit a particular problem. Default functions will be given, so not every user needs to override these functions. This structure also contains vectors of other objects including FINCH and DOGFISH objects to resolve the diffusion physics at both the macro- and micro-scale.

### 5.27.2 Member Data Documentation

#### 5.27.2.1 unsigned long int MONKFISH\_DATA::total\_steps = 0

Total number of steps taken by the algorithm (iterations and time steps)

#### 5.27.2.2 double MONKFISH\_DATA::time\_old = 0.0

Old value of time in the simulation (hrs)

#### 5.27.2.3 double MONKFISH\_DATA::time = 0.0

Current value of time in the simulation (hrs)

#### 5.27.2.4 bool MONKFISH\_DATA::Print2File = true

True = results to .txt; False = no printing.

5.27.2.5 `bool MONKFISH_DATA::Print2Console = true`

True = results to console; False = no printing.

5.27.2.6 `bool MONKFISH_DATA::DirichletBC = true`

False = uses film mass transfer for BC, True = Dirichlet BC.

5.27.2.7 `bool MONKFISH_DATA::NonLinear = false`

False = Solve directly, True = Solve iteratively.

5.27.2.8 `bool MONKFISH_DATA::haveMinMax = false`

True = know min and max fiber density, False = only know avg density (Used in ICs)

5.27.2.9 `bool MONKFISH_DATA::MultiScale = true`

True = solve single fiber model at nodes, False = solve equilibrium at nodes.

5.27.2.10 `int MONKFISH_DATA::level = 2`

Level of coupling between multiple scales (default = 2)

5.27.2.11 `double MONKFISH_DATA::t_counter = 0.0`

Counter for the time output.

5.27.2.12 `double MONKFISH_DATA::t_print`

Print output at every `t_print` time (hrs)

5.27.2.13 `int MONKFISH_DATA::NumComp`

Number of species to track.

5.27.2.14 `double MONKFISH_DATA::end_time`

Units: hours.

5.27.2.15 `double MONKFISH_DATA::total_sorption_old`

Old total adsorption per mass of woven nest (mg/g)

5.27.2.16 `double MONKFISH_DATA::total_sorption`

Current total adsorption per mass woven nest (mg/g)

5.27.2.17 `double MONKFISH_DATA::single_fiber_density`

Units: g/L.

5.27.2.18 `double MONKFISH_DATA::avg_fiber_density`

Units: g/L (Used in ICs)

5.27.2.19 `double MONKFISH_DATA::max_fiber_density`

Units: g/L (Used in ICs)

5.27.2.20 double MONKFISH\_DATA::min\_fiber\_density

Units: g/L (Used in ICs)

5.27.2.21 double MONKFISH\_DATA::max\_porosity

Units: -.

5.27.2.22 double MONKFISH\_DATA::min\_porosity

Units: -.

5.27.2.23 double MONKFISH\_DATA::domain\_diameter

Nominal diameter of the woven fiber ball - Units: cm.

5.27.2.24 FILE\* MONKFISH\_DATA::Output

Output file pointer for printing to text file.

5.27.2.25 double(\* MONKFISH\_DATA::eval\_eps)(int i, int l, const void \*user\_data)

Function pointer to evaluate the porosity of the woven bundle of fibers.

5.27.2.26 double(\* MONKFISH\_DATA::eval\_rho)(int i, int l, const void \*user\_data)

Function pointer to evaluate the fiber density in the domain.

5.27.2.27 double(\* MONKFISH\_DATA::eval\_Dex)(int i, int l, const void \*user\_data)

Function pointer to evaluate the interparticle diffusivity.

5.27.2.28 double(\* MONKFISH\_DATA::eval\_ads)(int i, int l, const void \*user\_data)

Function pointer to evaluate the adsorption strength for the macro-scale.

5.27.2.29 double(\* MONKFISH\_DATA::eval\_Ret)(int i, int l, const void \*user\_data)

Function pointer to evaluate the retardation coefficient for the macro-scale.

5.27.2.30 double(\* MONKFISH\_DATA::eval\_Cex)(int i, const void \*user\_data)

Function pointer to evaluate the exterior concentration for the domain.

5.27.2.31 double(\* MONKFISH\_DATA::eval\_kf)(int i, const void \*user\_data)

Function pointer to evaluate the film mass transfer coefficient for the macro-scale.

5.27.2.32 const void\* MONKFISH\_DATA::user\_data

User supplied data function to evaluate the function pointers (Default = [MONKFISH\\_DATA](#))

5.27.2.33 std::vector<FINCH\_DATA> MONKFISH\_DATA::finch\_dat

FINCH data structures to solve each species interparticle diffusion equation.

5.27.2.34 std::vector<MONKFISH\_PARAM> MONKFISH\_DATA::param\_dat

MONKFISH parameter data structure for each species adsorbing.

5.27.2.35 `std::vector<DOGFISH_DATA> MONKFISH_DATA::dog_dat`

DOGFISH data structures for each node in the macro-scale problem.

The documentation for this struct was generated from the following file:

- [monkfish.h](#)

## 5.28 MONKFISH\_PARAM Struct Reference

Data structure for species specific information and parameters.

```
#include <monkfish.h>
```

### Public Attributes

- double [interparticle\\_diffusion](#)  
*Units:  $\text{cm}^2/\text{hr}$ .*
- double [exterior\\_concentration](#)  
*Units: mol/L.*
- double [exterior\\_transfer\\_coeff](#)  
*Units: cm/hr.*
- double [sorbed\\_molefraction](#)  
*Units: -.*
- double [initial\\_sorption](#)  
*Units: mg/g.*
- double [sorption\\_bc](#)  
*Units: mg/g.*
- double [intraparticle\\_diffusion](#)  
*Units:  $\text{um}^2/\text{hr}$ .*
- double [film\\_transfer\\_coeff](#)  
*Units: um/hr.*
- [Matrix](#)< double > [avg\\_sorption](#)  
*Units: mg/g.*
- [Matrix](#)< double > [avg\\_sorption\\_old](#)  
*Units: mg/g.*
- [Molecule species](#)  
*Species in the liquid phase.*

### 5.28.1 Detailed Description

Data structure for species specific information and parameters.

C-style object to hold information associated with the different species present in the interparticle diffusion problem. Each species may have different diffusivities, mass transfer coefficients, etc. Average adsorption for each species will be held in matrix objects.

### 5.28.2 Member Data Documentation

5.28.2.1 `double MONKFISH_PARAM::interparticle_diffusion`

Units:  $\text{cm}^2/\text{hr}$ .



5.28.2.2 double MONKFISH\_PARAM::exterior\_concentration

Units: mol/L.

5.28.2.3 double MONKFISH\_PARAM::exterior\_transfer\_coeff

Units: cm/hr.

5.28.2.4 double MONKFISH\_PARAM::sorbed\_molefraction

Units: -.

5.28.2.5 double MONKFISH\_PARAM::initial\_sorption

Units: mg/g.

5.28.2.6 double MONKFISH\_PARAM::sorption\_bc

Units: mg/g.

5.28.2.7 double MONKFISH\_PARAM::intraparticle\_diffusion

Units:  $\mu\text{m}^2/\text{hr}$ .

5.28.2.8 double MONKFISH\_PARAM::film\_transfer\_coeff

Units:  $\mu\text{m}/\text{hr}$ .

5.28.2.9 Matrix<double> MONKFISH\_PARAM::avg\_sorption

Units: mg/g.

5.28.2.10 Matrix<double> MONKFISH\_PARAM::avg\_sorption\_old

Units: mg/g.

5.28.2.11 Molecule MONKFISH\_PARAM::species

Species in the liquid phase.

The documentation for this struct was generated from the following file:

- [monkfish.h](#)

## 5.29 mSPD\_DATA Struct Reference

MSPD Data Structure.

```
#include <magpie.h>
```

### Public Attributes

- double [s](#)  
*Area shape factor.*
- double [v](#)  
*van der Waals Volume ( $\text{cm}^3/\text{mol}$ )*
- double [eMax](#)  
*Maximum lateral interaction energy (J/mol)*
- std::vector< double > [eta](#)

Binary interaction parameter matrix ( $i,j$ )

- double [gama](#)

Activity coefficient calculated from mSPD.

### 5.29.1 Detailed Description

MSPD Data Structure.

C-Style object holding all parameter information associated with the Modified Spreading Pressure Dependent (SPD) activity model. Each species in the gas phase will have one of these objects.

### 5.29.2 Member Data Documentation

#### 5.29.2.1 double mSPD\_DATA::s

Area shape factor.

#### 5.29.2.2 double mSPD\_DATA::v

van der Waals Volume ( $\text{cm}^3/\text{mol}$ )

#### 5.29.2.3 double mSPD\_DATA::eMax

Maximum lateral interaction energy ( $\text{J/mol}$ )

#### 5.29.2.4 std::vector<double> mSPD\_DATA::eta

Binary interaction parameter matrix ( $i,j$ )

#### 5.29.2.5 double mSPD\_DATA::gama

Activity coefficient calculated from mSPD.

The documentation for this struct was generated from the following file:

- [magpie.h](#)

## 5.30 NUM\_JAC\_DATA Struct Reference

Data structure to form a numerical jacobian matrix with finite differences.

```
#include <lark.h>
```

### Public Attributes

- double [eps](#) = sqrt(DBL\_EPSILON)

Perturbation value.

- [Matrix](#)< double > [Fx](#)

Vector of function evaluations at  $x$ .

- [Matrix](#)< double > [Fxp](#)

Vector of function evaluations at  $x+eps$ .

- [Matrix](#)< double > [dxj](#)

Vector of perturbed  $x$  values.

## 5.30.1 Detailed Description

Data structure to form a numerical jacobian matrix with finite differences.

C-style object to be used in conjunction with the Numerical Jacobian algorithm. This algorithm will use double-precision finite-differences to formulate an approximate Jacobian matrix at the given variable state for the given residual/non-linear function.

## 5.30.2 Member Data Documentation

5.30.2.1 `double NUM_JAC_DATA::eps = sqrt(DBL_EPSILON)`

Perturbation value.

5.30.2.2 `Matrix<double> NUM_JAC_DATA::Fx`

Vector of function evaluations at x.

5.30.2.3 `Matrix<double> NUM_JAC_DATA::Fxp`

Vector of function evaluations at x+eps.

5.30.2.4 `Matrix<double> NUM_JAC_DATA::dxj`

Vector of perturbed x values.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.31 OPTRANS\_DATA Struct Reference

Data structure for implementation of linear operator transposition.

```
#include <lark.h>
```

## Public Attributes

- `Matrix< double > li`  
*The ith column vector of the identity operator.*
- `Matrix< double > Ai`  
*The ith column vector of the user's linear operator.*

## 5.31.1 Detailed Description

Data structure for implementation of linear operator transposition.

C-style object used in conjunction with the Operator Transpose algorithm to form an action of  $A^T r$  when A is only available as a linear operator and not a matrix. This is a sub-routine required by GCR and GMRESR to stabilize the outer iterations.

## 5.31.2 Member Data Documentation

5.31.2.1 `Matrix<double> OPTRANS_DATA::li`

The ith column vector of the identity operator.

## 5.31.2.2 Matrix&lt;double&gt; OPTRANS\_DATA::Ai

The ith column vector of the user's linear operator.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.32 PCG\_DATA Struct Reference

Data structure for implementation of the PCG algorithms for symmetric linear systems.

```
#include <lark.h>
```

## Public Attributes

- int [maxit](#) = 0  
*Maximum allowable iterations - default = min(vector\_size,1000)*
- int [iter](#) = 0  
*Actual number of iterations taken.*
- double [alpha](#)  
*Step size for new solution.*
- double [beta](#)  
*Step size for new search direction.*
- double [tol\\_rel](#) = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double [tol\\_abs](#) = 1e-6  
*Absolute tolerance for convergence - default = 1e-6.*
- double [res](#)  
*Absolute residual norm.*
- double [relres](#)  
*Relative residual norm.*
- double [relres\\_base](#)  
*Initial residual norm.*
- double [bestres](#)  
*Best found residual norm.*
- bool [Output](#) = true  
*True = print messages to console.*
- Matrix< double > [x](#)  
*Current solution to the linear system.*
- Matrix< double > [bestx](#)  
*Best found solution to the linear system.*
- Matrix< double > [r](#)  
*Residual vector for the linear system.*
- Matrix< double > [r\\_old](#)  
*Previous residual vector.*
- Matrix< double > [z](#)  
*Preconditioned residual vector (result of precon function)*
- Matrix< double > [z\\_old](#)  
*Previous preconditioned residual vector.*
- Matrix< double > [p](#)  
*Search direction.*
- Matrix< double > [Ap](#)  
*Result of matrix-vector multiplication.*

### 5.32.1 Detailed Description

Data structure for implementation of the PCG algorithms for symmetric linear systems.

C-style object used in conjunction with the Preconditioned Conjugate Gradient (PCG) algorithm to iteratively solve a symmetric linear system of equations. This algorithm is optimal if your linear system is symmetric, but will not work at all if your system is asymmetric. For asymmetric systems, use one of the other linear methods.

### 5.32.2 Member Data Documentation

#### 5.32.2.1 `int PCG_DATA::maxit = 0`

Maximum allowable iterations - default = min(vector\_size,1000)

#### 5.32.2.2 `int PCG_DATA::iter = 0`

Actual number of iterations taken.

#### 5.32.2.3 `double PCG_DATA::alpha`

Step size for new solution.

#### 5.32.2.4 `double PCG_DATA::beta`

Step size for new search direction.

#### 5.32.2.5 `double PCG_DATA::tol_rel = 1e-6`

Relative tolerance for convergence - default = 1e-6.

#### 5.32.2.6 `double PCG_DATA::tol_abs = 1e-6`

Absolution tolerance for convergence - default = 1e-6.

#### 5.32.2.7 `double PCG_DATA::res`

Absolute residual norm.

#### 5.32.2.8 `double PCG_DATA::relres`

Relative residual norm.

#### 5.32.2.9 `double PCG_DATA::relres_base`

Initial residual norm.

#### 5.32.2.10 `double PCG_DATA::bestres`

Best found residual norm.

#### 5.32.2.11 `bool PCG_DATA::Output = true`

True = print messages to console.

#### 5.32.2.12 `Matrix<double> PCG_DATA::x`

Current solution to the linear system.

#### 5.32.2.13 `Matrix<double> PCG_DATA::bestx`

Best found solution to the linear system.

**5.32.2.14** `Matrix<double> PCG_DATA::r`

Residual vector for the linear system.

**5.32.2.15** `Matrix<double> PCG_DATA::r_old`

Previous residual vector.

**5.32.2.16** `Matrix<double> PCG_DATA::z`

Preconditioned residual vector (result of precon function)

**5.32.2.17** `Matrix<double> PCG_DATA::z_old`

Previous preconditioned residual vector.

**5.32.2.18** `Matrix<double> PCG_DATA::p`

Search direction.

**5.32.2.19** `Matrix<double> PCG_DATA::Ap`

Result of matrix-vector multiplication.

The documentation for this struct was generated from the following file:

- [lark.h](#)

**5.33** PeriodicTable Class Reference

Class object that store a digital copy of all [Atom](#) objects.

```
#include <eel.h>
```

**Public Member Functions**

- [PeriodicTable](#) ()  
*Default Constructor - Build Perodic Table.*
- [~PeriodicTable](#) ()  
*Default Destructor - Destroy the table.*
- [PeriodicTable](#) (int \*n, int N)  
*Construct a partial table from a list of atomic numbers.*
- [PeriodicTable](#) (std::vector< std::string > &Symbol)  
*Construct a partial table from a vector of atom symbols.*
- [PeriodicTable](#) (std::vector< int > &n)  
*Construct a partial table from a vector of atomic numbers.*
- void [DisplayTable](#) ()  
*Displays the periodic table via symbols.*

**Protected Attributes**

- std::vector< [Atom](#) > [Table](#)  
*Storage vector for all atoms in the table.*

#### Private Attributes

- int [number\\_elements](#)  
*Number of atom objects being stored.*

#### 5.33.1 Detailed Description

Class object that store a digital copy of all [Atom](#) objects.

C++ class object to hold digitally registered [Atom](#) objects. All registered atoms (Hydrogen to Ununoctium) are stored as in a vector. Currently, this object is unused, but could be modified to be explorable and used as a constant referece for all atoms in the table.

#### 5.33.2 Constructor & Destructor Documentation

##### 5.33.2.1 PeriodicTable::PeriodicTable ( )

Default Constructor - Build Perodic Table.

##### 5.33.2.2 PeriodicTable::~~PeriodicTable ( )

Default Destructor - Destroy the table.

##### 5.33.2.3 PeriodicTable::PeriodicTable ( int \* *n*, int *N* )

Construct a partial table from a list of atomic numbers.

##### 5.33.2.4 PeriodicTable::PeriodicTable ( std::vector< std::string > & *Symbol* )

Construct a partial table from a vector of atom symbols.

##### 5.33.2.5 PeriodicTable::PeriodicTable ( std::vector< int > & *n* )

Construct a partial table from a vector of atomic numbers.

#### 5.33.3 Member Function Documentation

##### 5.33.3.1 void PeriodicTable::DisplayTable ( )

Displays the periodic table via symbols.

#### 5.33.4 Member Data Documentation

##### 5.33.4.1 std::vector<Atom> PeriodicTable::Table [protected]

Storage vector for all atoms in the table.

##### 5.33.4.2 int PeriodicTable::number\_elements [private]

Number of atom objects being stored.

The documentation for this class was generated from the following file:

- [eel.h](#)

## 5.34 PICARD\_DATA Struct Reference

Data structure for the implementation of a Picard or Fixed-Point iteration for non-linear systems.

```
#include <lark.h>
```

### Public Attributes

- int `maxit` = 0  
*Maximum allowable iterations - default = min(3\*vec\_size,1000)*
- int `iter` = 0  
*Actual number of iterations.*
- double `tol_rel` = 1e-6  
*Relative tolerance for convergence - default = 1e-6.*
- double `tol_abs` = 1e-6  
*Absolution tolerance for convergence - default = 1e-6.*
- double `res`  
*Residual norm of the iterate.*
- double `relres`  
*Relative residual norm of the iterate.*
- double `relres_base`  
*Initial residual norm.*
- double `bestres`  
*Best found residual norm.*
- bool `Output` = true  
*True = print messages to console.*
- `Matrix`< double > `x0`  
*Previous iterate solution vector.*
- `Matrix`< double > `bestx`  
*Best found solution vector.*
- `Matrix`< double > `r`  
*Residual of the non-linear system.*

### 5.34.1 Detailed Description

Data structure for the implementation of a Picard or Fixed-Point iteration for non-linear systems.

C-style object used in conjunction with the Picard algorithm for solving a non-linear system of equations. This is an extraordinarily simple iterative method by which a weak or loose form of the non-linear system is solved based on an initial guess. User must supplied a residual function for the non-linear system and a function representing the weak solution. Generally, this method is less efficient than Newton methods, but is significantly cheaper.

### 5.34.2 Member Data Documentation

#### 5.34.2.1 int PICARD\_DATA::maxit = 0

Maximum allowable iterations - default = min(3\*vec\_size,1000)

#### 5.34.2.2 int PICARD\_DATA::iter = 0

Actual number of iterations.

#### 5.34.2.3 double PICARD\_DATA::tol\_rel = 1e-6

Relative tolerance for convergence - default = 1e-6.



## 5.34.2.4 double PICARD\_DATA::tol\_abs = 1e-6

Absolution tolerance for convergence - default = 1e-6.

## 5.34.2.5 double PICARD\_DATA::res

Residual norm of the iterate.

## 5.34.2.6 double PICARD\_DATA::relres

Relative residual norm of the iterate.

## 5.34.2.7 double PICARD\_DATA::relres\_base

Initial residual norm.

## 5.34.2.8 double PICARD\_DATA::bestres

Best found residual norm.

## 5.34.2.9 bool PICARD\_DATA::Output = true

True = print messages to console.

## 5.34.2.10 Matrix&lt;double&gt; PICARD\_DATA::x0

Previous iterate solution vector.

## 5.34.2.11 Matrix&lt;double&gt; PICARD\_DATA::bestx

Best found solution vector.

## 5.34.2.12 Matrix&lt;double&gt; PICARD\_DATA::r

Residual of the non-linear system.

The documentation for this struct was generated from the following file:

- [lark.h](#)

## 5.35 PJFNK\_DATA Struct Reference

Data structure for the implementation of the PJFNK algorithm for non-linear systems.

```
#include <lark.h>
```

## Public Attributes

- int [nl\\_iter](#) = 0  
*Number of non-linear iterations.*
- int [l\\_iter](#) = 0  
*Number of linear iterations.*
- int [fun\\_call](#) = 0  
*Actual number of function calls made.*
- int [nl\\_maxit](#) = 0  
*Maximum allowable non-linear steps.*
- int [linear\\_solver](#) = -1  
*Flag to denote which linear solver to use - default = PJFNK Chooses.*

- double [nl\\_tol\\_abs](#) = 1e-6  
*Absolute Convergence tolerance for non-linear system - default = 1e-6.*
- double [nl\\_tol\\_rel](#) = 1e-6  
*Relative Convergence tol for the non-linear system - default = 1e-6.*
- double [lin\\_tol\\_rel](#) = 1e-6  
*Relative tolerance of the linear solver - default = 1e-6.*
- double [lin\\_tol\\_abs](#) = 1e-6  
*Absolute tolerance of the linear solver - default = 1e-6.*
- double [nl\\_res](#)  
*Absolute redidual norm for the non-linear system.*
- double [nl\\_relres](#)  
*Relative residual for the non-linear system.*
- double [nl\\_res\\_base](#)  
*Initial residual norm for the non-linear system.*
- double [nl\\_bestres](#)  
*Best found residual norm.*
- double [eps](#) = sqrt(DBL\_EPSILON)  
*Value of epsilon used jacvec - default = sqrt(DBL\_EPSILON)*
- bool [NL\\_Output](#) = true  
*True = print PJFNK messages to console.*
- bool [L\\_Output](#) = false  
*True = print Linear messages to console.*
- bool [LineSearch](#) = false  
*True = use Backtracking Linesearch for global convergence.*
- bool [Bounce](#) = false  
*True = allow Linesearch to go outside local well, False = Strict local convergence.*
- [Matrix](#)< double > [F](#)  
*Stored fuction evaluation at x (also the residual)*
- [Matrix](#)< double > [Fv](#)  
*Stored function evaluation at x+eps\*v.*
- [Matrix](#)< double > [v](#)  
*Stored vector of x+eps\*v.*
- [Matrix](#)< double > [x](#)  
*Current solution vector for the non-linear system.*
- [Matrix](#)< double > [bestx](#)  
*Best found solution vector to the non-linear system.*
- [GMRESLP\\_DATA](#) [gmreslp\\_dat](#)  
*Data structure for the GMRESLP method.*
- [PCG\\_DATA](#) [pcg\\_dat](#)  
*Data structure for the PCG method.*
- [BiCGSTAB\\_DATA](#) [bicgstab\\_dat](#)  
*Data structure for the BiCGSTAB method.*
- [CGS\\_DATA](#) [cgs\\_dat](#)  
*Data structure for the CGS method.*
- [GMRESRP\\_DATA](#) [gmresrp\\_dat](#)  
*Data structure for the GMRESRP method.*
- [GCR\\_DATA](#) [gcr\\_dat](#)  
*Data structure for the GCR method.*
- [GMRESR\\_DATA](#) [gmresr\\_dat](#)  
*Data structure for the GMRESR method.*
- [KMS\\_DATA](#) [kms\\_dat](#)

*Data structure for the KMS method.*

- [BACKTRACK\\_DATA](#) `backtrack_dat`

*Data structure for the Backtracking Linesearch algorithm.*

- `const void *` [res\\_data](#)

*Data structure pointer for user's residual data.*

- `const void *` [precon\\_data](#)

*Data structure pointer for user's preconditioning data.*

- `int(* funeval )(const Matrix< double > &x, Matrix< double > &F, const void *res\_data)`

*Function pointer for the user's function  $F(x)$  using there data.*

- `int(* precon )(const Matrix< double > &r, Matrix< double > &p, const void *precon\_data)`

*Function pointer for the user's preconditioning function for the linear system.*

### 5.35.1 Detailed Description

Data structure for the implementation of the PJFNK algorithm for non-linear systems.

C-style object to be used in conjunction with the Preconditioned Jacobian-Free Newton-Krylov (PJFNK) method for solving a non-linear system of equations. You can use any of the Krylov methods listed in the `krylov_method` enum to solve the linear sub-problem. When FOM is specified as the Krylov method, this algorithm becomes equivalent to an exact Newton method. If no Krylov method is specified, then the algorithm will try to pick a method based on the problem size and availability of preconditioning.

### 5.35.2 Member Data Documentation

#### 5.35.2.1 `int PJFNK_DATA::nl_iter = 0`

Number of non-linear iterations.

#### 5.35.2.2 `int PJFNK_DATA::l_iter = 0`

Number of linear iterations.

#### 5.35.2.3 `int PJFNK_DATA::fun_call = 0`

Actual number of function calls made.

#### 5.35.2.4 `int PJFNK_DATA::nl_maxit = 0`

Maximum allowable non-linear steps.

#### 5.35.2.5 `int PJFNK_DATA::linear_solver = -1`

Flag to denote which linear solver to use - default = PJFNK Chooses.

#### 5.35.2.6 `double PJFNK_DATA::nl_tol_abs = 1e-6`

Absolute Convergence tolerance for non-linear system - default = 1e-6.

#### 5.35.2.7 `double PJFNK_DATA::nl_tol_rel = 1e-6`

Relative Convergence tol for the non-linear system - default = 1e-6.

#### 5.35.2.8 `double PJFNK_DATA::lin_tol_rel = 1e-6`

Relative tolerance of the linear solver - default = 1e-6.

#### 5.35.2.9 `double PJFNK_DATA::lin_tol_abs = 1e-6`

Absolute tolerance of the linear solver - default = 1e-6.

5.35.2.10 double PJFNK\_DATA::nl\_res

Absolute residual norm for the non-linear system.

5.35.2.11 double PJFNK\_DATA::nl\_relres

Relative residual for the non-linear system.

5.35.2.12 double PJFNK\_DATA::nl\_res\_base

Initial residual norm for the non-linear system.

5.35.2.13 double PJFNK\_DATA::nl\_bestres

Best found residual norm.

5.35.2.14 double PJFNK\_DATA::eps = sqrt(DBL\_EPSILON)

Value of epsilon used jacvec - default = sqrt(DBL\_EPSILON)

5.35.2.15 bool PJFNK\_DATA::NL\_Output = true

True = print PJFNK messages to console.

5.35.2.16 bool PJFNK\_DATA::L\_Output = false

True = print Linear messages to console.

5.35.2.17 bool PJFNK\_DATA::LineSearch = false

True = use Backtracking Linesearch for global convergence.

5.35.2.18 bool PJFNK\_DATA::Bounce = false

True = allow Linesearch to go outside local well, False = Strict local convergence.

5.35.2.19 Matrix<double> PJFNK\_DATA::F

Stored function evaluation at x (also the residual)

5.35.2.20 Matrix<double> PJFNK\_DATA::Fv

Stored function evaluation at  $x + \text{eps} * v$ .

5.35.2.21 Matrix<double> PJFNK\_DATA::v

Stored vector of  $x + \text{eps} * v$ .

5.35.2.22 Matrix<double> PJFNK\_DATA::x

Current solution vector for the non-linear system.

5.35.2.23 Matrix<double> PJFNK\_DATA::bestx

Best found solution vector to the non-linear system.

5.35.2.24 GMRESLP\_DATA PJFNK\_DATA::gmreslp\_dat

Data structure for the GMRESLP method.

**5.35.2.25 PCG\_DATA PJFNK\_DATA::pcg\_dat**

Data structure for the PCG method.

**5.35.2.26 BiCGSTAB\_DATA PJFNK\_DATA::bicgstab\_dat**

Data structure for the BiCGSTAB method.

**5.35.2.27 CGS\_DATA PJFNK\_DATA::cgs\_dat**

Data structure for the CGS method.

**5.35.2.28 GMRESRP\_DATA PJFNK\_DATA::gmresrp\_dat**

Data structure for the GMRESRP method.

**5.35.2.29 GCR\_DATA PJFNK\_DATA::gcr\_dat**

Data structure for the GCR method.

**5.35.2.30 GMRESR\_DATA PJFNK\_DATA::gmresr\_dat**

Data structure for the GMRESR method.

**5.35.2.31 KMS\_DATA PJFNK\_DATA::kms\_dat**

Data structure for the KMS method.

**5.35.2.32 BACKTRACK\_DATA PJFNK\_DATA::backtrack\_dat**

Data structure for the Backtracking Linesearch algorithm.

**5.35.2.33 const void\* PJFNK\_DATA::res\_data**

Data structure pointer for user's residual data.

**5.35.2.34 const void\* PJFNK\_DATA::precon\_data**

Data structure pointer for user's preconditioning data.

**5.35.2.35 int(\* PJFNK\_DATA::funeval)(const Matrix< double > &x, Matrix< double > &F, const void \*res\_data)**

Function pointer for the user's function F(x) using there data.

**5.35.2.36 int(\* PJFNK\_DATA::precon)(const Matrix< double > &r, Matrix< double > &p, const void \*precon\_data)**

Function pointer for the user's preconditioning function for the linear system.

The documentation for this struct was generated from the following file:

- [lark.h](#)

**5.36 PURE\_GAS Struct Reference**

Data structure holding all the parameters for each pure gas spieces.

```
#include <egret.h>
```

**Public Attributes**

- double [molecular\\_weight](#)

- Given: molecular weights (g/mol)
- double [Sutherland\\_Temp](#)
- Given: Sutherland's Reference Temperature (K)
- double [Sutherland\\_Const](#)
- Given: Sutherland's Constant (K)
- double [Sutherland\\_Viscosity](#)
- Given: Sutherland's Reference Viscosity (g/cm/s)
- double [specific\\_heat](#)
- Given: Specific heat of the gas (J/g/K)
- double [molecular\\_diffusion](#)
- Calculated: molecular diffusivities (cm<sup>2</sup>/s)
- double [dynamic\\_viscosity](#)
- Calculated: dynamic viscosities (g/cm/s)
- double [density](#)
- Calculated: gas densities (g/cm<sup>3</sup>) {use RE3}.
- double [Schmidt](#)
- Calculated: Value of the Schmidt number (-)

#### 5.36.1 Detailed Description

Data structure holding all the parameters for each pure gas species.

C-style object that holds the constants and parameters associated with each pure gas species in the overall mixture. This information is used in conjunction with the kinetic theory of gases to produce approximations to many different gas properties needed in simulating gas dynamics, mobility of a gas through porous media, as well as some kinetic adsorption parameters such as diffusivities.

#### 5.36.2 Member Data Documentation

##### 5.36.2.1 double PURE\_GAS::molecular\_weight

Given: molecular weights (g/mol)

##### 5.36.2.2 double PURE\_GAS::Sutherland\_Temp

Given: Sutherland's Reference Temperature (K)

##### 5.36.2.3 double PURE\_GAS::Sutherland\_Const

Given: Sutherland's Constant (K)

##### 5.36.2.4 double PURE\_GAS::Sutherland\_Viscosity

Given: Sutherland's Reference Viscosity (g/cm/s)

##### 5.36.2.5 double PURE\_GAS::specific\_heat

Given: Specific heat of the gas (J/g/K)

##### 5.36.2.6 double PURE\_GAS::molecular\_diffusion

Calculated: molecular diffusivities (cm<sup>2</sup>/s)

##### 5.36.2.7 double PURE\_GAS::dynamic\_viscosity

Calculated: dynamic viscosities (g/cm/s)

## 5.36.2.8 double PURE\_GAS::density

Calculated: gas densities (g/cm<sup>3</sup>) {use RE3}.

## 5.36.2.9 double PURE\_GAS::Schmidt

Calculated: Value of the Schmidt number (-)

The documentation for this struct was generated from the following file:

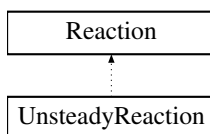
- [egret.h](#)

## 5.37 Reaction Class Reference

[Reaction](#) Object.

```
#include <shark.h>
```

Inheritance diagram for Reaction:



## Public Member Functions

- [Reaction](#) ()  
*Default constructor.*
- [~Reaction](#) ()  
*Default destructor.*
- void [Initialize\\_Object](#) (MasterSpeciesList &List)  
*Function to initialize the [Reaction](#) object from the [MasterSpeciesList](#).*
- void [Display\\_Info](#) ()  
*Display the reaction information.*
- void [Set\\_Stoichiometric](#) (int i, double v)  
*Set the ith stoichiometric value.*
- void [Set\\_Equilibrium](#) (double logK)  
*Set the equilibrium constant in log(K) units.*
- void [Set\\_Enthalpy](#) (double H)  
*Set the enthalpy of the reaction (J/mol)*
- void [Set\\_Entropy](#) (double S)  
*Set the entropy of the reaction (J/K/mol)*
- void [Set\\_EnthalpyANDEntropy](#) (double H, double S)  
*Set both the enthalpy and entropy (J/mol) & (J/K/mol)*
- void [Set\\_Energy](#) (double G)  
*Set the Gibb's free energy of reaction (J/mol)*
- void [checkSpeciesEnergies](#) ()  
*Function to check MasterList Reference for species energy info.*
- void [calculateEnergies](#) ()
- void [calculateEquilibrium](#) (double T)  
*Function to calculate the equilibrium constant based on temperature in K.*
- bool [haveEquilibrium](#) ()

*Function to return true if equilibrium constant is given or can be calculated.*

- double [Get\\_Stoichiometric](#) (int i)  
*Fetch the ith stoichiometric value.*
- double [Get\\_Equilibrium](#) ()  
*Fetch the equilibrium constant (logK)*
- double [Get\\_Enthalpy](#) ()  
*Fetch the enthalpy of the reaction (J/mol)*
- double [Get\\_Entropy](#) ()  
*Fetch the entropy of the reaction (J/K/mol)*
- double [Get\\_Energy](#) ()  
*Fetch the energy of the reaction (J/mol)*
- double [Eval\\_Residual](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama)

#### Protected Attributes

- [MasterSpeciesList](#) \* [List](#)  
*Pointer to a master species object.*
- std::vector< double > [Stoichiometric](#)  
*Vector of stoichiometric constants corresponding to species list.*
- double [Equilibrium](#)  
*Equilibrium constant for the reaction (logK)*
- double [enthalpy](#)  
*Reaction enthalpy (J/mol)*
- double [entropy](#)  
*Reaction entropy (J/K/mol)*
- double [energy](#)  
*Gibb's Free energy of reaction (J/mol)*
- bool [CanCalcHS](#)  
*True if all molecular info is available to calculate dH and dS.*
- bool [CanCalcG](#)  
*True if all molecular info is available to calculate dG.*
- bool [HaveHS](#)  
*True if dH and dS is given, or can be calculated.*
- bool [HaveG](#)  
*True if dG is given, or can be calculated.*
- bool [HaveEquil](#)  
*True as long as Equilibrium is given, or can be calculated.*

#### 5.37.1 Detailed Description

[Reaction](#) Object.

C++ style object that holds data and functions associated with standard chemical reactions...

i.e.,  $aA + bB \rightleftharpoons cC + dD$

These reactions are assumed steady state and are characterized by stoichiometry coefficients and equilibrium/stability constants. Types of reactions that these are valid for would be acid/base reactions, metal-ligand complexation reactions, oxidation-reduction reactions, Henry's Law phase changes, and more. Reactions that this may not be suitable for include mechanisms, adsorption, and precipitation. Those types of reactions would be better handled by more specific objects that inherit from this object.

If all species in the reaction are registered and known species in [mola.h](#) AND have known formation energies, then the equilibrium constants for that particular reaction will be calculated based on the species involved in the reaction. However, if using some custom molecule objects, then the reaction equilibrium may not be able to be automatically formed by the routine. In this case, you would need to also supply the equilibrium constant for the particular reaction.



## 5.37.2 Constructor &amp; Destructor Documentation

## 5.37.2.1 Reaction::Reaction ( )

Default constructor.

## 5.37.2.2 Reaction::~~Reaction ( )

Default destructor.

## 5.37.3 Member Function Documentation

## 5.37.3.1 void Reaction::Initialize\_Object ( MasterSpeciesList &amp; List )

Function to initialize the [Reaction](#) object from the [MasterSpeciesList](#).

## 5.37.3.2 void Reaction::Display\_Info ( )

Display the reaction information.

5.37.3.3 void Reaction::Set\_Stoichiometric ( int *i*, double *v* )

Set the *i*th stoichiometric value.

This function will set the stoichiometric constant of the *i*th species in the master list to the given value of *v*. All values of *v* are set to zero unless overridden by this function.

## Parameters

<i>i</i>	index of the species in the <a href="#">MasterSpeciesList</a>
<i>v</i>	value of the stoichiometric constant for that species in the reaction

5.37.3.4 void Reaction::Set\_Equilibrium ( double *logK* )

Set the equilibrium constant in log(*K*) units.

5.37.3.5 void Reaction::Set\_Enthalpy ( double *H* )

Set the enthalpy of the reaction (J/mol)

5.37.3.6 void Reaction::Set\_Entropy ( double *S* )

Set the entropy of the reaction (J/K/mol)

5.37.3.7 void Reaction::Set\_EnthalpyANDEntropy ( double *H*, double *S* )

Set both the enthalpy and entropy (J/mol) & (J/K/mol)

5.37.3.8 void Reaction::Set\_Energy ( double *G* )

Set the Gibb's free energy of reaction (J/mol)

## 5.37.3.9 void Reaction::checkSpeciesEnergies ( )

Function to check MasterList Reference for species energy info.

This function will go through the stoichiometry of this reaction and check the molecules in the [MasterSpeciesList](#) that correspond to the species present in this reaction for the existence of their formation energies. Based on the states of those energies, it will note internally whether or not it can determine the equilibrium constants based solely on individual species information. If it cannot, then the user must provide either the reaction energies to form the equilibrium constant or the equilibrium constant itself. Function to calculate and set the energy of the reaction

**5.37.3.10 void Reaction::calculateEnergies ( )**

If the energies of the reaction can be determined from the individual species in the reaction, then this function uses that information. Otherwise, it sets the energies equal to the constants given to the object by the user.

**5.37.3.11 void Reaction::calculateEquilibrium ( double *T* )**

Function to calculate the equilibrium constant based on temperature in K.

**5.37.3.12 bool Reaction::haveEquilibrium ( )**

Function to return true if equilibrium constant is given or can be calculated.

**5.37.3.13 double Reaction::Get\_Stoichiometric ( int *i* )**

Fetch the *i*th stoichiometric value.

**5.37.3.14 double Reaction::Get\_Equilibrium ( )**

Fetch the equilibrium constant (logK)

**5.37.3.15 double Reaction::Get\_Enthalpy ( )**

Fetch the enthalpy of the reaction (J/mol)

**5.37.3.16 double Reaction::Get\_Entropy ( )**

Fetch the entropy of the reaction (J/K/mol)

**5.37.3.17 double Reaction::Get\_Energy ( )**

Fetch the energy of the reaction (J/mol)

Evaluate a residual for the reaction given variable  $x=\log(C)$  and activity coefficients *gama*

**5.37.3.18 double Reaction::Eval\_Residual ( const Matrix< double > & *x*, const Matrix< double > & *gama* )**

This function will calculate the reaction residual from this object's stoichiometry, equilibrium constant,  $\log(C)$  concentrations, and activity coefficients.

**Parameters**

<i>x</i>	matrix of the $\log(C)$ concentration values at the current non-linear step
<i>gama</i>	matrix of activity coefficients for each species at the current non-linear step

**5.37.4 Member Data Documentation****5.37.4.1 MasterSpeciesList\* Reaction::List [protected]**

Pointer to a master species object.

**5.37.4.2 std::vector<double> Reaction::Stoichiometric [protected]**

Vector of stoichiometric constants corresponding to species list.

**5.37.4.3 double Reaction::Equilibrium [protected]**

Equilibrium constant for the reaction (logK)

**5.37.4.4 double Reaction::enthalpy [protected]**

[Reaction](#) enthalpy (J/mol)

5.37.4.5 double Reaction::entropy [protected]

Reaction entropy (J/K/mol)

5.37.4.6 double Reaction::energy [protected]

Gibb's Free energy of reaction (J/mol)

5.37.4.7 bool Reaction::CanCalcHS [protected]

True if all molecular info is available to calculate dH and dS.

5.37.4.8 bool Reaction::CanCalcG [protected]

True if all molecular info is available to calculate dG.

5.37.4.9 bool Reaction::HaveHS [protected]

True if dH and dS is given, or can be calculated.

5.37.4.10 bool Reaction::HaveG [protected]

True if dG is given, or can be calculated.

5.37.4.11 bool Reaction::HaveEquil [protected]

True as long as Equilibrium is given, or can be calculated.

The documentation for this class was generated from the following file:

- [shark.h](#)

## 5.38 SCOPSOWL\_DATA Struct Reference

Primary data structure for SCOPSOWL simulations.

```
#include <scopsowl.h>
```

### Public Attributes

- unsigned long int [total\\_steps](#)  
*Running total of all calculation steps.*
- int [coord\\_macro](#)  
*Coordinate system for large pellet.*
- int [coord\\_micro](#)  
*Coordinate system for small crystal (if any)*
- int [level](#) = 2  
*Level of coupling between the different scales (default = 2)*
- double [sim\\_time](#)  
*Stopping time for the simulation (hrs)*
- double [t\\_old](#)  
*Old time of the simulations (hrs)*
- double [t](#)  
*Current time of the simulations (hrs)*
- double [t\\_counter](#) = 0.0  
*Counter for the time output.*
- double [t\\_print](#)

- Print output at every t\_print time (hrs)*
- bool `Print2File` = true  
*True = results to .txt; False = no printing.*
  - bool `Print2Console` = true  
*True = results to console; False = no printing.*
  - bool `SurfDiff` = true  
*True = includes SKUA simulation if Heterogeneous; False = only uses MAGPIE.*
  - bool `Heterogeneous` = true  
*True = pellet is made of binder and crystals, False = all one phase.*
  - double `gas_velocity`  
*Superficial Gas Velocity around pellet (cm/s)*
  - double `total_pressure`  
*Gas phase total pressure (kPa)*
  - double `gas_temperature`  
*Gas phase temperature (K)*
  - double `pellet_radius`  
*Nominal radius of the pellet - macroscale domain (cm)*
  - double `crystal_radius`  
*Nominal radius of the crystal - microscale domain (um)*
  - double `char_macro`  
*Characteristic size for macro scale (cm or cm<sup>2</sup>) - only if pellet is not spherical.*
  - double `char_micro`  
*Characteristic size for micro scale (um or um<sup>2</sup>) - only if crystal is not spherical.*
  - double `binder_fraction`  
*Volume of binder per total volume of pellet (-)*
  - double `binder_porosity`  
*Volume of pores per volume of binder (-)*
  - double `binder_poresize`  
*Nominal radius of the binder pores (cm)*
  - double `pellet_density`  
*Mass of the pellet per volume of pellet (kg/L)*
  - bool `DirichletBC` = false  
*True = Dirichlet BC; False = Neumann BC.*
  - bool `NonLinear` = true  
*True = Non-linear solver; False = Linear solver.*
  - std::vector< double > `y`  
*Outside mole fractions of each component (-)*
  - std::vector< double > `tempy`  
*Temporary place holder for gas mole fractions in other locations (-)*
  - FILE \* `OutputFile`  
*Output file pointer to the output file for postprocesses.*
  - double(\* `eval_ads`)(int i, int l, const void \*`user_data`)  
*Function pointer for evaluating adsorption (mol/kg)*
  - double(\* `eval_retard`)(int i, int l, const void \*`user_data`)  
*Function pointer for evaluating retardation (-)*
  - double(\* `eval_diff`)(int i, int l, const void \*`user_data`)  
*Function pointer for evaluating pore diffusion (cm<sup>2</sup>/hr)*
  - double(\* `eval_surfDiff`)(int i, int l, const void \*`user_data`)  
*Function pointer for evaluating surface diffusion (um<sup>2</sup>/hr)*
  - double(\* `eval_kf`)(int i, const void \*`user_data`)  
*Function pointer for evaluating film mass transfer (cm/hr)*

- const void \* [user\\_data](#)  
*Data structure for users info to calculate parameters.*
- [MIXED\\_GAS](#) \* [gas\\_dat](#)  
*Pointer to the [MIXED\\_GAS](#) data structure (may or may not be used)*
- [MAGPIE\\_DATA](#) [magpie\\_dat](#)  
*Data structure for a magpie problem (to be used if not using skua)*
- std::vector< [FINCH\\_DATA](#) > [finch\\_dat](#)  
*Data structure for pore adsorption kinetics for all species (u in mol/L)*
- std::vector< [SCOPSOWL\\_PARAM\\_DATA](#) > [param\\_dat](#)  
*Data structure for parameter info for all species.*
- std::vector< [SKUA\\_DATA](#) > [skua\\_dat](#)  
*Data structure holding a skua object for all nodes (each skua has an object for each species)*

### 5.38.1 Detailed Description

Primary data structure for SCOPSOWL simulations.

C-style object holding necessary information to run a SCOPSOWL simulation. SCOPSOWL is a multi-scale problem involving PDE solution for the macro-scale adsorbent pellet and the micro-scale adsorbent crystals. As such, each SCOPSOWL simulation involves multiple SKUA simulations at the nodes in the macro-scale domain. Alternatively, if the user wishes to specify that the adsorbent is homogeneous, then you can run SCOPSOWL as a single-scale problem. Additionally, you can simplify the model by assuming that the micro-scale diffusion is very fast, and therefore replace each SKUA simulation with a simpler MAGPIE evaluation. Details on running SCOPSOWL with the various options will be discussed in the SCOPSOWL\_SCENARIOS function.

### 5.38.2 Member Data Documentation

#### 5.38.2.1 unsigned long int SCOPSOWL\_DATA::total\_steps

Running total of all calculation steps.

#### 5.38.2.2 int SCOPSOWL\_DATA::coord\_macro

Coordinate system for large pellet.

#### 5.38.2.3 int SCOPSOWL\_DATA::coord\_micro

Coordinate system for small crystal (if any)

#### 5.38.2.4 int SCOPSOWL\_DATA::level = 2

Level of coupling between the different scales (default = 2)

#### 5.38.2.5 double SCOPSOWL\_DATA::sim\_time

Stopping time for the simulation (hrs)

#### 5.38.2.6 double SCOPSOWL\_DATA::t\_old

Old time of the simulations (hrs)

#### 5.38.2.7 double SCOPSOWL\_DATA::t

Current time of the simulations (hrs)

#### 5.38.2.8 double SCOPSOWL\_DATA::t\_counter = 0.0

Counter for the time output.

5.38.2.9 double SCOPSOWL\_DATA::t\_print

Print output at every t\_print time (hrs)

5.38.2.10 bool SCOPSOWL\_DATA::Print2File = true

True = results to .txt; False = no printing.

5.38.2.11 bool SCOPSOWL\_DATA::Print2Console = true

True = results to console; False = no printing.

5.38.2.12 bool SCOPSOWL\_DATA::SurfDiff = true

True = includes SKUA simulation if Heterogeneous; False = only uses MAGPIE.

5.38.2.13 bool SCOPSOWL\_DATA::Heterogeneous = true

True = pellet is made of binder and crystals, False = all one phase.

5.38.2.14 double SCOPSOWL\_DATA::gas\_velocity

Superficial Gas Velocity around pellet (cm/s)

5.38.2.15 double SCOPSOWL\_DATA::total\_pressure

Gas phase total pressure (kPa)

5.38.2.16 double SCOPSOWL\_DATA::gas\_temperature

Gas phase temperature (K)

5.38.2.17 double SCOPSOWL\_DATA::pellet\_radius

Nominal radius of the pellet - macroscale domain (cm)

5.38.2.18 double SCOPSOWL\_DATA::crystal\_radius

Nominal radius of the crystal - microscale domain (um)

5.38.2.19 double SCOPSOWL\_DATA::char\_macro

Characteristic size for macro scale (cm or  $\text{cm}^2$ ) - only if pellet is not spherical.

5.38.2.20 double SCOPSOWL\_DATA::char\_micro

Characteristic size for micro scale (um or  $\text{um}^2$ ) - only if crystal is not spherical.

5.38.2.21 double SCOPSOWL\_DATA::binder\_fraction

Volume of binder per total volume of pellet (-)

5.38.2.22 double SCOPSOWL\_DATA::binder\_porosity

Volume of pores per volume of binder (-)

5.38.2.23 double SCOPSOWL\_DATA::binder\_poresize

Nominal radius of the binder pores (cm)

5.38.2.24 `double SCOPSOWL_DATA::pellet_density`

Mass of the pellet per volume of pellet (kg/L)

5.38.2.25 `bool SCOPSOWL_DATA::DirichletBC = false`

True = Dirichlet BC; False = Neumann BC.

5.38.2.26 `bool SCOPSOWL_DATA::NonLinear = true`

True = Non-linear solver; False = Linear solver.

5.38.2.27 `std::vector<double> SCOPSOWL_DATA::y`

Outside mole fractions of each component (-)

5.38.2.28 `std::vector<double> SCOPSOWL_DATA::tempy`

Temporary place holder for gas mole fractions in other locations (-)

5.38.2.29 `FILE* SCOPSOWL_DATA::OutputFile`

Output file pointer to the output file for postprocesses.

5.38.2.30 `double(* SCOPSOWL_DATA::eval_ads)(int i, int l, const void *user_data)`

Function pointer for evaluating adsorption (mol/kg)

5.38.2.31 `double(* SCOPSOWL_DATA::eval_retard)(int i, int l, const void *user_data)`

Function pointer for evaluating retardation (-)

5.38.2.32 `double(* SCOPSOWL_DATA::eval_diff)(int i, int l, const void *user_data)`

Function pointer for evaluating pore diffusion ( $\text{cm}^2/\text{hr}$ )

5.38.2.33 `double(* SCOPSOWL_DATA::eval_surfDiff)(int i, int l, const void *user_data)`

Function pointer for evaluating surface diffusion ( $\text{um}^2/\text{hr}$ )

5.38.2.34 `double(* SCOPSOWL_DATA::eval_kf)(int i, const void *user_data)`

Function pointer for evaluating film mass transfer ( $\text{cm}/\text{hr}$ )

5.38.2.35 `const void* SCOPSOWL_DATA::user_data`

Data structure for users info to calculate parameters.

5.38.2.36 `MIXED_GAS* SCOPSOWL_DATA::gas_dat`

Pointer to the [MIXED\\_GAS](#) data structure (may or may not be used)

5.38.2.37 `MAGPIE_DATA SCOPSOWL_DATA::magpie_dat`

Data structure for a magpie problem (to be used if not using skua)

5.38.2.38 `std::vector<FINCH_DATA> SCOPSOWL_DATA::finch_dat`

Data structure for pore adsorption kinetics for all species (u in mol/L)

5.38.2.39 `std::vector<SCOPSOWL_PARAM_DATA> SCOPSOWL_DATA::param_dat`

Data structure for parameter info for all species.

5.38.2.40 `std::vector<SKUA_DATA> SCOPSOWL_DATA::skua_dat`

Data structure holding a skua object for all nodes (each skua has an object for each species)

The documentation for this struct was generated from the following file:

- [scopsowl.h](#)

## 5.39 SCOPSOWL\_OPT\_DATA Struct Reference

Data structure for the SCOPSOWL optimization routine.

```
#include <scopsowl_opt.h>
```

### Public Attributes

- int [num\\_curves](#)  
*Number of adsorption curves to analyze.*
- int [evaluation](#)  
*Number of times the eval function has been called for a single curve.*
- unsigned long int [total\\_eval](#)  
*Total number of evaluations needed for completion.*
- int [current\\_points](#)  
*Number of points in the current curve.*
- int [num\\_params](#) = 1  
*Number of adjustable parameters for the current curve (currently only supports 1)*
- int [diffusion\\_type](#)  
*Flag to identify type of diffusion function to use.*
- int [adsorb\\_index](#)  
*Component index for adsorbable species.*
- int [max\\_guess\\_iter](#) = 20  
*Maximum allowed guess iterations (default = 20)*
- bool [Optimize](#)  
*True = run optimization, False = run a comparison.*
- bool [Rough](#)  
*True = use only a rough estimate, False = run full optimization.*
- double [current\\_temp](#)  
*Temperature for current curve.*
- double [current\\_press](#)  
*Partial pressure for current curve.*
- double [current\\_equil](#)  
*Equilibrium data point for the current curve.*
- double [simulation\\_equil](#)  
*Equilibrium simulation point for the current curve.*
- double [max\\_bias](#)  
*Positive maximum bias plausible for fitting.*
- double [min\\_bias](#)  
*Negative minimum bias plausible for fitting.*
- double [e\\_norm](#)



- *Euclidean norm of current fit.*  
double [f\\_bias](#)
- *Function bias of current fit.*  
double [e\\_norm\\_old](#)
- *Euclidean norm of the previous fit.*  
double [f\\_bias\\_old](#)
- *Function bias of the previous fit.*  
double [param\\_guess](#)
- *Parameter guess for the surface/crystal diffusivity.*  
double [param\\_guess\\_old](#)
- *Parameter guess for the previous curve.*  
double [rel\\_tol\\_norm](#) = 0.01
- *Tolerance for convergence of the guess norm.*  
double [abs\\_tol\\_bias](#) = 1.0
- *Tolerance for convergence of the guess bias.*  
std::vector< double > [y\\_base](#)
- *Gas phase mole fractions in absense of adsorbing species.*  
std::vector< double > [q\\_data](#)
- *Amount adsorbed at a particular point in current curve.*  
std::vector< double > [q\\_sim](#)
- *Amount adsorbed based on the simulation.*  
std::vector< double > [t](#)
- *Time points in the current curve.*  
FILE \* [ParamFile](#)
- *Output file for parameter results.*  
FILE \* [CompareFile](#)
- *Output file for comparison of results.*  
[SCOPSOWL\\_DATA owl\\_dat](#)
- *Data structure for the SCOPSOWL simulation.*

### 5.39.1 Detailed Description

Data structure for the SCOPSOWL optimization routine.

C-style object holding information about the optimization routine as well as the standard SCOPSOWL\_DATA structure for SCOPSOWL simulations.

### 5.39.2 Member Data Documentation

#### 5.39.2.1 int SCOPSOWL\_OPT\_DATA::num\_curves

Number of adsorption curves to analyze.

#### 5.39.2.2 int SCOPSOWL\_OPT\_DATA::evaluation

Number of times the eval function has been called for a single curve.

#### 5.39.2.3 unsigned long int SCOPSOWL\_OPT\_DATA::total\_eval

Total number of evaluations needed for completion.

#### 5.39.2.4 int SCOPSOWL\_OPT\_DATA::current\_points

Number of points in the current curve.

5.39.2.5 int SCOPSOWL\_OPT\_DATA::num\_params = 1

Number of adjustable parameters for the current curve (currently only supports 1)

5.39.2.6 int SCOPSOWL\_OPT\_DATA::diffusion\_type

Flag to identify type of diffusion function to use.

5.39.2.7 int SCOPSOWL\_OPT\_DATA::adsorb\_index

Component index for adsorbable species.

5.39.2.8 int SCOPSOWL\_OPT\_DATA::max\_guess\_iter = 20

Maximum allowed guess iterations (default = 20)

5.39.2.9 bool SCOPSOWL\_OPT\_DATA::Optimize

True = run optimization, False = run a comparison.

5.39.2.10 bool SCOPSOWL\_OPT\_DATA::Rough

True = use only a rough estimate, False = run full optimization.

5.39.2.11 double SCOPSOWL\_OPT\_DATA::current\_temp

Temperature for current curve.

5.39.2.12 double SCOPSOWL\_OPT\_DATA::current\_press

Partial pressure for current curve.

5.39.2.13 double SCOPSOWL\_OPT\_DATA::current\_equil

Equilibrium data point for the current curve.

5.39.2.14 double SCOPSOWL\_OPT\_DATA::simulation\_equil

Equilibrium simulation point for the current curve.

5.39.2.15 double SCOPSOWL\_OPT\_DATA::max\_bias

Positive maximum bias plausible for fitting.

5.39.2.16 double SCOPSOWL\_OPT\_DATA::min\_bias

Negative minimum bias plausible for fitting.

5.39.2.17 double SCOPSOWL\_OPT\_DATA::e\_norm

Euclidean norm of current fit.

5.39.2.18 double SCOPSOWL\_OPT\_DATA::f\_bias

Function bias of current fit.

5.39.2.19 double SCOPSOWL\_OPT\_DATA::e\_norm\_old

Euclidean norm of the previous fit.

5.39.2.20 double SCOPSOWL\_OPT\_DATA::f\_bias\_old

Function bias of the previous fit.

5.39.2.21 double SCOPSOWL\_OPT\_DATA::param\_guess

Parameter guess for the surface/crystal diffusivity.

5.39.2.22 double SCOPSOWL\_OPT\_DATA::param\_guess\_old

Parameter guess for the previous curve.

5.39.2.23 double SCOPSOWL\_OPT\_DATA::rel\_tol\_norm = 0.01

Tolerance for convergence of the guess norm.

5.39.2.24 double SCOPSOWL\_OPT\_DATA::abs\_tol\_bias = 1.0

Tolerance for convergence of the guess bias.

5.39.2.25 std::vector<double> SCOPSOWL\_OPT\_DATA::y\_base

Gas phase mole fractions in absense of adsorbing species.

5.39.2.26 std::vector<double> SCOPSOWL\_OPT\_DATA::q\_data

Amount adsorbed at a particular point in current curve.

5.39.2.27 std::vector<double> SCOPSOWL\_OPT\_DATA::q\_sim

Amount adsorbed based on the simulation.

5.39.2.28 std::vector<double> SCOPSOWL\_OPT\_DATA::t

Time points in the current curve.

5.39.2.29 FILE\* SCOPSOWL\_OPT\_DATA::ParamFile

Output file for parameter results.

5.39.2.30 FILE\* SCOPSOWL\_OPT\_DATA::CompareFile

Output file for comparison of results.

5.39.2.31 SCOPSOWL\_DATA SCOPSOWL\_OPT\_DATA::owl\_dat

Data structure for the SCOPSOWL simulation.

The documentation for this struct was generated from the following file:

- [scopsowl\\_opt.h](#)

## 5.40 SCOPSOWL\_PARAM\_DATA Struct Reference

Data structure for the species' parameters in SCOPSOWL.

```
#include <scopsowl.h>
```

### Public Attributes

- [Matrix< double > qAvg](#)

- Average adsorbed amount for a species at each node (mol/kg)*

  - `Matrix`< double > `qAvg_old`

*Old Average adsorbed amount for a species at each node (mol/kg)*
- `Matrix`< double > `Qst`

*Heat of adsorption for all nodes (J/mol)*
- `Matrix`< double > `Qst_old`

*Old Heat of adsorption for all nodes (J/mol)*
- `Matrix`< double > `dq_dc`

*Storage vector for current adsorption slope/strength (dq/dc) (L/kg)*
- double `xIC`

*Initial conditions for adsorbed molefractions.*
- double `qIntegralAvg`

*Integral average of adsorption over the entire pellet (mol/kg)*
- double `qIntegralAvg_old`

*Old Integral average of adsorption over the entire pellet (mol/kg)*
- double `QstAvg`

*Integral average heat of adsorption (J/mol)*
- double `QstAvg_old`

*Old integral average heat of adsorption (J/mol)*
- double `qo`

*Boundary value of adsorption if using Dirichlet BCs (mol/kg)*
- double `Qsto`

*Boundary value of adsorption heat if using Dirichlet BCs (J/mol)*
- double `dq_dco`

*Boundary value of adsorption slope for Dirichlet BCs (L/kg)*
- double `pore_diffusion`

*Value for constant pore diffusion (cm<sup>2</sup>/hr)*
- double `film_transfer`

*Value for constant film mass transfer (cm/hr)*
- double `activation_energy`

*Activation energy for surface diffusion (J/mol)*
- double `ref_diffusion`

*Reference state surface diffusivity (um<sup>2</sup>/hr)*
- double `ref_temperature`

*Reference temperature for empirical adjustments (K)*
- double `affinity`

*Affinity parameter used in empirical adjustments (-)*
- double `ref_pressure`
- bool `Adsorbable`

*True = species can adsorb; False = species cannot adsorb.*
- std::string `speciesName`

*String to hold the name of each species.*

#### 5.40.1 Detailed Description

Data structure for the species' parameters in SCOPSOWL.

C-style object that holds information on all species for a particular SCOPSOWL simulation. Initial conditions, kinetic parameters, and interim matrix objects are stored here for use in various SCOPSOWL functions.

#### 5.40.2 Member Data Documentation

##### 5.40.2.1 Matrix<double> SCOPSOWL\_PARAM\_DATA::qAvg

Average adsorbed amount for a species at each node (mol/kg)

##### 5.40.2.2 Matrix<double> SCOPSOWL\_PARAM\_DATA::qAvg\_old

Old Average adsorbed amount for a species at each node (mol/kg)

##### 5.40.2.3 Matrix<double> SCOPSOWL\_PARAM\_DATA::Qst

Heat of adsorption for all nodes (J/mol)

##### 5.40.2.4 Matrix<double> SCOPSOWL\_PARAM\_DATA::Qst\_old

Old Heat of adsorption for all nodes (J/mol)

##### 5.40.2.5 Matrix<double> SCOPSOWL\_PARAM\_DATA::dq\_dc

Storage vector for current adsorption slope/strength (dq/dc) (L/kg)

##### 5.40.2.6 double SCOPSOWL\_PARAM\_DATA::xIC

Initial conditions for adsorbed molefractions.

##### 5.40.2.7 double SCOPSOWL\_PARAM\_DATA::qIntegralAvg

Integral average of adsorption over the entire pellet (mol/kg)

##### 5.40.2.8 double SCOPSOWL\_PARAM\_DATA::qIntegralAvg\_old

Old Integral average of adsorption over the entire pellet (mol/kg)

##### 5.40.2.9 double SCOPSOWL\_PARAM\_DATA::QstAvg

Integral average heat of adsorption (J/mol)

##### 5.40.2.10 double SCOPSOWL\_PARAM\_DATA::QstAvg\_old

Old integral average heat of adsorption (J/mol)

##### 5.40.2.11 double SCOPSOWL\_PARAM\_DATA::qo

Boundary value of adsorption if using Dirichlet BCs (mol/kg)

##### 5.40.2.12 double SCOPSOWL\_PARAM\_DATA::Qsto

Boundary value of adsorption heat if using Dirichlet BCs (J/mol)

##### 5.40.2.13 double SCOPSOWL\_PARAM\_DATA::dq\_dco

Boundary value of adsorption slope for Dirichlet BCs (L/kg)

##### 5.40.2.14 double SCOPSOWL\_PARAM\_DATA::pore\_diffusion

Value for constant pore diffusion ( $\text{cm}^2/\text{hr}$ )

##### 5.40.2.15 double SCOPSOWL\_PARAM\_DATA::film\_transfer

Value for constant film mass transfer (cm/hr)

5.40.2.16 double SCOPSOWL\_PARAM\_DATA::activation\_energy

Activation energy for surface diffusion (J/mol)

5.40.2.17 double SCOPSOWL\_PARAM\_DATA::ref\_diffusion

Reference state surface diffusivity ( $\text{um}^2/\text{hr}$ )

5.40.2.18 double SCOPSOWL\_PARAM\_DATA::ref\_temperature

Reference temperature for empirical adjustments (K)

5.40.2.19 double SCOPSOWL\_PARAM\_DATA::affinity

Affinity parameter used in empirical adjustments (-)

5.40.2.20 double SCOPSOWL\_PARAM\_DATA::ref\_pressure

5.40.2.21 bool SCOPSOWL\_PARAM\_DATA::Adsorbable

True = species can adsorb; False = species cannot adsorb.

5.40.2.22 std::string SCOPSOWL\_PARAM\_DATA::speciesName

String to hold the name of each species.

The documentation for this struct was generated from the following file:

- [scopsowl.h](#)

## 5.41 SHARK\_DATA Struct Reference

Data structure for SHARK simulations.

```
#include <shark.h>
```

### Public Attributes

- [MasterSpeciesList](#) [MasterList](#)  
*Master List of species object.*
- std::vector< [Reaction](#) > [ReactionList](#)  
*Equilibrium reaction objects.*
- std::vector< [MassBalance](#) > [MassBalanceList](#)  
*Mass balance objects.*
- std::vector< [UnsteadyReaction](#) > [UnsteadyList](#)  
*Unsteady [Reaction](#) objects.*
- std::vector< [AdsorptionReaction](#) > [AdsorptionList](#)  
*Equilibrium Adsorption [Reaction](#) Objects.*
- std::vector< double(\*)(<const [Matrix](#)< double > &x, [SHARK\\_DATA](#) \*shark\_dat, const void \*data) > [OtherList](#)  
*Array of Other Residual functions to be defined by user.*
- int [numvar](#)  
*Total number of functions and species.*
- int [num\\_ssr](#)  
*Number of steady-state reactions.*

- int `num_mbe`  
*Number of mass balance equations.*
- int `num_usr` = 0  
*Number of unsteady-state reactions.*
- int `num_ssao` = 0  
*Number of steady-state adsorption objects.*
- std::vector< int > `num_ssar`  
*List of the numbers of reactions in each adsorption object.*
- std::vector< std::string > `ads_names`  
*List of the adsorbent object names.*
- int `num_other` = 0  
*Number of other functions to be used (default is always 0)*
- int `act_fun` = IDEAL  
*Flag denoting the activity function to use (default is IDEAL)*
- int `totalsteps` = 0  
*Total number of iterations.*
- int `totalcalls` = 0  
*Total number of residual function calls.*
- int `timesteps` = 0  
*Number of time steps taken to complete simulation.*
- int `pH_index` = -1  
*Contains the index of the pH variable (set internally)*
- int `pOH_index` = -1  
*Contains the index of the pOH variable (set internally)*
- double `simulationtime` = 0.0  
*Time to simulate unsteady reactions for (default = 0.0 hrs)*
- double `dt` = 0.1  
*Time step size (hrs)*
- double `dt_min` = sqrt(DBL\_EPSILON)  
*Minimum allowable step size.*
- double `t_out` = 0.0  
*Time increment by which file output is made (default = print all time steps)*
- double `t_count` = 0.0  
*Running count of time increments.*
- double `time` = 0.0  
*Current value of time (starts from t = 0.0 hrs)*
- double `time_old` = 0.0  
*Previous value of time (start from t = 0.0 hrs)*
- double `pH` = 7.0  
*Value of pH if needed (default = 7)*
- double `pH_step` = 0.5  
*Value by which to increment pH when doing a speciation curve (default = 0.5)*
- double `volume` = 1.0  
*Volume of the domain in liters (default = 1 L)*
- double `Norm` = 0.0  
*Current value of euclidean norm in solution.*
- double `dielectric_const` = 78.325  
*Dielectric constant used in many activity models (default: water = 78.325 (1/K))*
- double `relative_permittivity` = 80.1  
*Relative permittivity of the medium (default: water = 80.1 (-))*
- double `temperature` = 298.15

- Solution temperature (default = 25 oC or 298.15 K)*

  - bool `steadystate` = true  
*True = solve steady problem; False = solve transient problem.*
  - bool `TimeAdaptivity` = false  
*True = solve using variable time step.*
  - bool `const_pH` = false  
*True = set pH to a constant; False = solve for pH.*
  - bool `SpeciationCurve` = false  
*True = runs a series of constant pH steady-state problems to produce curves.*
  - bool `Console_Output` = true  
*True = display output to console.*
  - bool `File_Output` = false  
*True = write output to a file.*
  - bool `Contains_pH` = false  
*True = system contains pH as a variable (set internally)*
  - bool `Contains_pOH` = false  
*True = system contains pOH as a variable (set internally)*
  - bool `Converged` = false  
*True = system converged within tolerance.*
  - bool `LocalMin` = true  
*True = allow the system to settle for a local minimum if tolerance not reached.*
  - `Matrix`< double > `X_old`  
*Solution vector for old time step - log(C)*
  - `Matrix`< double > `X_new`  
*Solution vector for current time step - log(C)*
  - `Matrix`< double > `Conc_old`  
*Concentration vector for old time step - 10<sup>x</sup>.*
  - `Matrix`< double > `Conc_new`  
*Concentration vector for current time step - 10<sup>x</sup>.*
  - `Matrix`< double > `activity_new`  
*Activity matrix for current time step.*
  - `Matrix`< double > `activity_old`  
*Activity matrix from prior time step.*
  - `int(* EvalActivity)(const Matrix< double > &x, Matrix< double > &F, const void *data)`  
*Function pointer to evaluate activity coefficients.*
  - `int(* Residual)(const Matrix< double > &x, Matrix< double > &F, const void *data)`  
*Function pointer to evaluate all residuals in the system.*
  - `int(* lin_precon)(const Matrix< double > &r, Matrix< double > &p, const void *data)`  
*Function pointer to form a linear preconditioning operation for the Jacobian.*
  - `PJFNK_DATA Newton_data`  
*Data structure for the Newton-Krylov solver (see [lark.h](#))*
  - `const void * activity_data`  
*User defined data structure for an activity model.*
  - `const void * residual_data`  
*User defined data structure for the residual function.*
  - `const void * precon_data`  
*User defined data structure for preconditioning.*
  - `const void * other_data`  
*User define data structure used for user defined residuals.*
  - `FILE * OutputFile`  
*Output File pointer.*
  - `yaml_cpp_class yaml_object`  
*yaml object to read and access digitized yaml documents (see [yaml\\_wrapper.h](#))*



## 5.41.1 Detailed Description

Data structure for SHARK simulations.

C-style object holding data and function pointers associated with solving aqueous speciation and reaction kinetics. This object couples all other objects available in [shark.h](#) in order to provide residual calculations for each individual function that makes up the overall system model. Those residuals are brought together inside the residual function and fed into the [lark.h](#) PJFNK solver routine. That solver then attempts to find a solution to all non-linear variables simultaneously. Any function or data pointers in this structure can be overridden to change how you interface with and solve the problem. Users may also provide a set of custom residual functions through the "OtherList" vector object. Those residual function must all have the same format.

## 5.41.2 Member Data Documentation

## 5.41.2.1 MasterSpeciesList SHARK\_DATA::MasterList

Master List of species object.

## 5.41.2.2 std::vector&lt;Reaction&gt; SHARK\_DATA::ReactionList

Equilibrium reaction objects.

## 5.41.2.3 std::vector&lt;MassBalance&gt; SHARK\_DATA::MassBalanceList

Mass balance objects.

## 5.41.2.4 std::vector&lt;UnsteadyReaction&gt; SHARK\_DATA::UnsteadyList

Unsteady [Reaction](#) objects.

## 5.41.2.5 std::vector&lt;AdsorptionReaction&gt; SHARK\_DATA::AdsorptionList

Equilibrium Adsorption [Reaction](#) Objects.

## 5.41.2.6 std::vector&lt; double (\*) (const Matrix&lt;double&gt; &amp;x, SHARK\_DATA \*shark\_dat, const void \*data) &gt; SHARK\_DATA::OtherList

Array of Other Residual functions to be defined by user.

This list of function pointers can be declared and set up by the user in order to add to or change the behavior of the SHARK system. Each one must be declared setup individually by the user. They will be called by the `shark_residual` function when needed. Alternatively, the user is free to provide their own `shark_residual` function for the overall system.

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>shark_dat</i>	pointer to the <a href="#">SHARK_DATA</a> data structure
<i>data</i>	pointer to a user defined data structure that is used to evaluate this residual

## 5.41.2.7 int SHARK\_DATA::numvar

Total number of functions and species.

## 5.41.2.8 int SHARK\_DATA::num\_ssr

Number of steady-state reactions.

## 5.41.2.9 int SHARK\_DATA::num\_mbe

Number of mass balance equations.

5.41.2.10 int SHARK\_DATA::num\_usr = 0

Number of unsteady-state reactions.

5.41.2.11 int SHARK\_DATA::num\_ssao = 0

Number of steady-state adsorption objects.

5.41.2.12 std::vector<int> SHARK\_DATA::num\_ssar

List of the numbers of reactions in each adsorption object.

5.41.2.13 std::vector<std::string> SHARK\_DATA::ads\_names

List of the adsorbent object names.

5.41.2.14 int SHARK\_DATA::num\_other = 0

Number of other functions to be used (default is always 0)

5.41.2.15 int SHARK\_DATA::act\_fun = IDEAL

Flag denoting the activity function to use (default is IDEAL)

5.41.2.16 int SHARK\_DATA::totalsteps = 0

Total number of iterations.

5.41.2.17 int SHARK\_DATA::totalcalls = 0

Total number of residual function calls.

5.41.2.18 int SHARK\_DATA::timesteps = 0

Number of time steps taken to complete simulation.

5.41.2.19 int SHARK\_DATA::pH\_index = -1

Contains the index of the pH variable (set internally)

5.41.2.20 int SHARK\_DATA::pOH\_index = -1

Contains the index of the pOH variable (set internally)

5.41.2.21 double SHARK\_DATA::simulationtime = 0.0

Time to simulate unsteady reactions for (default = 0.0 hrs)

5.41.2.22 double SHARK\_DATA::dt = 0.1

Time step size (hrs)

5.41.2.23 double SHARK\_DATA::dt\_min = sqrt(DBL\_EPSILON)

Minimum allowable step size.

5.41.2.24 double SHARK\_DATA::t\_out = 0.0

Time increment by which file output is made (default = print all time steps)

5.41.2.25 double SHARK\_DATA::t\_count = 0.0

Running count of time increments.

5.41.2.26 double SHARK\_DATA::time = 0.0

Current value of time (starts from t = 0.0 hrs)

5.41.2.27 double SHARK\_DATA::time\_old = 0.0

Previous value of time (start from t = 0.0 hrs)

5.41.2.28 double SHARK\_DATA::pH = 7.0

Value of pH if needed (default = 7)

5.41.2.29 double SHARK\_DATA::pH\_step = 0.5

Value by which to increment pH when doing a speciation curve (default = 0.5)

5.41.2.30 double SHARK\_DATA::volume = 1.0

Volume of the domain in liters (default = 1 L)

5.41.2.31 double SHARK\_DATA::Norm = 0.0

Current value of euclidean norm in solution.

5.41.2.32 double SHARK\_DATA::dielectric\_const = 78.325

Dielectric constant used in many activity models (default: water = 78.325 (1/K))

5.41.2.33 double SHARK\_DATA::relative\_permittivity = 80.1

Relative permittivity of the medium (default: water = 80.1 (-))

5.41.2.34 double SHARK\_DATA::temperature = 298.15

Solution temperature (default = 25 oC or 298.15 K)

5.41.2.35 bool SHARK\_DATA::steadystate = true

True = solve steady problem; False = solve transient problem.

5.41.2.36 bool SHARK\_DATA::TimeAdaptivity = false

True = solve using variable time step.

5.41.2.37 bool SHARK\_DATA::const\_pH = false

True = set pH to a constant; False = solve for pH.

5.41.2.38 bool SHARK\_DATA::SpeciationCurve = false

True = runs a series of constant pH steady-state problems to produce curves.

5.41.2.39 bool SHARK\_DATA::Console\_Output = true

True = display output to console.

5.41.2.40 `bool SHARK_DATA::File_Output = false`

True = write output to a file.

5.41.2.41 `bool SHARK_DATA::Contains_pH = false`

True = system contains pH as a variable (set internally)

5.41.2.42 `bool SHARK_DATA::Contains_pOH = false`

True = system contains pOH as a variable (set internally)

5.41.2.43 `bool SHARK_DATA::Converged = false`

True = system converged within tolerance.

5.41.2.44 `bool SHARK_DATA::LocalMin = true`

True = allow the system to settle for a local minimum if tolerance not reached.

5.41.2.45 `Matrix<double> SHARK_DATA::X_old`

Solution vector for old time step -  $\log(C)$

5.41.2.46 `Matrix<double> SHARK_DATA::X_new`

Solution vector for current time step -  $\log(C)$

5.41.2.47 `Matrix<double> SHARK_DATA::Conc_old`

Concentration vector for old time step -  $10^x$ .

5.41.2.48 `Matrix<double> SHARK_DATA::Conc_new`

Concentration vector for current time step -  $10^x$ .

5.41.2.49 `Matrix<double> SHARK_DATA::activity_new`

Activity matrix for current time step.

5.41.2.50 `Matrix<double> SHARK_DATA::activity_old`

Activity matrix from prior time step.

5.41.2.51 `int(* SHARK_DATA::EvalActivity)(const Matrix< double > &x, Matrix< double > &F, const void *data)`

Function pointer to evaluate activity coefficients.

This function pointer is called within the `shark_residual` function to calculate and modify the `activity_new` matrix entries. When using the SHARK default options, this function pointer will be automatically set to a cooresponding activity function for the list of valid functions from the `valid_act` enum. User may override this function pointer if they desire. Must be overridden after calling the `setup` function.

#### Parameters

<i>x</i>	matrix of the $\log(C)$ concentration values at the current non-linear step
<i>F</i>	matrix of activity coefficients that are to be altered by this function
<i>data</i>	pointer to a data structure needed to evaluate the activity model

5.41.2.52 `int(* SHARK_DATA::Residual)(const Matrix< double > &x, Matrix< double > &F, const void *data)`

Function pointer to evaluate all residuals in the system.

This function will be fed into the PJFNK solver (see [lark.h](#)) to solve the non-linear system of equations. By default, this pointer will be the shark\_residual function (see below). However, the user may override the function and provide their own residuals for the PJFNK solver to operate on.

#### Parameters

$x$	matrix of the log(C) concentration values at the current non-linear step
$F$	matrix of residuals that are to be altered from the functions in the system
<i>data</i>	pointer to a data structure needed to evaluate the activity model

5.41.2.53 `int(* SHARK_DATA::lin_precon)(const Matrix< double > &r, Matrix< double > &p, const void *data)`

Function pointer to form a linear preconditioning operation for the Jacobian.

This function will be fed into the linear solver used for each non-linear step in PJFNK (see [lark.h](#)). By default, we cannot provide any linear preconditioner, because we do not know the form or sparsity of the Jacobian before hand. It will be the user's responsibility to form their own preconditioner until we can figure out a generic way to precondition the system.

5.41.2.54 `PJFNK_DATA SHARK_DATA::Newton_data`

Data structure for the Newton-Krylov solver (see [lark.h](#))

5.41.2.55 `const void* SHARK_DATA::activity_data`

User defined data structure for an activity model.

5.41.2.56 `const void* SHARK_DATA::residual_data`

User defined data structure for the residual function.

5.41.2.57 `const void* SHARK_DATA::precon_data`

User defined data structure for preconditioning.

5.41.2.58 `const void* SHARK_DATA::other_data`

User define data structure used for user defined residuals.

5.41.2.59 `FILE* SHARK_DATA::OutputFile`

Output File pointer.

5.41.2.60 `yaml_cpp_class SHARK_DATA::yaml_object`

yaml object to read and access digitized yaml documents (see [yaml\\_wrapper.h](#))

The documentation for this struct was generated from the following file:

- [shark.h](#)

## 5.42 SKUA\_DATA Struct Reference

Data structure for all simulation information in SKUA.

```
#include <skua.h>
```

#### Public Attributes

- unsigned long int [total\\_steps](#)

- Running total of all calculation steps.*

  - int [coord](#)

*Used to determine the coordinates of the problem.*
- double [sim\\_time](#)

*Stopping time for the simulation (hrs)*
- double [t\\_old](#)

*Old time of the simulations (hrs)*
- double [t](#)

*Current time of the simulations (hrs)*
- double [t\\_counter](#) = 0.0

*Counts for print times for output (hrs)*
- double [t\\_print](#)

*Prints out every t\_print time (hrs)*
- double [qTn](#)

*Old total amounts adsorbed (mol/kg)*
- double [qTnp1](#)

*New total amounts adsorbed (mol/kg)*
- bool [Print2File](#) = true

*True = results to .txt; False = no printing.*
- bool [Print2Console](#) = true

*True = results to console; False = no printing.*
- double [gas\\_velocity](#)

*Superficial Gas Velocity around pellet (cm/s)*
- double [pellet\\_radius](#)

*Nominal radius of the pellet/crystal (um)*
- double [char\\_measure](#)

*Length or Area if in Cylindrical or Cartesian coordinates (um or um<sup>2</sup>)*
- bool [DirichletBC](#) = true

*True = Dirichlet BC; False = Neumann BC.*
- bool [NonLinear](#) = true

*True = Non-linear solver; False = Linear solver.*
- std::vector< double > [y](#)

*Outside mole fractions of each component (-)*
- FILE \* [OutputFile](#)

*Output file pointer to the output file.*
- double(\* [eval\\_diff](#))(int i, int l, const void \*[user\\_data](#))

*Function pointer for evaluating surface diffusivity.*
- double(\* [eval\\_kf](#))(int i, const void \*[user\\_data](#))

*Function pointer for evaluating film mass transfer.*
- const void \* [user\\_data](#)

*Data structure for user's information needed in parameter functions.*
- [MAGPIE\\_DATA](#) [magpie\\_dat](#)

*Data structure for adsorption equilibria (see [magpie.h](#))*
- [MIXED\\_GAS](#) \* [gas\\_dat](#)

*Pointer to the [MIXED\\_GAS](#) data structure (see [egret.h](#))*
- std::vector< [FINCH\\_DATA](#) > [finch\\_dat](#)

*Data structure for adsorption kinetics (see [finch.h](#))*
- std::vector< [SKUA\\_PARAM](#) > [param\\_dat](#)

*Data structure for SKUA specific parameters.*

### 5.42.1 Detailed Description

Data structure for all simulation information in SKUA.

C-style object holding all data, functions, and other objects needed to successfully run a SKUA simulation. This object holds system information, such as boundary condition type, adsorbent size, and total adsorption, and also contains structure for EGRET ([egret.h](#)), FINCH ([finch.h](#)), and MAGPIE ([magpie.h](#)) calculations. Function pointers for evaluation of the surface diffusivity and film mass transfer coefficients can be overridden by the user to change the behavior of the SKUA simulation. However, defaults are also provided for these functions.

### 5.42.2 Member Data Documentation

#### 5.42.2.1 unsigned long int SKUA\_DATA::total\_steps

Running total of all calculation steps.

#### 5.42.2.2 int SKUA\_DATA::coord

Used to determine the coordinates of the problem.

#### 5.42.2.3 double SKUA\_DATA::sim\_time

Stopping time for the simulation (hrs)

#### 5.42.2.4 double SKUA\_DATA::t\_old

Old time of the simulations (hrs)

#### 5.42.2.5 double SKUA\_DATA::t

Current time of the simulations (hrs)

#### 5.42.2.6 double SKUA\_DATA::t\_counter = 0.0

Counts for print times for output (hrs)

#### 5.42.2.7 double SKUA\_DATA::t\_print

Prints out every t\_print time (hrs)

#### 5.42.2.8 double SKUA\_DATA::qTn

Old total amounts adsorbed (mol/kg)

#### 5.42.2.9 double SKUA\_DATA::qTnp1

New total amounts adsorbed (mol/kg)

#### 5.42.2.10 bool SKUA\_DATA::Print2File = true

True = results to .txt; False = no printing.

#### 5.42.2.11 bool SKUA\_DATA::Print2Console = true

True = results to console; False = no printing.

#### 5.42.2.12 double SKUA\_DATA::gas\_velocity

Superficial Gas Velocity around pellet (cm/s)

5.42.2.13 `double SKUA_DATA::pellet_radius`

Nominal radius of the pellet/crystal (um)

5.42.2.14 `double SKUA_DATA::char_measure`

Length or Area if in Cylindrical or Cartesian coordinates (um or um<sup>2</sup>)

5.42.2.15 `bool SKUA_DATA::DirichletBC = true`

True = Dirichlet BC; False = Neumann BC.

5.42.2.16 `bool SKUA_DATA::NonLinear = true`

True = Non-linear solver; False = Linear solver.

5.42.2.17 `std::vector<double> SKUA_DATA::y`

Outside mole fractions of each component (-)

5.42.2.18 `FILE* SKUA_DATA::OutputFile`

Output file pointer to the output file.

5.42.2.19 `double(* SKUA_DATA::eval_diff)(int i, int l, const void *user_data)`

Function pointer for evaluating surface diffusivity.

5.42.2.20 `double(* SKUA_DATA::eval_kf)(int i, const void *user_data)`

Function pointer for evaluating film mass transfer.

5.42.2.21 `const void* SKUA_DATA::user_data`

Data structure for user's information needed in parameter functions.

5.42.2.22 `MAGPIE_DATA SKUA_DATA::magpie_dat`

Data structure for adsorption equilibria (see [magpie.h](#))

5.42.2.23 `MIXED_GAS* SKUA_DATA::gas_dat`

Pointer to the [MIXED\\_GAS](#) data structure (see [egret.h](#))

5.42.2.24 `std::vector<FINCH_DATA> SKUA_DATA::finch_dat`

Data structure for adsorption kinetics (see [finch.h](#))

5.42.2.25 `std::vector<SKUA_PARAM> SKUA_DATA::param_dat`

Data structure for SKUA specific parameters.

The documentation for this struct was generated from the following file:

- [skua.h](#)

## 5.43 SKUA\_OPT\_DATA Struct Reference

Data structure for the SKUA Optimization Routine.

```
#include <skua_opt.h>
```



## Public Attributes

- int [num\\_curves](#)  
*Number of adsorption curves to analyze.*
- int [evaluation](#)  
*Number of times the eval function has been called for a single curve.*
- unsigned long int [total\\_eval](#)  
*Total number of evaluations needed for completion.*
- int [current\\_points](#)  
*Number of points in the current curve.*
- int [num\\_params](#) = 1  
*Number of adjustable parameters for the current curve.*
- int [diffusion\\_type](#)  
*Flag to identify type of diffusion function to use.*
- int [adsorb\\_index](#)  
*Component index for adsorbable species.*
- int [max\\_guess\\_iter](#) = 20  
*Maximum allowed guess iterations (default = 20)*
- bool [Optimize](#)  
*True = run optimization, False = run a comparison.*
- bool [Rough](#)  
*True = use only a rough estimate, False = run full optimization.*
- double [current\\_temp](#)  
*Temperature for current curve.*
- double [current\\_press](#)  
*Partial pressure for current curve.*
- double [current\\_equil](#)  
*Equilibrium data point for the current curve.*
- double [simulation\\_equil](#)  
*Equilibrium simulation point for the current curve.*
- double [max\\_bias](#)  
*Positive maximum bias plausible for fitting.*
- double [min\\_bias](#)  
*Negative minimum bias plausible for fitting.*
- double [e\\_norm](#)  
*Euclidean norm of current fit.*
- double [f\\_bias](#)  
*Function bias of current fit.*
- double [e\\_norm\\_old](#)  
*Euclidean norm of the previous fit.*
- double [f\\_bias\\_old](#)  
*Function bias of the previous fit.*
- double [param\\_guess](#)  
*Parameter guess for the surface/crystal diffusivity.*
- double [param\\_guess\\_old](#)  
*Parameter guess for the previous curve.*
- double [rel\\_tol\\_norm](#) = 0.1  
*Tolerance for convergence of the guess norm.*
- double [abs\\_tol\\_bias](#) = 0.1  
*Tolerance for convergence of the guess bias.*
- std::vector< double > [y\\_base](#)

- *Gas phase mole fractions in absense of adsorbing species.*  
std::vector< double > [q\\_data](#)
- *Amount adsorbed at a particular point in current curve.*  
std::vector< double > [q\\_sim](#)
- *Amount adsorbed based on the simulation.*  
std::vector< double > [t](#)
- *Time points in the current curve.*  
FILE \* [ParamFile](#)
- *Output file for parameter results.*  
FILE \* [CompareFile](#)
- *Output file for comparison of results.*  
[SKUA\\_DATA skua\\_dat](#)
- *Data structure for the SKUA simulation.*

#### 5.43.1 Detailed Description

Data structure for the SKUA Optimization Routine.

C-style object holding data and pointers necessary for running a SKUA optimization. It contains information about the type of optimization requested, the current status of the optimization, the data being compared against, and the [SKUA\\_DATA](#) object for the evaluation of a SKUA simulation. The pointers in the structure are for the two output files produced by the routine: (i) parameter results and (ii) model comparison results.

#### 5.43.2 Member Data Documentation

##### 5.43.2.1 int SKUA\_OPT\_DATA::num\_curves

Number of adsorption curves to analyze.

##### 5.43.2.2 int SKUA\_OPT\_DATA::evaluation

Number of times the eval function has been called for a single curve.

##### 5.43.2.3 unsigned long int SKUA\_OPT\_DATA::total\_eval

Total number of evaluations needed for completion.

##### 5.43.2.4 int SKUA\_OPT\_DATA::current\_points

Number of points in the current curve.

##### 5.43.2.5 int SKUA\_OPT\_DATA::num\_params = 1

Number of adjustable parameters for the current curve.

##### 5.43.2.6 int SKUA\_OPT\_DATA::diffusion\_type

Flag to identify type of diffusion function to use.

##### 5.43.2.7 int SKUA\_OPT\_DATA::adsorb\_index

Component index for adsorbable species.

##### 5.43.2.8 int SKUA\_OPT\_DATA::max\_guess\_iter = 20

Maximum allowed guess iterations (default = 20)

**5.43.2.9 bool SKUA\_OPT\_DATA::Optimize**

True = run optimization, False = run a comparison.

**5.43.2.10 bool SKUA\_OPT\_DATA::Rough**

True = use only a rough estimate, False = run full optimization.

**5.43.2.11 double SKUA\_OPT\_DATA::current\_temp**

Temperature for current curve.

**5.43.2.12 double SKUA\_OPT\_DATA::current\_press**

Partial pressure for current curve.

**5.43.2.13 double SKUA\_OPT\_DATA::current\_equil**

Equilibrium data point for the current curve.

**5.43.2.14 double SKUA\_OPT\_DATA::simulation\_equil**

Equilibrium simulation point for the current curve.

**5.43.2.15 double SKUA\_OPT\_DATA::max\_bias**

Positive maximum bias plausible for fitting.

**5.43.2.16 double SKUA\_OPT\_DATA::min\_bias**

Negative minimum bias plausible for fitting.

**5.43.2.17 double SKUA\_OPT\_DATA::e\_norm**

Euclidean norm of current fit.

**5.43.2.18 double SKUA\_OPT\_DATA::f\_bias**

Function bias of current fit.

**5.43.2.19 double SKUA\_OPT\_DATA::e\_norm\_old**

Euclidean norm of the previous fit.

**5.43.2.20 double SKUA\_OPT\_DATA::f\_bias\_old**

Function bias of the previous fit.

**5.43.2.21 double SKUA\_OPT\_DATA::param\_guess**

Parameter guess for the surface/crystal diffusivity.

**5.43.2.22 double SKUA\_OPT\_DATA::param\_guess\_old**

Parameter guess for the previous curve.

**5.43.2.23 double SKUA\_OPT\_DATA::rel\_tol\_norm = 0.1**

Tolerance for convergence of the guess norm.

5.43.2.24 `double SKUA_OPT_DATA::abs_tol_bias = 0.1`

Tolerance for convergence of the guess bias.

5.43.2.25 `std::vector<double> SKUA_OPT_DATA::y_base`

Gas phase mole fractions in absense of adsorbing species.

5.43.2.26 `std::vector<double> SKUA_OPT_DATA::q_data`

Amount adsorbed at a particular point in current curve.

5.43.2.27 `std::vector<double> SKUA_OPT_DATA::q_sim`

Amount adsorbed based on the simulation.

5.43.2.28 `std::vector<double> SKUA_OPT_DATA::t`

Time points in the current curve.

5.43.2.29 `FILE* SKUA_OPT_DATA::ParamFile`

Output file for parameter results.

5.43.2.30 `FILE* SKUA_OPT_DATA::CompareFile`

Output file for comparison of results.

5.43.2.31 `SKUA_DATA SKUA_OPT_DATA::skua_dat`

Data structure for the SKUA simulation.

The documentation for this struct was generated from the following file:

- [skua\\_opt.h](#)

## 5.44 SKUA\_PARAM Struct Reference

Data structure for species' parameters in SKUA.

```
#include <skua.h>
```

### Public Attributes

- double [activation\\_energy](#)
- double [ref\\_diffusion](#)
- double [ref\\_temperature](#)
- double [affinity](#)
- double [ref\\_pressure](#)
- double [film\\_transfer](#)
- double [xIC](#)
- double [y\\_eff](#)
- double [Qstn](#)
- double [Qstnp1](#)
- double [xn](#)
- double [xnp1](#)
- bool [Adsorbable](#)
- std::string [speciesName](#)

## 5.44.1 Detailed Description

Data structure for species' parameters in SKUA.

C-style object holding data and parameters associated with the gas/solid species in the overall SKUA system. These parameters are used in to modify surface diffusivity with temperature, establish film mass transfer coefficients, formulate the initial conditions, and store solution results for heat of adsorption and adsorbed mole fractions. One of these objects will be created for each species in the gas system.

## 5.44.2 Member Data Documentation

5.44.2.1 `double SKUA_PARAM::activation_energy`

5.44.2.2 `double SKUA_PARAM::ref_diffusion`

5.44.2.3 `double SKUA_PARAM::ref_temperature`

5.44.2.4 `double SKUA_PARAM::affinity`

5.44.2.5 `double SKUA_PARAM::ref_pressure`

5.44.2.6 `double SKUA_PARAM::film_transfer`

5.44.2.7 `double SKUA_PARAM::xIC`

5.44.2.8 `double SKUA_PARAM::y_eff`

5.44.2.9 `double SKUA_PARAM::Qstn`

5.44.2.10 `double SKUA_PARAM::Qstnp1`

5.44.2.11 `double SKUA_PARAM::xn`

5.44.2.12 `double SKUA_PARAM::xnp1`

5.44.2.13 `bool SKUA_PARAM::Adsorbable`

5.44.2.14 `std::string SKUA_PARAM::speciesName`

The documentation for this struct was generated from the following file:

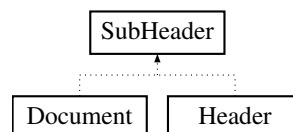
- [skua.h](#)

## 5.45 SubHeader Class Reference

Object for the Lowest level of [Header](#) for the `yaml_wrapper`.

```
#include <yaml_wrapper.h>
```

Inheritance diagram for SubHeader:



## Public Member Functions

- [SubHeader](#) ()  
*Default Constructor.*
- [~SubHeader](#) ()  
*Default Destructor.*
- [SubHeader](#) (const [SubHeader](#) &subheader)  
*Copy constructor.*
- [SubHeader](#) (const [KeyValueMap](#) &map)  
*Construction by existing map.*
- [SubHeader](#) (std::string name)  
*Construction by name only.*
- [SubHeader](#) (std::string name, const [KeyValueMap](#) &map)  
*Construction by name and map.*
- [SubHeader](#) & [operator=](#) (const [SubHeader](#) &sub)  
*Equals overload.*
- [ValueTypePair](#) & [operator\[\]](#) (const std::string key)  
*Return the ValueType reference at the given key.*
- [ValueTypePair](#) [operator\[\]](#) (const std::string key) const  
*Return the ValueType at the give key.*
- [KeyValueMap](#) & [getMap](#) ()  
*Returns reference to the [KeyValueMap](#) object.*
- void [clear](#) ()  
*Empty out data contents.*
- void [addPair](#) (std::string key, std::string val)  
*Adds a pair object to the map (with only strings)*
- void [addPair](#) (std::string key, std::string val, int type)  
*Adds a pair object and asserts a type.*
- void [setName](#) (std::string name)  
*Sets the name of the subheader.*
- void [setAlias](#) (std::string alias)  
*Set the alias without type specification.*
- void [setAlias](#) (std::string alias, int state)  
*Sets the alias and state of the subheader.*
- void [setNameAliasPair](#) (std::string name, std::string alias, int state)  
*Sets the name and alias of the subheader.*
- void [setState](#) (int state)  
*Sets the state of the subheader.*
- void [DisplayContents](#) ()  
*Display the contents of the subheader.*
- std::string [getName](#) ()  
*Return the name of the subheader.*
- std::string [getAlias](#) ()  
*Return the alias of the subheader, if one exists.*
- bool [isAlias](#) ()  
*Returns true if subheader is an alias.*
- bool [isAnchor](#) ()  
*Returns true if subheader is an anchor.*
- int [getState](#) ()  
*Returns the state of the subheader.*

## Protected Attributes

- [KeyValueMap Data\\_Map](#)  
*A Map of Keys and Values.*
- `std::string name`  
*Name of the subheader.*
- `std::string alias`  
*Name of the alias for the subheader.*
- `int state`  
*State of the header.*

## 5.45.1 Detailed Description

Object for the Lowest level of [Header](#) for the `yaml_wrapper`.

C++ Object for sub-headers in a yaml document. This object contains a [KeyValueMap](#) that holds a set of key-value pairs for data listed under a sub-header in yaml files. It is the lowest allowable recursion of headers in a yaml document and so is the base class for [Header](#) and [Document](#), which themselves can contain [KeyValueMaps](#) as well as maps for other header-like objects.

SubHeaders are recognized by a unique name and/or alias while being put together in other higher document structures. Additionally, each header or sub-header will have a state to denote whether the object is a yaml alias, anchor, or niether. This is used in the yaml documents to ensure that aliases for anchors have the correct data moved over into the new structures.

## 5.45.2 Constructor &amp; Destructor Documentation

## 5.45.2.1 SubHeader::SubHeader ( )

Default Constructor.

## 5.45.2.2 SubHeader::~~SubHeader ( )

Default Destructor.

## 5.45.2.3 SubHeader::SubHeader ( const SubHeader &amp; subheader )

Copy constructor.

## 5.45.2.4 SubHeader::SubHeader ( const KeyValueMap &amp; map )

Construction by existing map.

## 5.45.2.5 SubHeader::SubHeader ( std::string name )

Construction by name only.

## 5.45.2.6 SubHeader::SubHeader ( std::string name, const KeyValueMap &amp; map )

Construction by name and map.

## 5.45.3 Member Function Documentation

## 5.45.3.1 SubHeader&amp; SubHeader::operator= ( const SubHeader &amp; sub )

Equals overload.

**5.45.3.2 ValueTypePair& SubHeader::operator[] ( const std::string key )**

Return the ValueType reference at the given key.

**5.45.3.3 ValueTypePair SubHeader::operator[] ( const std::string key ) const**

Return the ValueType at the give key.

**5.45.3.4 KeyValueMap& SubHeader::getMap ( )**

Returns reference to the [KeyValueMap](#) object.

**5.45.3.5 void SubHeader::clear ( )**

Empty out data contents.

**5.45.3.6 void SubHeader::addPair ( std::string key, std::string val )**

Adds a pair object to the map (with only strings)

**5.45.3.7 void SubHeader::addPair ( std::string key, std::string val, int type )**

Adds a pair object and asserts a type.

**5.45.3.8 void SubHeader::setName ( std::string name )**

Sets the name of the subheader.

**5.45.3.9 void SubHeader::setAlias ( std::string alias )**

Set the alias without type specification.

**5.45.3.10 void SubHeader::setAlias ( std::string alias, int state )**

Sets the alias and state of the subheader.

**5.45.3.11 void SubHeader::setNameAliasPair ( std::string name, std::string alias, int state )**

Sets the name and alias of the subheader.

**5.45.3.12 void SubHeader::setState ( int state )**

Sets the state of the subheader.

**5.45.3.13 void SubHeader::DisplayContents ( )**

Display the contents of the subheader.

**5.45.3.14 std::string SubHeader::getName ( )**

Return the name of the subheader.

**5.45.3.15 std::string SubHeader::getAlias ( )**

Return the alias of the subheader, if one exists.

**5.45.3.16 bool SubHeader::isAlias ( )**

Returns true if subheader is an alias.



## 5.45.3.17 bool SubHeader::isAnchor ( )

Returns true if subheader is an anchor.

## 5.45.3.18 int SubHeader::getState ( )

Returns the state of the subheader.

## 5.45.4 Member Data Documentation

## 5.45.4.1 KeyValueType SubHeader::Data\_Map [protected]

A Map of Keys and Values.

## 5.45.4.2 std::string SubHeader::name [protected]

Name of the subheader.

## 5.45.4.3 std::string SubHeader::alias [protected]

Name of the alias for the subheader.

## 5.45.4.4 int SubHeader::state [protected]

State of the header.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 5.46 SYSTEM\_DATA Struct Reference

System Data Structure.

```
#include <magpie.h>
```

## Public Attributes

- double [T](#)  
*System Temperature (K)*
- double [PT](#)  
*Total Pressure (kPa)*
- double [qT](#)  
*Total Amount adsorbed (mol/kg)*
- double [PI](#)  
*Total Lumped Spreading Pressure (mol/kg)*
- double [pi](#)  
*Actual Spreading pressure (J/m<sup>2</sup>)*
- double [As](#)  
*Specific surface area of adsorbent (m<sup>2</sup>/kg)*
- int [N](#)  
*Total Number of Components.*
- int [I](#)
- int [J](#)
- int [K](#)  
*Special indices used to keep track of sub-systems.*

- unsigned long int `total_eval`  
*Counter to keep track of total number of non-linear steps.*
- double `avg_norm`  
*Used to store all norms from evaluations then average at end of run.*
- double `max_norm`  
*Used to store the maximum e.norm calculated from non-linear iterations.*
- int `Sys`  
*Number of sub-systems to solve.*
- int `Par`  
*Number of binary parameters to solve for.*
- bool `Recover`  
*If Recover == false, standard GPAST using y's as knowns.*
- bool `Carrier`  
*If there is an inert carrier gas, Carrier == true.*
- bool `Ideal`  
*If the behavior of the system is determined to be ideal, then Ideal == true.*
- bool `Output`  
*Boolean to suppress output if desired (true = display, false = no display).*

#### 5.46.1 Detailed Description

System Data Structure.

C-style object holding all the data associated with the overall system to be modeled.

#### 5.46.2 Member Data Documentation

##### 5.46.2.1 double SYSTEM\_DATA::T

System Temperature (K)

##### 5.46.2.2 double SYSTEM\_DATA::PT

Total Pressure (kPa)

##### 5.46.2.3 double SYSTEM\_DATA::qT

Total Amount adsorbed (mol/kg)

##### 5.46.2.4 double SYSTEM\_DATA::PI

Total Lumped Spreading Pressure (mol/kg)

##### 5.46.2.5 double SYSTEM\_DATA::pi

Actual Spreading pressure (J/m<sup>2</sup>)

##### 5.46.2.6 double SYSTEM\_DATA::As

Specific surface area of adsorbent (m<sup>2</sup>/kg)

##### 5.46.2.7 int SYSTEM\_DATA::N

Total Number of Components.

5.46.2.8 int SYSTEM\_DATA::I

5.46.2.9 int SYSTEM\_DATA::J

5.46.2.10 int SYSTEM\_DATA::K

Special indices used to keep track of sub-systems.

5.46.2.11 unsigned long int SYSTEM\_DATA::total\_eval

Counter to keep track of total number of non-linear steps.

5.46.2.12 double SYSTEM\_DATA::avg\_norm

Used to store all norms from evaluations then average at end of run.

5.46.2.13 double SYSTEM\_DATA::max\_norm

Used to store the maximum e.norm calculated from non-linear iterations.

5.46.2.14 int SYSTEM\_DATA::Sys

Number of sub-systems to solve.

5.46.2.15 int SYSTEM\_DATA::Par

Number of binary parameters to solve for.

5.46.2.16 bool SYSTEM\_DATA::Recover

If Recover == false, standard GPAST using y's as knowns.

5.46.2.17 bool SYSTEM\_DATA::Carrier

If there is an inert carrier gas, Carrier == true.

5.46.2.18 bool SYSTEM\_DATA::Ideal

If the behavior of the system is determined to be ideal, then Ideal == true.

5.46.2.19 bool SYSTEM\_DATA::Output

Boolean to suppress output if desired (true = display, false = no display).

The documentation for this struct was generated from the following file:

- [magpie.h](#)

## 5.47 TRAJECTORY\_DATA Struct Reference

Data structure holding constants and parameters need in trajectory analysis.

```
#include <Trajectory.h>
```

### Public Attributes

- double [mu\\_0](#) = 12.57e-7  
*permeability of free space, H/m*
- double [rho\\_f](#) = 1000.0  
*Fluid density, Kg/m3.*

- double `eta` = 0.001  
*Dynamic viscosity, Kg/m-s.*
- double `Hamaker` = 1.3e-21  
*Hamaker constant for ferric oxide particles.*
- double `Temp` = 298  
*Temperature, Kelvin.*
- double `k` = 1.38e-23  
*Boltzmann constant.*
- double `Rs` = 0.0026925  
*separator radius, m*
- double `L` = 0.0611  
*0.05separator length, m*
- double `porosity` = 0.8979  
*0.965separator porosity*
- double `V_separator`  
*volume of separator, m<sup>3</sup>*
- double `a` = 33.0e-6  
*Wire radius,m.*
- double `V_wire`  
*Total wire volume, m<sup>3</sup>.*
- double `L_wire`  
*Total wire length, m.*
- double `A_separator`  
*(Alex, Put something here)*
- double `A_wire`  
*(Alex, Put something here)*
- double `B0` = 1.0  
*Applied magnetic induction,T.*
- double `H0`  
*(Alex, Put something here)*
- double `Ms` = 0.6  
*Saturated magnetization,T.*
- double `b` = 0.25e-6  
*Particle radius,m.*
- double `chi_p` = 3.87e-6  
*Volume magnetic susceptibility, dimensionless.*
- double `rho_p` = 8700.0  
*Particle density, Kg/m3.*
- double `Q_in`  
*Volumetric fluid flow, m<sup>3</sup>/sec.*
- double `V0`  
*Superficial velocity,m/s.*
- double `Y_initial` = 20.0  
*initial position in Y-axis, Y=y/a, dimensionless*
- double `dt`  
*Time step size.*
- double `M`  
*(Alex, Put something here)*
- double `mp`  
*Particle Mass, Kg.*
- double `beta`

- *Friction coefficient per unit mass.*
- double `q_bar`  
(Alex, Put something here)
- double `sigma_v`  
*Take square root to get actual value for sigma v.*
- double `sigma_vz`  
(Alex, Put something here)
- double `sigma_z`  
*Take square root for actual value of sigma z.*
- double `sigma_n`  
(Alex, Put something here)
- double `sigma_m`  
(Alex, Put something here)
- double `n_rand`  
(Alex, Put something here)
- double `m_rand`  
(Alex, Put something here)
- double `s_rand`  
(Alex, Put something here)
- double `t_rand`  
(Alex, Put something here)
- `Matrix< double > POL`
- `Matrix< double > H`
- `Matrix< double > dX`
- `Matrix< double > dY`  
(Alex, Put something here)
- `Matrix< double > X`
- `Matrix< double > Y`  
(Alex, Put something here)
- `Matrix< int > Cap`  
(Alex, Put something here)

#### 5.47.1 Detailed Description

Data structure holding constants and parameters need in trajectory analysis.

Alex, please provide details here...

#### 5.47.2 Member Data Documentation

##### 5.47.2.1 double TRAJECTORY\_DATA::mu\_0 = 12.57e-7

permeability of free space, H/m

##### 5.47.2.2 double TRAJECTORY\_DATA::rho\_f = 1000.0

Fluid density, Kg/m3.

##### 5.47.2.3 double TRAJECTORY\_DATA::eta = 0.001

Dynamic viscosity, Kg/m-s.

##### 5.47.2.4 double TRAJECTORY\_DATA::Hamaker = 1.3e-21

Hamaker constant for ferric oxide particles.

5.47.2.5 double TRAJECTORY\_DATA::Temp = 298

Temperature, Kelvin.

5.47.2.6 double TRAJECTORY\_DATA::k = 1.38e-23

Boltzmann constant.

5.47.2.7 double TRAJECTORY\_DATA::Rs = 0.0026925

separator radius, m

5.47.2.8 double TRAJECTORY\_DATA::L = 0.0611

0.05separator length, m

5.47.2.9 double TRAJECTORY\_DATA::porosity = 0.8979

0.965separator porosity

5.47.2.10 double TRAJECTORY\_DATA::V\_separator

volume of separator, m<sup>3</sup>

5.47.2.11 double TRAJECTORY\_DATA::a = 33.0e-6

Wire radius,m.

5.47.2.12 double TRAJECTORY\_DATA::V\_wire

Total wire volume, m<sup>3</sup>.

5.47.2.13 double TRAJECTORY\_DATA::L\_wire

Total wire length, m.

5.47.2.14 double TRAJECTORY\_DATA::A\_separator

(Alex, Put something here)

5.47.2.15 double TRAJECTORY\_DATA::A\_wire

(Alex, Put something here)

5.47.2.16 double TRAJECTORY\_DATA::B0 = 1.0

Applied magnetic induction,T.

5.47.2.17 double TRAJECTORY\_DATA::H0

(Alex, Put something here)

5.47.2.18 double TRAJECTORY\_DATA::Ms = 0.6

Saturated magnetization,T.

5.47.2.19 double TRAJECTORY\_DATA::b = 0.25e-6

Particle radius,m.

5.47.2.20 double TRAJECTORY\_DATA::chi\_p = 3.87e-6

Volume magnetic susceptibility, dimensionless.

5.47.2.21 double TRAJECTORY\_DATA::rho\_p = 8700.0

Particle density, Kg/m3.

5.47.2.22 double TRAJECTORY\_DATA::Q\_in

Volumetric fluid flow, m<sup>3</sup>/sec.

5.47.2.23 double TRAJECTORY\_DATA::V0

Superficial velocity, m/s.

5.47.2.24 double TRAJECTORY\_DATA::Y\_initial = 20.0

initial position in Y-axis, Y=y/a, dimensionless

5.47.2.25 double TRAJECTORY\_DATA::dt

Time step size.

5.47.2.26 double TRAJECTORY\_DATA::M

(Alex, Put something here)

5.47.2.27 double TRAJECTORY\_DATA::mp

Particle Mass, Kg.

5.47.2.28 double TRAJECTORY\_DATA::beta

Friction coefficient per unit mass.

5.47.2.29 double TRAJECTORY\_DATA::q\_bar

(Alex, Put something here)

5.47.2.30 double TRAJECTORY\_DATA::sigma\_v

Take square root to get actual value for sigma v.

5.47.2.31 double TRAJECTORY\_DATA::sigma\_vz

(Alex, Put something here)

5.47.2.32 double TRAJECTORY\_DATA::sigma\_z

Take square root for actual value of sigma z.

5.47.2.33 double TRAJECTORY\_DATA::sigma\_n

(Alex, Put something here)

5.47.2.34 double TRAJECTORY\_DATA::sigma\_m

(Alex, Put something here)

5.47.2.35 double TRAJECTORY\_DATA::n\_rand

(Alex, Put something here)

5.47.2.36 double TRAJECTORY\_DATA::m\_rand

(Alex, Put something here)

5.47.2.37 double TRAJECTORY\_DATA::s\_rand

(Alex, Put something here)

5.47.2.38 double TRAJECTORY\_DATA::t\_rand

(Alex, Put something here)

5.47.2.39 Matrix<double> TRAJECTORY\_DATA::POL

5.47.2.40 Matrix<double> TRAJECTORY\_DATA::H

5.47.2.41 Matrix<double> TRAJECTORY\_DATA::dX

5.47.2.42 Matrix<double> TRAJECTORY\_DATA::dY

(Alex, Put something here)

5.47.2.43 Matrix<double> TRAJECTORY\_DATA::X

5.47.2.44 Matrix<double> TRAJECTORY\_DATA::Y

(Alex, Put something here)

5.47.2.45 Matrix<int> TRAJECTORY\_DATA::Cap

(Alex, Put something here)

The documentation for this struct was generated from the following file:

- [Trajectory.h](#)

## 5.48 UI\_DATA Struct Reference

Data structure holding the UI arguments.

```
#include <ui.h>
```

### Public Attributes

- [ValueTypePair value\\_type](#)  
*Data pair for input, tells what the input is and it's type.*
- std::vector< std::string > [user\\_input](#)  
*What is read in from the console at any point.*
- std::vector< std::string > [input\\_files](#)  
*A vector of input file names and directories given by user.*
- std::string [path](#)  
*Path to where input files are located.*
- int [count](#) = 0  
*Number of times a questing has been asked.*



- int `max` = 3  
*Maximum allowable recursions of a question.*
- int `option`  
*Current option choosen by the user.*
- bool `Path` = false  
*True if user gives path as an option.*
- bool `Files` = false  
*True if user gives input files as an option.*
- bool `MissingArg` = true  
*True if an input argument is missing; False if everything is ok.*
- bool `BasicUI` = true  
*True if using Basic UI; False if using Advanced UI.*
- int `argc`  
*Number of console arguments given on input.*
- const char \* `argv` []  
*Actual console arguments given at execution.*

#### 5.48.1 Detailed Description

Data structure holding the UI arguments.

C-Style object for interfacing with users request upon execution of the program. User input is stored in objects below and a series of booleans is used to determine how and what to execute.

#### 5.48.2 Member Data Documentation

##### 5.48.2.1 `ValueTypePair UI_DATA::value_type`

Data pair for input, tells what the input is and it's type.

##### 5.48.2.2 `std::vector<std::string> UI_DATA::user_input`

What is read in from the console at any point.

##### 5.48.2.3 `std::vector<std::string> UI_DATA::input_files`

A vector of input file names and directories given by user.

##### 5.48.2.4 `std::string UI_DATA::path`

Path to where input files are located.

##### 5.48.2.5 `int UI_DATA::count = 0`

Number of times a questing has been asked.

##### 5.48.2.6 `int UI_DATA::max = 3`

Maximum allowable recursions of a question.

##### 5.48.2.7 `int UI_DATA::option`

Current option choosen by the user.

##### 5.48.2.8 `bool UI_DATA::Path = false`

True if user gives path as an option.

5.48.2.9 `bool UI_DATA::Files = false`

True if user gives input files as an option.

5.48.2.10 `bool UI_DATA::MissingArg = true`

True if an input argument is missing; False if everything is ok.

5.48.2.11 `bool UI_DATA::BasicUI = true`

True if using Basic UI; False if using Advanced UI.

5.48.2.12 `int UI_DATA::argc`

Number of console arguments given on input.

5.48.2.13 `const char* UI_DATA::argv[]`

Actual console arguments given at execution.

The documentation for this struct was generated from the following file:

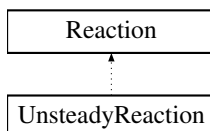
- [ui.h](#)

## 5.49 UnsteadyReaction Class Reference

Unsteady [Reaction](#) Object (inherits from [Reaction](#))

```
#include <shark.h>
```

Inheritance diagram for UnsteadyReaction:



## Public Member Functions

- [UnsteadyReaction](#) ()  
*Default Constructor.*
- [~UnsteadyReaction](#) ()  
*Default Destructor.*
- void [Initialize\\_Object](#) ([MasterSpeciesList](#) &[List](#))  
*Function to initialize the [UnsteadyReaction](#) object from the [MasterSpeciesList](#).*
- void [Display\\_Info](#) ()  
*Display the unsteady reaction information.*
- void [Set\\_Species\\_Index](#) (int i)  
*Set the Unsteady species index by number.*
- void [Set\\_Species\\_Index](#) (std::string formula)  
*Set the Unsteady species index by formula.*
- void [Set\\_Stoichiometric](#) (int i, double v)  
*Set the ith stoichiometric value (see [Reaction](#) object)*
- void [Set\\_Equilibrium](#) (double v)  
*Set the equilibrium constant (logK) (see [Reaction](#) object)*

- void [Set\\_Enthalpy](#) (double H)  
*Set the enthalpy of the reaction (J/mol) (see [Reaction](#) object)*
- void [Set\\_Entropy](#) (double S)  
*Set the entropy of the reaction (J/K/mol) (see [Reaction](#) object)*
- void [Set\\_EnthalpyANDEntropy](#) (double H, double S)  
*Set both the enthalpy and entropy (J/mol) & (J/K/mol) (see [Reaction](#) object)*
- void [Set\\_Energy](#) (double G)  
*Set the Gibbs free energy of reaction (J/mol) (see [Reaction](#) object)*
- void [Set\\_InitialValue](#) (double ic)  
*Set the initial value of the unsteady variable.*
- void [Set\\_MaximumValue](#) (double max)  
*Set the maximum value of the unsteady variable to a given value max (mol/L)*
- void [Set\\_Forward](#) (double forward)  
*Set the forward rate for the reaction (mol/L/hr)*
- void [Set\\_Reverse](#) (double reverse)  
*Set the reverse rate for the reaction (mol/L/hr)*
- void [Set\\_ForwardRef](#) (double Fref)  
*Set the forward reference rate (mol/L/hr)*
- void [Set\\_ReverseRef](#) (double Rref)  
*Set the reverse reference rate (mol/L/hr)*
- void [Set\\_ActivationEnergy](#) (double E)  
*Set the activation energy for the reaction (J/mol)*
- void [Set\\_Affinity](#) (double b)  
*Set the temperature affinity parameter for the reaction.*
- void [Set\\_TimeStep](#) (double dt)  
*Set the time step for the current simulation.*
- void [checkSpeciesEnergies](#) ()  
*Function to check [MasterSpeciesList](#) for species energy info (see [Reaction](#) object)*
- void [calculateEnergies](#) ()  
*Function to calculate the energy of the reaction (see [Reaction](#) object)*
- void [calculateEquilibrium](#) (double T)  
*Function to calculate the equilibrium constant (see [Reaction](#) object)*
- void [calculateRate](#) (double T)  
*Function to calculate the rate constant based on given temperature.*
- bool [haveEquilibrium](#) ()  
*True if equilibrium constant is given or can be calculated (see [Reaction](#) object)*
- bool [haveRate](#) ()  
*Function to return true if you have the forward or reverse rate calculated.*
- int [Get\\_Species\\_Index](#) ()  
*Fetch the index of the Unsteady species.*
- double [Get\\_Stoichiometric](#) (int i)  
*Fetch the ith stoichiometric value.*
- double [Get\\_Equilibrium](#) ()  
*Fetch the equilibrium constant (logK)*
- double [Get\\_Enthalpy](#) ()  
*Fetch the enthalpy of the reaction.*
- double [Get\\_Entropy](#) ()  
*Fetch the entropy of the reaction.*
- double [Get\\_Energy](#) ()  
*Fetch the energy of the reaction.*
- double [Get\\_InitialValue](#) ()

- Fetch the initial value of the variable.*

  - double [Get\\_MaximumValue](#) ()

*Fetch the maximum value of the variable.*
- double [Get\\_Forward](#) ()

*Fetch the forward rate.*
- double [Get\\_Reverse](#) ()

*Fetch the reverse rate.*
- double [Get\\_ForwardRef](#) ()

*Fetch the forward reference rate.*
- double [Get\\_ReverseRef](#) ()

*Fetch the reverse reference rate.*
- double [Get\\_ActivationEnergy](#) ()

*Fetch the activation energy for the reaction.*
- double [Get\\_Affinity](#) ()

*Fetch the temperature affinity for the reaction.*
- double [Get\\_TimeStep](#) ()

*Fetch the time step.*
- double [Eval\\_ReactionRate](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama)

*Calculate reaction rate (dC/dt) from concentrations and activities.*
- double [Eval\\_Residual](#) (const [Matrix](#)< double > &x\_new, const [Matrix](#)< double > &x\_old, const [Matrix](#)< double > &gama\_new, const [Matrix](#)< double > &gama\_old)

*Calculate the unsteady residual for the reaction using and implicit time discretization.*
- double [Eval\\_Residual](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama)

*Calculate the steady-state residual for this reaction (see [Reaction](#) object)*
- double [Eval\\_IC\\_Residual](#) (const [Matrix](#)< double > &x)

*Calculate the unsteady residual for initial conditions.*
- double [Explicit\\_Eval](#) (const [Matrix](#)< double > &x, const [Matrix](#)< double > &gama)

*Return an approximate explicit solution to our unsteady variable (mol/L)*

#### Protected Attributes

- double [initial\\_value](#)

*Initial value given at t=0 (in mol/L)*
- double [max\\_value](#)

*Maximum value plausible (in mol/L)*
- double [forward\\_rate](#)

*Forward reaction rate constant (in (mol/L)<sup>n</sup>/hr)*
- double [reverse\\_rate](#)

*Reverse reaction rate constant (in (mol/L)<sup>n</sup>/hr)*
- double [forward\\_ref\\_rate](#)

*Forward reference rate constant (in (mol/L)<sup>n</sup>/hr)*
- double [reverse\\_ref\\_rate](#)

*Reverse reference rate constant (in (mol/L)<sup>n</sup>/hr)*
- double [activation\\_energy](#)

*Activation or barrier energy for the reaction (J/mol)*
- double [temperature\\_affinity](#)

*Temperature affinity parameter (dimensionless)*
- double [time\\_step](#)

*Time step size for current step.*
- bool [HaveForward](#)

*True if can calculate, or was given the forward rate.*

- bool [HaveReverse](#)  
*True if can calculate, or was given the reverse rate.*
- bool [HaveForRef](#)  
*True if given the forward reference rate.*
- bool [HaveRevRef](#)  
*True if given the reverse reference rate.*
- int [species\\_index](#)  
*Index in MasterList of Unsteady Species.*

#### Additional Inherited Members

##### 5.49.1 Detailed Description

Unsteady [Reaction](#) Object (inherits from [Reaction](#))

C++ style object that holds data and functions associated with unsteady chemical reactions...

i.e.,  $aA + bB \xleftarrow{\text{reverse}} \text{forward} \xrightarrow{\text{reverse}} cC + dD$

This is essentially the same as the steady reaction, but we now have a forward and reverse reaction rate to deal with. It should be noted that this is a very simple kinetic reaction model based on splitting an overall equilibrium reaction into an overall forward and reverse reaction model. Therefore, it is not expected that this representation of the reaction will provide high accuracy results for reaction kinetics, but should at least provide an overall idea of the process occurring.

##### 5.49.2 Constructor & Destructor Documentation

###### 5.49.2.1 UnsteadyReaction::UnsteadyReaction ( )

Default Constructor.

###### 5.49.2.2 UnsteadyReaction::~~UnsteadyReaction ( )

Default Destructor.

##### 5.49.3 Member Function Documentation

###### 5.49.3.1 void UnsteadyReaction::Initialize\_Object ( MasterSpeciesList & List )

Function to initialize the [UnsteadyReaction](#) object from the [MasterSpeciesList](#).

###### 5.49.3.2 void UnsteadyReaction::Display\_Info ( )

Display the unsteady reaction information.

###### 5.49.3.3 void UnsteadyReaction::Set\_Species\_Index ( int i )

Set the Unsteady species index by number.

This function will set the unsteady species index by the index *i* given. That given index must correspond to the index of the species in the [MasterSpeciesList](#) that is being considered as the unsteady species.

#### Parameters

<i>i</i>	index of the unsteady species in the <a href="#">MasterSpeciesList</a>
----------	--

**5.49.3.4 void UnsteadyReaction::Set\_Species\_Index ( std::string *formula* )**

Set the Unsteady species index by formula.

This function will check the [MasterSpeciesList](#) for the molecule object that has the given formula, then set the unsteady species index based on the index of that species in the master list.

**Parameters**

<i>formula</i>	molecular formula of the unsteady species (see <a href="#">mola.h</a> for standard formatting)
----------------	--

**5.49.3.5 void UnsteadyReaction::Set\_Stoichiometric ( int *i*, double *v* )**

Set the *i*th stoichiometric value (see [Reaction](#) object)

**5.49.3.6 void UnsteadyReaction::Set\_Equilibrium ( double *v* )**

Set the equilibrium constant (logK) (see [Reaction](#) object)

**5.49.3.7 void UnsteadyReaction::Set\_Enthalpy ( double *H* )**

Set the enthalpy of the reaction (J/mol) (see [Reaction](#) object)

**5.49.3.8 void UnsteadyReaction::Set\_Entropy ( double *S* )**

Set the entropy of the reaction (J/K/mol) (see [Reaction](#) object)

**5.49.3.9 void UnsteadyReaction::Set\_EnthalpyANDEntropy ( double *H*, double *S* )**

Set both the enthalpy and entropy (J/mol) & (J/K/mol) (see [Reaction](#) object)

**5.49.3.10 void UnsteadyReaction::Set\_Energy ( double *G* )**

Set the Gibb's free energy of reaction (J/mol) (see [Reaction](#) object)

**5.49.3.11 void UnsteadyReaction::Set\_InitialValue ( double *ic* )**

Set the initial value of the unsteady variable.

This function sets the initial concentration value for the unsteady species to the given value *ic* (mol/L). Only unsteady species need to be given an initial value. All other species initial values for the overall system is setup based on a speciation calculation performed while holding the unsteady variables constant at their respective initial values.

**Parameters**

<i>ic</i>	initial concentration value for the unsteady object (mol/L)
-----------	---

**5.49.3.12 void UnsteadyReaction::Set\_MaximumValue ( double *max* )**

Set the maximum value of the unsteady variable to a given value *max* (mol/L)

This function will be called internally to help bound the unsteady variable to reasonable maximum values. That maximum is usually based on the mass balances for the current non-linear iteration.

**Parameters**

<i>max</i>	maximum allowable value for the unsteady variable (mol/L)
------------	---

**5.49.3.13 void UnsteadyReaction::Set\_Forward ( double *forward* )**

Set the forward rate for the reaction (mol/L/hr)

5.49.3.14 void UnsteadyReaction::Set\_Reverse ( double *reverse* )

Set the reverse rate for the reaction (mol/L/hr)

5.49.3.15 void UnsteadyReaction::Set\_ForwardRef ( double *Fref* )

Set the forward reference rate (mol/L/hr)

Unlike just setting the forward rate, this function sets a reference forward rate of the reaction that can be used to correct the overall forward rate based on system temperature and Arrhenius Rate Equation constants.

## Parameters

<i>Fref</i>	forward reference rate constant (mol/L/hr)
-------------	--

5.49.3.16 void UnsteadyReaction::Set\_ReverseRef ( double *Rref* )

Set the reverse reference rate (mol/L/hr)

Unlike just setting the reverse rate, this function sets a reference reverse rate of the reaction that can be used to correct the overall reverse rate based on system temperature and Arrhenius Rate Equation constants.

## Parameters

<i>Rref</i>	reverse reference rate constant (mol/L/hr)
-------------	--

5.49.3.17 void UnsteadyReaction::Set\_ActivationEnergy ( double *E* )

Set the activation energy for the reaction (J/mol)

This function will set the activation energy for the reaction to the given value of E. Note that we will only set one value for activation energy, even though there are rates for forward and reverse reactions. This is because we use the ratio of the rates and the equilibrium constant to establish the other rate. Therefore, we only need either the forward or reverse rate and the equilibrium constant to set all the rates.

## Parameters

<i>E</i>	activation energy for the forward or reverse rate, depending on which was given
----------	---

5.49.3.18 void UnsteadyReaction::Set\_Affinity ( double *b* )

Set the temperature affinity parameter for the reaction.

This function will set the temperature affinity for the reaction to the given value of b. Note that we will only set one value for temperature affinity, even though there are rates for forward and reverse reactions. This is because we use the ratio of the rates and the equilibrium constant to establish the other rate. Therefore, we only need either the forward or reverse rate and the equilibrium constant to set all the rates.

## Parameters

<i>b</i>	temperature affinity for the forward or reverse rate, depending on which was given
----------	--

5.49.3.19 void UnsteadyReaction::Set\_TimeStep ( double *dt* )

Set the time step for the current simulation.

## 5.49.3.20 void UnsteadyReaction::checkSpeciesEnergies ( )

Function to check [MasterSpeciesList](#) for species energy info (see [Reaction](#) object)

5.49.3.21 void UnsteadyReaction::calculateEnergies ( )

Function to calculate the energy of the reaction (see [Reaction](#) object)

5.49.3.22 void UnsteadyReaction::calculateEquilibrium ( double  $T$  )

Function to calculate the equilibrium constant (see [Reaction](#) object)

5.49.3.23 void UnsteadyReaction::calculateRate ( double  $T$  )

Function to calculate the rate constant based on given temperature.

This function will calculate and set either the forward or reverse rate for the unsteady reaction based on what information was given. If the forward rate information was given, then it sets the reverse rate and visa versa. If nothing was set correctly, an error will occur.

#### Parameters

$T$	temperature of the system in Kelvin
-----	-------------------------------------

5.49.3.24 bool UnsteadyReaction::haveEquilibrium ( )

True if equilibrium constant is given or can be calculated (see [Reaction](#) object)

5.49.3.25 bool UnsteadyReaction::haveRate ( )

Function to return true if you have the forward or reverse rate calculated.

5.49.3.26 int UnsteadyReaction::Get\_Species\_Index ( )

Fetch the index of the Unsteady species.

5.49.3.27 double UnsteadyReaction::Get\_Stoichiometric ( int  $i$  )

Fetch the  $i$ th stoichiometric value.

5.49.3.28 double UnsteadyReaction::Get\_Equilibrium ( )

Fetch the equilibrium constant (logK)

5.49.3.29 double UnsteadyReaction::Get\_Enthalpy ( )

Fetch the enthalpy of the reaction.

5.49.3.30 double UnsteadyReaction::Get\_Entropy ( )

Fetch the entropy of the reaction.

5.49.3.31 double UnsteadyReaction::Get\_Energy ( )

Fetch the energy of the reaction.

5.49.3.32 double UnsteadyReaction::Get\_InitialValue ( )

Fetch the initial value of the variable.

5.49.3.33 double UnsteadyReaction::Get\_MaximumValue ( )

Fetch the maximum value of the variable.



5.49.3.34 `double UnsteadyReaction::Get_Forward ( )`

Fetch the forward rate.

5.49.3.35 `double UnsteadyReaction::Get_Reverse ( )`

Fetch the reverse rate.

5.49.3.36 `double UnsteadyReaction::Get_ForwardRef ( )`

Fetch the forward reference rate.

5.49.3.37 `double UnsteadyReaction::Get_ReverseRef ( )`

Fetch the reverse reference rate.

5.49.3.38 `double UnsteadyReaction::Get_ActivationEnergy ( )`

Fetch the activation energy for the reaction.

5.49.3.39 `double UnsteadyReaction::Get_Affinity ( )`

Fetch the temperature affinity for the reaction.

5.49.3.40 `double UnsteadyReaction::Get_TimeStep ( )`

Fetch the time step.

5.49.3.41 `double UnsteadyReaction::Eval_ReactionRate ( const Matrix< double > & x, const Matrix< double > & gama )`

Calculate reaction rate (dC/dt) from concentrations and activities.

This function calculates the right hand side of the unsteady reaction equation based on the available rates, the current values of the non-linear variables ( $x=\log(C)$ ), and the activity coefficients (*gama*).

#### Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>gama</i>	matrix of activity coefficients for each species at the current non-linear step

5.49.3.42 `double UnsteadyReaction::Eval_Residual ( const Matrix< double > & x_new, const Matrix< double > & x_old, const Matrix< double > & gama_new, const Matrix< double > & gama_old )`

Calculate the unsteady residual for the reaction using and implicit time discretization.

This function uses the current time step and states of the non-linear variables and activities to form the residual contribution of the unsteady reaction. The time dependent functions are discretized using an implicit finite difference for best stability.

#### Parameters

<i>x_new</i>	matrix of the log(C) concentration values at the current non-linear step
<i>gama_new</i>	matrix of activity coefficients for each species at the current non-linear step
<i>x_old</i>	matrix of the log(C) concentration values at the previous non-linear step
<i>gama_old</i>	matrix of activity coefficients for each species at the previous non-linear step

5.49.3.43 `double UnsteadyReaction::Eval_Residual ( const Matrix< double > & x, const Matrix< double > & gama )`

Calculate the steady-state residual for this reaction (see [Reaction](#) object)

**5.49.3.44** `double UnsteadyReaction::Eval_IC_Residual ( const Matrix< double > & x )`

Calculate the unsteady residual for initial conditions.

Setting the initial conditions for all variables in the system requires a speciation calculation. However, we want the unsteady variables to be set to their respective initial conditions. Using this residual function imposes an equality constraint on those non-linear, unsteady variables allowing the rest of the speciation problem to be solved via PJFNK iterations.

**Parameters**

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
----------	--

**5.49.3.45** `double UnsteadyReaction::Explicit_Eval ( const Matrix< double > & x, const Matrix< double > & gama )`

Return an approximate explicit solution to our unsteady variable (mol/L)

This function will approximate the concentration of the unsteady variables based on an explicit time discretization. The purpose of this function is to try to provide the PJFNK method with a good initial guess for the values of the non-linear, unsteady variables. If we do not provide a good initial guess to these variables, then the PJFNK method may not converge to the correct solution, because the unsteady problem is the most difficult to solve.

**Parameters**

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>gama</i>	matrix of activity coefficients for each species at the current non-linear step

**5.49.4 Member Data Documentation****5.49.4.1** `double UnsteadyReaction::initial_value` [protected]

Initial value given at t=0 (in mol/L)

**5.49.4.2** `double UnsteadyReaction::max_value` [protected]

Maximum value plausible (in mol/L)

**5.49.4.3** `double UnsteadyReaction::forward_rate` [protected]

Forward reaction rate constant (in (mol/L)<sup>n</sup>/hr)

**5.49.4.4** `double UnsteadyReaction::reverse_rate` [protected]

Reverse reaction rate constant (in (mol/L)<sup>n</sup>/hr)

**5.49.4.5** `double UnsteadyReaction::forward_ref_rate` [protected]

Forward reference rate constant (in (mol/L)<sup>n</sup>/hr)

**5.49.4.6** `double UnsteadyReaction::reverse_ref_rate` [protected]

Reverse reference rate constant (in (mol/L)<sup>n</sup>/hr)

**5.49.4.7** `double UnsteadyReaction::activation_energy` [protected]

Activation or barrier energy for the reaction (J/mol)

**5.49.4.8** `double UnsteadyReaction::temperature_affinity` [protected]

Temperature affinity parameter (dimensionless)

## 5.49.4.9 double UnsteadyReaction::time\_step [protected]

Time step size for current step.

## 5.49.4.10 bool UnsteadyReaction::HaveForward [protected]

True if can calculate, or was given the forward rate.

## 5.49.4.11 bool UnsteadyReaction::HaveReverse [protected]

True if can calculate, or was given the reverse rate.

## 5.49.4.12 bool UnsteadyReaction::HaveForRef [protected]

True if given the forward reference rate.

## 5.49.4.13 bool UnsteadyReaction::HaveRevRef [protected]

True if given the reverse reference rate.

## 5.49.4.14 int UnsteadyReaction::species\_index [protected]

Index in MasterList of Unsteady Species.

The documentation for this class was generated from the following file:

- [shark.h](#)

## 5.50 ValueTypePair Class Reference

Value-Type Pair object to recognize data type of a string that was read.

```
#include <yaml_wrapper.h>
```

## Public Member Functions

- [ValueTypePair](#) ()  
*Default constructor.*
- [~ValueTypePair](#) ()  
*Default destructor.*
- [ValueTypePair](#) (const std::pair< std::string, int > &vt)  
*Constructor by pair.*
- [ValueTypePair](#) (std::string value, int type)  
*Construction by string and int.*
- [ValueTypePair](#) (const [ValueTypePair](#) &vt)  
*Copy constructor.*
- [ValueTypePair](#) & [operator=](#) (const [ValueTypePair](#) &vt)  
*Equals operator overload.*
- void [editValue](#) (std::string value)  
*Edits value to pair with UNKNOWN type.*
- void [editPair](#) (std::string value, int type)  
*Creates a paired Value-Type from the given args.*
- void [findType](#) ()  
*Determines the data type of the object.*
- void [assertType](#) (int type)  
*Forces a specific data type.*

- void [DisplayPair](#) ()  
*Display the pair information.*
- std::string [getString](#) ()  
*Returns the value of the pair as a string.*
- bool [getBool](#) ()  
*Returns the value of the pair as a bool.*
- double [getDouble](#) ()  
*Returns the value of the pair as a double.*
- int [getInt](#) ()  
*Returns the value of the pair as an int.*
- std::string [getValue](#) ()  
*Returns the value of the pair as it was given.*
- int [getType](#) ()  
*Returns the type of the pair.*
- std::pair< std::string, int > & [getPair](#) ()  
*Returns reference to the actual pair object.*

**Private Attributes**

- std::pair< std::string, int > [Value\\_Type](#)  
*pair object holding the Value and Type info*
- int [type](#)  
*Type of the value.*

**5.50.1 Detailed Description**

Value-Type Pair object to recognize data type of a string that was read.

C++ Object that creates a pair between a read in value as a string and an enum denoting what the data type of that string is. This object is primarily used in the other yamI\_wrapper objects, but can also be used for any string that you want to parse to identify it's type. The supported types are denoted in the data\_type enum and can be determined automatically by the [findType\(\)](#) function or can be specified by the [assertType\(\)](#) function.

**5.50.2 Constructor & Destructor Documentation****5.50.2.1 [ValueTypePair::ValueTypePair](#) ( )**

Default constructor.

**5.50.2.2 [ValueTypePair::~~ValueTypePair](#) ( )**

Default destructor.

**5.50.2.3 [ValueTypePair::ValueTypePair](#) ( const std::pair< std::string, int > & vt )**

Constructor by pair.

**5.50.2.4 [ValueTypePair::ValueTypePair](#) ( std::string value, int type )**

Construction by string and int.

**5.50.2.5 [ValueTypePair::ValueTypePair](#) ( const [ValueTypePair](#) & vt )**

Copy constructor.

### 5.50.3 Member Function Documentation

#### 5.50.3.1 **ValueTypePair& ValueTypePair::operator= ( const ValueTypePair & vt )**

Equals operator overload.

#### 5.50.3.2 **void ValueTypePair::editValue ( std::string value )**

Edits value to pair with UNKOWN type.

#### 5.50.3.3 **void ValueTypePair::editPair ( std::string value, int type )**

Creates a paired Value-Type from the given args.

#### 5.50.3.4 **void ValueTypePair::findType ( )**

Determines the data type of the object.

#### 5.50.3.5 **void ValueTypePair::assertType ( int type )**

Forces a specific data type.

#### 5.50.3.6 **void ValueTypePair::DisplayPair ( )**

Display the pair information.

#### 5.50.3.7 **std::string ValueTypePair::getString ( )**

Returns the value of the pair as a string.

#### 5.50.3.8 **bool ValueTypePair::getBool ( )**

Returns the value of the pair as a bool.

#### 5.50.3.9 **double ValueTypePair::getDouble ( )**

Returns the value of the pair as a double.

#### 5.50.3.10 **int ValueTypePair::getInt ( )**

Returns the value of the pair as an int.

#### 5.50.3.11 **std::string ValueTypePair::getValue ( )**

Returns the value of the pair as it was given.

#### 5.50.3.12 **int ValueTypePair::getType ( )**

Returns the type of the pair.

#### 5.50.3.13 **std::pair<std::string,int>& ValueTypePair::getPair ( )**

Returns reference to the actual pair object.

### 5.50.4 Member Data Documentation

#### 5.50.4.1 **std::pair<std::string,int> ValueTypePair::Value\_Type [private]**

pair object holding the Value and Type info

## 5.50.4.2 int ValueTypePair::type [private]

Type of the value.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 5.51 yaml\_cpp\_class Class Reference

Primary object used when reading and digitally storing yaml files.

```
#include <yaml_wrapper.h>
```

## Public Member Functions

- [yaml\\_cpp\\_class](#) ()  
*Default constructor.*
- [~yaml\\_cpp\\_class](#) ()  
*Default destructor.*
- int [setInputFile](#) (const char \*file)  
*Set the input file to be read.*
- int [readInputFile](#) ()  
*Reads through input file and stores into [YamlWrapper](#).*
- int [cleanup](#) ()  
*Deletes yaml\_c objects and closes the input file.*
- int [executeYamlRead](#) (const char \*file)  
*Runs the full execution of initialization, reading, and cleaning.*
- [YamlWrapper](#) & [getYamlWrapper](#) ()  
*Returns reference to the [YamlWrapper](#) Object.*
- void [DisplayContents](#) ()  
*Print out the contents of the read to the console window.*

## Private Attributes

- [YamlWrapper](#) [yaml\\_wrapper](#)  
*[YamlWrapper](#) object where digital file is stored.*
- FILE \* [input\\_file](#)  
*Function pointer to the yaml formatted file.*
- const char \* [file\\_name](#)  
*Name of the file to be parsed and read.*
- [yaml\\_parser\\_t](#) [token\\_parser](#)  
*C-YAML parser object for token based parsing.*
- [yaml\\_token\\_t](#) [current\\_token](#)  
*C-YAML token object for the current token in the file.*
- [yaml\\_token\\_t](#) [previous\\_token](#)  
*C-YAML token object for the previous token in the file.*

## 5.51.1 Detailed Description

Primary object used when reading and digitally storing yaml files.

C++ Object that holds the [YamlWrapper](#) object and the C-YAML objects necessary for reading and parsing a yaml formatted file. This is the primary object that users are expected to work with when using [yaml\\_wrapper.h](#) to read input files. It contains functions necessary to setup a read instance, read and parse the input, place the parsed input results into the digital [YamlWrapper](#) object, and allow the user to query that object.

The two main functions that the typical user will need are: (i) [executeYamlRead\(\)](#) and (ii) [getYamlWrapper](#). Make sure that the read function was called prior to querying the [YamlWrapper](#) structure. Do not call the [cleanup\(\)](#) function if using [executeYamlRead\(\)](#). That function will be automatically called after the read is complete.

## 5.51.2 Constructor &amp; Destructor Documentation

5.51.2.1 `yaml_cpp_class::yaml_cpp_class ( )`

Default constructor.

5.51.2.2 `yaml_cpp_class::~yaml_cpp_class ( )`

Default destructor.

## 5.51.3 Member Function Documentation

5.51.3.1 `int yaml_cpp_class::setInputFile ( const char * file )`

Set the input file to be read.

5.51.3.2 `int yaml_cpp_class::readInputFile ( )`

Reads through input file and stores into [YamlWrapper](#).

5.51.3.3 `int yaml_cpp_class::cleanup ( )`

Deletes `yaml_c` objects and closes the input file.

5.51.3.4 `int yaml_cpp_class::executeYamlRead ( const char * file )`

Runs the full execution of initialization, reading, and cleaning.

5.51.3.5 `YamlWrapper& yaml_cpp_class::getYamlWrapper ( )`

Returns reference to the [YamlWrapper](#) Object.

5.51.3.6 `void yaml_cpp_class::DisplayContents ( )`

Print out the contents of the read to the console window.

## 5.51.4 Member Data Documentation

5.51.4.1 `YamlWrapper yaml_cpp_class::yaml_wrapper [private]`

[YamlWrapper](#) object where digital file is stored.

5.51.4.2 `FILE* yaml_cpp_class::input_file [private]`

Function pointer to the yaml formatted file.

5.51.4.3 `const char* yaml_cpp_class::file_name` [private]

Name of the file to be parsed and read.

5.51.4.4 `yaml_parser_t yaml_cpp_class::token_parser` [private]

C-YAML parser object for token based parsing.

5.51.4.5 `yaml_token_t yaml_cpp_class::current_token` [private]

C-YAML token object for the current token in the file.

5.51.4.6 `yaml_token_t yaml_cpp_class::previous_token` [private]

C-YAML token object for the previous token in the file.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 5.52 YamlWrapper Class Reference

Object for the entire yaml file holding all documents, header, sub-headers, keys, and values.

```
#include <yaml_wrapper.h>
```

### Public Member Functions

- [YamlWrapper](#) ()  
*Default constructor.*
- [~YamlWrapper](#) ()  
*Default destructor.*
- [YamlWrapper](#) (const [YamlWrapper](#) &yaml)  
*Copy constructor.*
- [YamlWrapper](#) (std::string key, const [Document](#) &doc)  
*Constructor by a single document.*
- [YamlWrapper](#) & [operator=](#) (const [YamlWrapper](#) &yaml)  
*Equals overload.*
- [Document](#) & [operator\(\)](#) (const std::string key)  
*Return the [Document](#) reference at the given key.*
- [Document](#) [operator\(\)](#) (const std::string key) const  
*Return the [Document](#) at the given key.*
- std::map< std::string, [Document](#) > & [getDocMap](#) ()  
*Return reference to the document map.*
- [Document](#) & [getDocument](#) (std::string key)  
*Return reference to the document at the key.*
- std::map< std::string, [Document](#) >::const\_iterator [end](#) () const  
*Returns a const iterator pointing to the end of the list.*
- std::map< std::string, [Document](#) >::iterator [end](#) ()  
*Returns an iterator pointing to the end of the list.*
- std::map< std::string, [Document](#) >::const\_iterator [begin](#) () const  
*Returns a const iterator pointing to the beginning of the list.*



- `std::map< std::string, Document >::iterator begin ()`  
*Returns an iterator pointing to the beginning of the list.*
- `void clear ()`  
*Clear out the yaml object.*
- `void resetKeys ()`  
*Resets all the keys in DocumentMap to match document names.*
- `void changeKey (std::string oldKey, std::string newKey)`  
*Change a given oldKey in the map to the newKey given.*
- `void revalidateAllKeys ()`  
*Resets and validates all keys in the structure.*
- `void DisplayContents ()`  
*Display the contents of the wrapper.*
- `void addDocKey (std::string key)`  
*Add a key to the document map.*
- `void copyAnchor2Alias (std::string alias, Document &ref)`  
*Find the anchor in the map, and copy to the Document reference given.*
- `int size ()`  
*Return the size of the document map.*
- `Document & getAnchoredDoc (std::string alias)`  
*Return the reference to the document that is anchored with the given alias.*
- `Document & getDocFromHeadAlias (std::string alias)`  
*Return reference to the document that contains the header with the given alias.*
- `Document & getDocFromSubAlias (std::string alias)`  
*Return reference to the document that contains the subheader with the given alias.*

#### Private Attributes

- `std::map< std::string, Document > Doc_Map`  
*Map of the documents contained within the wrapper.*

#### 5.52.1 Detailed Description

Object for the entire yaml file holding all documents, header, sub-headers, keys, and values.

C++ Object for the yaml file. This object holds a map of all Documents in the yaml file. Each document holds a map of Key-values and Headers. The Headers hold maps of Key-values and SubHeaders, and each SubHeader can hold more Key-values.

This object is used to represent a digital and queryable structure for all information contained within a yaml file. There are some limitations to what can be held here, and those limitations are based on the limitations in the C-YAML Library token parser. The main limitation is that the deepest level of allowable recursion in the file is SubHeader. Meaning that you are not allowed to have Sub-SubHeaders underneath a SubHeader object. This imposes a hard limit to number of nested lists that can be in a single Document object.

When using `yaml_cpp_class`, this object will generally be what you query into to get the information from your yaml input files. From this object, functions and operators are provided to give you the capability of querying down into any allowable level of the file by the keys that were used in the file. Be sure that you are querying the correct objects by the correct keys, otherwise errors and exceptions will be thrown.

#### 5.52.2 Constructor & Destructor Documentation

##### 5.52.2.1 YamlWrapper::YamlWrapper ( )

Default constructor.

### 5.52.2.2 YamlWrapper::~YamlWrapper ( )

Default destructor.

### 5.52.2.3 YamlWrapper::YamlWrapper ( const YamlWrapper & yml )

Copy constructor.

### 5.52.2.4 YamlWrapper::YamlWrapper ( std::string key, const Document & doc )

Constructor by a single document.

## 5.52.3 Member Function Documentation

### 5.52.3.1 YamlWrapper& YamlWrapper::operator= ( const YamlWrapper & yml )

Equals overload.

### 5.52.3.2 Document& YamlWrapper::operator() ( const std::string key )

Return the [Document](#) reference at the given key.

### 5.52.3.3 Document YamlWrapper::operator() ( const std::string key ) const

Return the [Document](#) at the given key.

### 5.52.3.4 std::map<std::string, Document>& YamlWrapper::getDocMap ( )

Return reference to the document map.

### 5.52.3.5 Document& YamlWrapper::getDocument ( std::string key )

Return reference to the document at the key.

### 5.52.3.6 std::map<std::string, Document>::const\_iterator YamlWrapper::end ( ) const

Returns a const iterator pointing to the end of the list.

### 5.52.3.7 std::map<std::string, Document>::iterator YamlWrapper::end ( )

Returns an iterator pointing to the end of the list.

### 5.52.3.8 std::map<std::string, Document>::const\_iterator YamlWrapper::begin ( ) const

Returns a const iterator pointing to the beginning of the list.

### 5.52.3.9 std::map<std::string, Document>::iterator YamlWrapper::begin ( )

Returns an iterator pointing to the beginning of the list.

### 5.52.3.10 void YamlWrapper::clear ( )

Clear out the yaml object.

### 5.52.3.11 void YamlWrapper::resetKeys ( )

Resets all the keys in DocumentMap to match document names.

### 5.52.3.12 void YamlWrapper::changeKey ( std::string oldKey, std::string newKey )

Change a given oldKey in the map to the newKey given.

5.52.3.13 void YamlWrapper::revalidateAllKeys ( )

Resets and validates all keys in the structure.

5.52.3.14 void YamlWrapper::DisplayContents ( )

Display the contents of the wrapper.

5.52.3.15 void YamlWrapper::addDocKey ( std::string key )

Add a key to the document map.

5.52.3.16 void YamlWrapper::copyAnchor2Alias ( std::string alias, Document & ref )

Find the anchor in the map, and copy to the [Document](#) reference given.

5.52.3.17 int YamlWrapper::size ( )

Return the size of the document map.

5.52.3.18 Document& YamlWrapper::getAnchoredDoc ( std::string alias )

Return the reference to the document that is anchored with the given alias.

5.52.3.19 Document& YamlWrapper::getDocFromHeadAlias ( std::string alias )

Return reference to the document that contains the header with the given alias.

5.52.3.20 Document& YamlWrapper::getDocFromSubAlias ( std::string alias )

Return reference to the document that contains the subheader with the given alias.

## 5.52.4 Member Data Documentation

5.52.4.1 std::map<std::string, Document> YamlWrapper::Doc\_Map [private]

Map of the documents contained within the wrapper.

The documentation for this class was generated from the following file:

- [yaml\\_wrapper.h](#)

## 6 File Documentation

### 6.1 dogfish.h File Reference

Diffusion Object Governing Fiber Interior Sorption History.

```
#include "finch.h"
#include "mola.h"
```

#### Classes

- struct [DOGFISH\\_PARAM](#)  
*Data structure for species-specific parameters.*
- struct [DOGFISH\\_DATA](#)  
*Primary data structure for running the DOGFISH application.*

## Functions

- void `print2file_species_header` (FILE \*Output, DOGFISH\_DATA \*dog\_dat, int i)  
*Function to print a species based header for the output file.*
- void `print2file_DOGFISH_header` (DOGFISH\_DATA \*dog\_dat)  
*Function to print a time and space header for the output file.*
- void `print2file_DOGFISH_result_old` (DOGFISH\_DATA \*dog\_dat)  
*Function to print out the old time results for the output file.*
- void `print2file_DOGFISH_result_new` (DOGFISH\_DATA \*dog\_dat)  
*Function to print out the new time results for the output file.*
- double `default_Retardation` (int i, int l, const void \*data)  
*Default function for the retardation coefficient.*
- double `default_IntraDiffusion` (int i, int l, const void \*data)  
*Default function for the intraparticle diffusion coefficient.*
- double `default_FilmMTCoeff` (int i, const void \*data)  
*Default function for the film mass transfer coefficient.*
- double `default_SurfaceConcentration` (int i, const void \*data)  
*Default function for the fiber surface concentration.*
- int `setup_DOGFISH_DATA` (FILE \*file, double(\*eval\_R)(int i, int l, const void \*user\_data), double(\*eval\_DI)(int i, int l, const void \*user\_data), double(\*eval\_kf)(int i, const void \*user\_data), double(\*eval\_qs)(int i, const void \*user\_data), const void \*user\_data, DOGFISH\_DATA \*dog\_dat)  
*Function will set up the memory and pointers for use in the DOGFISH simulations.*
- int `DOGFISH_Executioner` (DOGFISH\_DATA \*dog\_dat)  
*Function to serially call all other functions need to solve the system at one time step.*
- int `set_DOGFISH_ICs` (DOGFISH\_DATA \*dog\_dat)  
*Function called to evaluate the initial conditions for the time dependent problem.*
- int `set_DOGFISH_timestep` (DOGFISH\_DATA \*dog\_dat)  
*Function sets the time step size for the next step forward in the simulation.*
- int `DOGFISH_preprocesses` (DOGFISH\_DATA \*dog\_dat)  
*Function to perform preprocess actions to be used before calling any solver.*
- int `set_DOGFISH_params` (const void \*user\_data)  
*Function to calculate the values of all parameters for all species at all nodes.*
- int `DOGFISH_postprocesses` (DOGFISH\_DATA \*dog\_dat)  
*Function to perform post-solve actions such as printing out results.*
- int `DOGFISH_reset` (DOGFISH\_DATA \*dog\_dat)  
*Function to reset the matrices and vectors and prepare for next time step.*
- int `DOGFISH` (DOGFISH\_DATA \*dog\_dat)  
*Function performs all necessary steps to step the diffusion simulation through time.*
- int `DOGFISH_TESTS` ()  
*Running DOGFISH tests.*

## 6.1.1 Detailed Description

Diffusion Object Governing Fiber Interior Sorption History. dogfish.cpp

This set of objects and functions is used to numerically solve linear or non-linear diffusion physics of aqueous ions into cylindrical adsorbent fibers. Boundary conditions for this problem could be a film mass transfer, reaction, or dirichlet condition depending on the type of problem being solve.

## Warning

Functions and methods in this file are still under construction.

**Author**

Austin Ladshaw

**Date**

04/09/2015

**Copyright**

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

**6.1.2 Function Documentation****6.1.2.1 void print2file\_species\_header ( FILE \* *Output*, DOGFISH\_DATA \* *dog\_dat*, int *i* )**

Function to print a species based header for the output file.

**6.1.2.2 void print2file\_DOGFISH\_header ( DOGFISH\_DATA \* *dog\_dat* )**

Function to print a time and space header for the output file.

**6.1.2.3 void print2file\_DOGFISH\_result\_old ( DOGFISH\_DATA \* *dog\_dat* )**

Function to print out the old time results for the output file.

**6.1.2.4 void print2file\_DOGFISH\_result\_new ( DOGFISH\_DATA \* *dog\_dat* )**

Function to print out the new time results for the output file.

**6.1.2.5 double default\_Retardation ( int *i*, int *l*, const void \* *data* )**

Default function for the retardation coefficient.

The default retardation coefficient for this problem is 1.0 for all time and space. Therefore, this function will only ever return a 1.

**Parameters**

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>data</i>	pointer to the <a href="#">DOGFISH_DATA</a> structure

**6.1.2.6 double default\_IntraDiffusion ( int *i*, int *l*, const void \* *data* )**

Default function for the intraparticle diffusion coefficient.

The default intraparticle diffusivity is to assume that each species *i* has a constant diffusivity. Therefore, this function returns the value of the parameter `intraparticle_diffusion` from the [DOGFISH\\_PARAM](#) structure for each adsorbing species *i*. Each species may have a different diffusivity.

**Parameters**

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>data</i>	pointer to the <a href="#">DOGFISH_DATA</a> structure

6.1.2.7 double default\_FilmMTCoeff ( int *i*, const void \* *data* )

Default function for the film mass transfer coefficient.

The default film mass transfer coefficient will be to assume that this value is a constant for each species *i*. Therefore, this function returns the parameter value of film\_transfer\_coeff from the [DOGFISH\\_PARAM](#) structure for each adsorbing species *i*.

## Parameters

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>data</i>	pointer to the <a href="#">DOGFISH_DATA</a> structure

6.1.2.8 double default\_SurfaceConcentration ( int *i*, const void \* *data* )

Default function for the fiber surface concentration.

The default fiber surface concentration will be to assume that this value is a constant for each species *i*. Therefore, this function returns the parameter value of surface\_concentration from the [DOGFISH\\_PARAM](#) structure for each adsorbing species *i*.

## Parameters

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>data</i>	pointer to the <a href="#">DOGFISH_DATA</a> structure

6.1.2.9 int setup\_DOGFISH\_DATA ( FILE \* *file*, double (\*)(int *i*, int *l*, const void \* *user\_data*) *eval\_R*, double (\*)(int *i*, int *l*, const void \* *user\_data*) *eval\_DI*, double (\*)(int *i*, const void \* *user\_data*) *eval\_kf*, double (\*)(int *i*, const void \* *user\_data*) *eval\_qs*, const void \* *user\_data*, DOGFISH\_DATA \* *dog\_dat* )

Function will set up the memory and pointers for use in the DOGFISH simulations.

The pointers to the output file, parameter functions, and data structures are passed into this function to setup the problem in memory. This function must always be called prior to calling any other DOGFISH routine and after the [DOGFISH\\_DATA](#) structure has been initialized.

## Parameters

<i>file</i>	pointer to the output file to print out results
<i>eval_R</i>	function pointer for the retardation coefficient function
<i>eval_DI</i>	function pointer for the intraparticle diffusion function
<i>eval_kf</i>	function pointer for the film mass transfer function
<i>eval_qs</i>	function pointer for the surface concentration function
<i>user_data</i>	pointer for the user's own data structure (only if using custom functions)
<i>dog_dat</i>	pointer for the <a href="#">DOGFISH_DATA</a> structure

6.1.2.10 int DOGFISH\_Executioner ( DOGFISH\_DATA \* *dog\_dat* )

Function to serially call all other functions need to solve the system at one time step.

This function will call the DOGFISH\_preprocesses function, followed by the FINCH solver functions for each species *i*, then call the DOGFISH\_postprocesses function. After completion, this would have solved the diffusion physics for a single time step.

6.1.2.11 int set\_DOGFISH\_ICs ( DOGFISH\_DATA \* *dog\_dat* )

Function called to evaluate the initial conditions for the time dependent problem.

This function will use information in [DOGFISH\\_DATA](#) to setup the initial conditions, initial parameter values, and initial sorption averages for each species. This function always assumes a constant initial condition for the sorption of each species.

### 6.1.2.12 int set\_DOGFISH\_timestep ( DOGFISH\_DATA \* *dog\_dat* )

Function sets the time step size for the next step forward in the simulation.

This function will set the next time step size based on the spatial discretization of the fiber. Maximum time step size is locked at 0.5 hours.

### 6.1.2.13 int DOGFISH\_preprocesses ( DOGFISH\_DATA \* *dog\_dat* )

Function to perform preprocess actions to be used before calling any solver.

This function will call all of the parameter functions in order to establish boundary condition parameter values prior to calling the FINCH solvers.

### 6.1.2.14 int set\_DOGFISH\_params ( const void \* *user\_data* )

Function to calculate the values of all parameters for all species at all nodes.

This function is passed to the [FINCH\\_DATA](#) data structure and set as the setparams function pointer. FINCH calls this function during it's solver routine to setup the non-linear form of the problem and solve the non-linear system.

#### Parameters

<i>user_data</i>	this is actually the <a href="#">DOGFISH_DATA</a> structure, but is passed anonymously to FINCH
------------------	---

### 6.1.2.15 int DOGFISH\_postprocesses ( DOGFISH\_DATA \* *dog\_dat* )

Function to perform post-solve actions such as printing out results.

This function increments the total\_steps counter in [DOGFISH\\_DATA](#) to keep a running total of all solver steps taken. Additionally, it prints out the results of the current time simulation to the output file.

### 6.1.2.16 int DOGFISH\_reset ( DOGFISH\_DATA \* *dog\_dat* )

Function to reset the matrices and vectors and prepare for next time step.

This function will reset the matrix and vector information of [DOGFISH\\_DATA](#) and [FINCH\\_DATA](#) to prepare for the next simulation step in time.

### 6.1.2.17 int DOGFISH ( DOGFISH\_DATA \* *dog\_dat* )

Function performs all necessary steps to step the diffusion simulation through time.

This function calls the initial conditions, set time step, executioner, and reset functions to step the simulation through time. It will only exit when the simulation time is reached or if an error occurs.

### 6.1.2.18 int DOGFISH.TESTS ( )

Running DOGFISH tests.

This function is called from the UI to run a test simulation of DOGFISH. Output is stored in a DOGFISH\_TestOutput.txt file in a sub-directory "output" from the directory in which the executable was called.

## 6.2 eel.h File Reference

Easy-access Element Library.

```
#include <stdio.h>
#include <math.h>
#include <iostream>
#include <fstream>
#include <stdlib.h>
#include <vector>
#include <time.h>
#include <float.h>
#include <string>
#include "error.h"
```

### Classes

- class [Atom](#)  
*[Atom](#) object to hold information about specific atoms in the periodic table (click [Atom](#) to go to function definitions)*
- class [PeriodicTable](#)  
*Class object that store a digital copy of all [Atom](#) objects.*

### Functions

- int [EEL\\_TESTS](#) ()  
*Test function to exercise the class objects and check for errors.*

#### 6.2.1 Detailed Description

Easy-access Element Library. eel.cpp

This file contains two C++ objects: (i) [Atom](#) and (ii) [PeriodicTable](#).

The [Atom](#) class defines all relevant information necessary for dealing with actual atoms. However, this is not necessarily all the information that one may need for any simulation dealing with atoms. Instead, it is really just a place holder used to construct Molecules and hold oxidation state and molecular/atomic weight information.

The [PeriodicTable](#) class creates a digital version of a complete periodic table. Further development of this object can make it possible to query this structure for a particular atom upon user request.

### Warning

The [Atom](#) class is mostly complete, but the [PeriodicTable](#) object is just a place holder.

### Author

Austin Ladshaw

### Date

02/23/2015

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## 6.2.2 Function Documentation

## 6.2.2.1 int EEL\_TESTS ( )

Test function to exercise the class objects and check for errors.

## 6.3 egret.h File Reference

Estimation of Gas-phase pRopErTies.

```
#include "macaw.h"
```

## Classes

- struct [PURE\\_GAS](#)  
*Data structure holding all the parameters for each pure gas spieces.*
- struct [MIXED\\_GAS](#)  
*Data structure holding information necessary for computing mixed gas properties.*

## Macros

- #define [Rstd](#) 8.3144621  
*Gas Constant in J/K/mol (or) L\*kPa/K/mol (Standard Units)*
- #define [RE3](#) 8.3144621E+3  
*Gas Constant in cm<sup>3</sup>\*kPa/K/mol (Convenient for density calculations)*
- #define [Po](#) 100.0  
*Standard state pressure (kPa)*
- #define [Cstd](#)(p, T) ((p)/(Rstd\*T))  
*Calculation of concentration/density from partial pressure (Cstd = mol/L)*
- #define [CE3](#)(p, T) ((p)/(RE3\*T))  
*Calculation of concentration/density from partial pressure (CE3 = mol/cm<sup>3</sup>)*
- #define [Pstd](#)(c, T) ((c)\*Rstd\*T)  
*Calculation of partial pressure from concentration/density (c = mol/L)*
- #define [PE3](#)(c, T) ((c)\*RE3\*T)  
*Calculation of partial pressure from concentration/density (c = mol/cm<sup>3</sup>)*
- #define [Nu](#)(mu, rho) ((mu)/(rho))  
*Calculation of kinematic viscosity from dynamic viscosity and density (cm<sup>2</sup>/s)*
- #define [PSI](#)(T) (0.873143 + (0.000072375\*T))  
*Calculation of temperature correction factor for dynamic viscosity.*
- #define [Dp\\_ij](#)(Dij, PT) ((PT\*Dij)/Po)  
*Calculation of the corrected binary diffusivity (cm<sup>2</sup>/s)*
- #define [D\\_ij](#)(MWi, MWj, rhoi, rhoj, mui, muj) ( (4.0 / sqrt(2.0)) \* pow(((1/MWi)+(1/MWj)),0.5) ) / pow( (pow((pow((rhoi/(1.385\*mui)),2.0)/MWi),0.25)+ pow((pow((rhoj/(1.385\*muj)),2.0)/MWj),0.25)),2.0 )  
*Calculation of binary diffusion based on MW, density, and viscosity info (cm<sup>2</sup>/s)*
- #define [Mu](#)(muo, To, C, T) (muo \* ((To + C)/(T + C)) \* pow((T/To),1.5) )  
*Calculation of single species viscosity from Sutherland's Equ. (g/cm/s)*
- #define [D\\_ii](#)(rhoi, mui) (1.385\*mui/rhoi)  
*Calculation of self-diffusivity (cm<sup>2</sup>/s)*
- #define [ReNum](#)(u, L, nu) (u\*L/nu)  
*Calculation of the Reynold's Number (-)*
- #define [ScNum](#)(nu, D) (nu/D)

*Calculation of the Schmidt Number (-)*

- #define `FilmMTCoeff`(D, L, Re, Sc)  $((D/L)*(2.0 + (1.1*pow(Re,0.6)*pow(Sc,0.3))))$

*Calculation of film mass transfer coefficient (cm/s)*

## Functions

- int `initialize_data` (int N, `MIXED_GAS` \*gas\_dat)  
*Function to initialize the `MIXED_GAS` structure based on number of gas species.*
- int `set_variables` (double PT, double T, double us, double L, std::vector< double > &y, `MIXED_GAS` \*gas\_dat)  
*Function to set the values of the parameters in the gas phase.*
- int `calculate_properties` (`MIXED_GAS` \*gas\_dat)  
*Function to calculate the gas properties based on information in `MIXED_GAS`.*
- int `EGRET_TESTS` ()  
*Function runs a series of tests for the EGRET file.*

### 6.3.1 Detailed Description

Estimation of Gas-phase pRopErTies. egret.cpp

This file is responsible for estimating various temperature, pressure, and concentration dependent parameters to be used in other models for gas phase adsorption, mass transfer, and or mass transport. The goal of this file is to eliminate redundancies in code such that the higher level programs operate more efficiently and cleanly. Calculations made here are based on kinetic theory of gases, ideal gas law, and some empirical models that were developed to account for changes in density and viscosity with changes in temperature between standard temperatures and up to 1000 K.

#### Author

Austin Ladshaw

#### Date

01/29/2015

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### 6.3.2 Macro Definition Documentation

#### 6.3.2.1 #define Rstd 8.3144621

Gas Constant in J/K/mol (or) L\*kPa/K/mol (Standard Units)

#### 6.3.2.2 #define RE3 8.3144621E+3

Gas Constant in cm<sup>3</sup>\*kPa/K/mol (Convenient for density calculations)

#### 6.3.2.3 #define Po 100.0

Standard state pressure (kPa)

#### 6.3.2.4 #define Cstd( p, T ) ((p)/(Rstd\*T))

Calculation of concentration/density from partial pressure (Cstd = mol/L)

6.3.2.5 `#define CE3( p, T ) ((p)/(RE3*T))`

Calculation of concentration/density from partial pressure ( $CE3 = \text{mol}/\text{cm}^3$ )

6.3.2.6 `#define Pstd( c, T ) ((c)*Rstd*T)`

Calculation of partial pressure from concentration/density ( $c = \text{mol}/\text{L}$ )

6.3.2.7 `#define PE3( c, T ) ((c)*RE3*T)`

Calculation of partial pressure from concentration/density ( $c = \text{mol}/\text{cm}^3$ )

6.3.2.8 `#define Nu( mu, rho ) ((mu)/(rho))`

Calculation of kinematic viscosity from dynamic viscosity and density ( $\text{cm}^2/\text{s}$ )

6.3.2.9 `#define PSI( T ) (0.873143 + (0.000072375*T))`

Calculation of temperature correction factor for dynamic viscosity.

6.3.2.10 `#define Dp_ij( Dij, PT ) ((PT*Dij)/Po)`

Calculation of the corrected binary diffusivity ( $\text{cm}^2/\text{s}$ )

6.3.2.11 `#define D_ij( MWi, MWj, rhoi, rhoj, mui, muj ) ( (4.0 / sqrt(2.0)) * pow(((1/MWi)+(1/MWj)),0.5) ) / pow( pow((pow((rhoi/(1.385*mui)),2.0)/MWi),0.25)+ pow((pow((rhoj/(1.385*muj)),2.0)/MWj),0.25)),2.0 )`

Calculation of binary diffusion based on MW, density, and viscosity info ( $\text{cm}^2/\text{s}$ )

6.3.2.12 `#define Mu( muo, To, C, T ) (muo * ((To + C)/(T + C)) * pow((T/To),1.5) )`

Calculation of single species viscosity from Sutherland's Equ. ( $\text{g}/\text{cm}/\text{s}$ )

6.3.2.13 `#define D_ii( rhoi, mui ) (1.385*mui/rhoi)`

Calculation of self-diffusivity ( $\text{cm}^2/\text{s}$ )

6.3.2.14 `#define ReNum( u, L, nu ) (u*L/nu)`

Calculation of the Reynold's Number (-)

6.3.2.15 `#define ScNum( nu, D ) (nu/D)`

Calculation of the Schmidt Number (-)

6.3.2.16 `#define FilmMTCoeff( D, L, Re, Sc ) ((D/L)*(2.0 + (1.1*pow(Re,0.6)*pow(Sc,0.3))))`

Calculation of film mass transfer coefficient ( $\text{cm}/\text{s}$ )

### 6.3.3 Function Documentation

6.3.3.1 `int initialize_data ( int N, MIXED_GAS * gas_dat )`

Function to initialize the `MIXED_GAS` structure based on number of gas species.

This function will initialize the sizes of all vector objects in the `MIXED_GAS` structure based on the number of gas species indicated by N.

6.3.3.2 `int set_variables ( double PT, double T, double us, double L, std::vector< double > & y, MIXED_GAS * gas_dat )`

Function to set the values of the parameters in the gas phase.

The gas phase properties are a function of total pressure, gas temperature, gas velocity, characteristic length, and the mole fractions of each species in the gas phase. Prior to calculating the gas phase properties, these parameters must be set and updated as they change.

#### Parameters

<i>PT</i>	total gas pressure in kPa
<i>T</i>	gas temperature in K
<i>us</i>	gas velocity in cm/s
<i>L</i>	characteristic length in cm (this depends on the particular system)
<i>y</i>	vector of gas mole fractions of each species in the mixture
<i>gas_dat</i>	pointer to the <a href="#">MIXED_GAS</a> data structure

#### 6.3.3.3 int calculate\_properties ( MIXED\_GAS \* gas\_dat )

Function to calculate the gas properties based on information in [MIXED\\_GAS](#).

This function uses the kinetic theory of gases, combined with other semi-empirical models, to predict and approximate several properties of the mixed gas phase that might be necessary when running any gas dynamical simulation. This includes mass and energy transfer equations, as well as adsorption kinetics in porous adsorbents.

#### 6.3.3.4 int EGRET\_TESTS ( )

Function runs a series of tests for the EGRET file.

The test looks at a standard air with 5 primary species of interest and calculates the gas properties from 273 K to 373 K. This function can be called from the UI.

## 6.4 error.h File Reference

All error types are defined here.

```
#include <iostream>
```

#### Macros

- `#define mError(i)`

#### Enumerations

- `enum error_type {`  
`generic_error, file_dne, indexing_error, magpie_reverse_error,`  
`simulation_fail, invalid_components, invalid_boolean, invalid_molefraction,`  
`invalid_gas_sum, invalid_solid_sum, scenario_fail, out_of_bounds,`  
`non_square_matrix, dim_mis_match, empty_matrix, opt_no_support,`  
`invalid_fraction, ortho_check_fail, unstable_matrix, no_diffusion,`  
`negative_mass, negative_time, matvec_mis_match, arg_matrix_same,`  
`singular_matrix, matrix_too_small, invalid_size, nullptr_func,`  
`invalid_norm, vector_out_of_bounds, zero_vector, tensor_out_of_bounds,`  
`non_real_edge, nullptr_error, invalid_atom, invalid_proton,`  
`invalid_neutron, invalid_electron, invalid_valence, string_parse_error,`  
`unregistered_name, rxn_rate_error, invalid_species, duplicate_variable,`  
`missing_information, invalid_type, key_not_found, anchor_alias_dne,`  
`initial_error, not_a_token, read_error, invalid_console_input }`

*List of names for error type.*

## Functions

- void `error` (int flag)

*Error function customizes output message based on flag.*

### 6.4.1 Detailed Description

All error types are defined here. `error.cpp`

This file defines all the different errors that may occur in any simulation in any file. Those errors are recognized by an enum with is then passed through to the `error.cpp` file that customizes the error message to the console. A macro will also print out the file name and line number where the error occurred.

## Author

Austin Ladshaw

## Date

04/28/2014

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### 6.4.2 Macro Definition Documentation

#### 6.4.2.1 `#define mError( i )`

##### Value:

```
{error(i);  
std::cout << "Source: " << __FILE__ << "\nLine: " << __LINE__ << std::endl;}
```

### 6.4.3 Enumeration Type Documentation

#### 6.4.3.1 `enum error_type`

List of names for error type.

##### Enumerator

***generic\_error***  
***file\_dne***  
***indexing\_error***  
***magpie\_reverse\_error***  
***simulation\_fail***  
***invalid\_components***  
***invalid\_boolean***  
***invalid\_molefraction***  
***invalid\_gas\_sum***  
***invalid\_solid\_sum***  
***scenario\_fail***

*out\_of\_bounds*  
*non\_square\_matrix*  
*dim\_mis\_match*  
*empty\_matrix*  
*opt\_no\_support*  
*invalid\_fraction*  
*ortho\_check\_fail*  
*unstable\_matrix*  
*no\_diffusion*  
*negative\_mass*  
*negative\_time*  
*matvec\_mis\_match*  
*arg\_matrix\_same*  
*singular\_matrix*  
*matrix\_too\_small*  
*invalid\_size*  
*nullptr\_func*  
*invalid\_norm*  
*vector\_out\_of\_bounds*  
*zero\_vector*  
*tensor\_out\_of\_bounds*  
*non\_real\_edge*  
*nullptr\_error*  
*invalid\_atom*  
*invalid\_proton*  
*invalid\_neutron*  
*invalid\_electron*  
*invalid\_valence*  
*string\_parse\_error*  
*unregistered\_name*  
*rxn\_rate\_error*  
*invalid\_species*  
*duplicate\_variable*  
*missing\_information*  
*invalid\_type*  
*key\_not\_found*  
*anchor\_alias\_dne*  
*initial\_error*  
*not\_a\_token*  
*read\_error*  
*invalid\_console\_input*

### 6.4.4 Function Documentation

#### 6.4.4.1 void error ( int flag )

Error function customizes output message based on flag.

This error function is reference in the error.cpp file, but is not called by any other file. Instead, all other files call the `mError(i)` macro that expands into this error function call plus prints out the file name and line number where the error occurred.

## 6.5 finch.h File Reference

Flux-limiting Implicit Non-oscillatory Conservative High-resolution scheme.

```
#include "macaw.h"
#include "lark.h"
```

### Classes

- struct `FINCH_DATA`  
*Data structure for the FINCH object.*

### Enumerations

- enum `finch_solve_type` { `FINCH_Picard`, `LARK_Picard`, `LARK_PJFNK` }  
*List of enum options to define the solver type in FINCH.*
- enum `finch_coord_type` { `Cartesian`, `Cylindrical`, `Spherical` }  
*List of enum options to define the coordinate system in FINCH.*

### Functions

- double `max` (std::vector< double > &values)  
*Function returns the maximum in a list of values.*
- double `min` (std::vector< double > &values)  
*Function returns the minimum in a list of values.*
- double `minmod` (std::vector< double > &values)  
*Function returns the result of the minmod function acting on a list of values.*
- int `uTotal` (`FINCH_DATA` \*dat)  
*Function integrates the conserved quantity to return it's total in the domain.*
- int `uAverage` (`FINCH_DATA` \*dat)  
*Function integrates the conserved quantity to return it's average in the domain.*
- int `check_Mass` (`FINCH_DATA` \*dat)  
*Function checks the unp1 vector for negative values and will adjust if needed.*
- int `I_direct` (`FINCH_DATA` \*dat)  
*Function solves the discretized FINCH problem directly by assuming it is linear.*
- int `lark_picard_step` (const `Matrix`< double > &x, `Matrix`< double > &G, const void \*data)  
*Function to perform the necessary LARK Picard iterative method (not typically used)*
- int `nl_picard` (`FINCH_DATA` \*dat)  
*Function to solve the discretized FINCH problem iteratively by assuming it is non-linear.*

- int [setup\\_FINCH\\_DATA](#) (int(\*user\_callroutine)(const void \*user\_data), int(\*user\_setic)(const void \*user\_data), int(\*user\_timestep)(const void \*user\_data), int(\*user\_preprocess)(const void \*user\_data), int(\*user\_solve)(const void \*user\_data), int(\*user\_setparams)(const void \*user\_data), int(\*user\_discretize)(const void \*user\_data), int(\*user\_bcs)(const void \*user\_data), int(\*user\_res)(const [Matrix](#)< double > &x, [Matrix](#)< double > &res, const void \*user\_data), int(\*user\_precon)(const [Matrix](#)< double > &b, [Matrix](#)< double > &p, const void \*user\_data), int(\*user\_postprocess)(const void \*user\_data), int(\*user\_reset)(const void \*user\_data), [FINCH\\_DATA](#) \*dat, const void \*param\_data)  
*Function to setup memory and set user defined functions into the FINCH object.*
- void [print2file\\_dim\\_header](#) (FILE \*Output, [FINCH\\_DATA](#) \*dat)  
*Function will print out a dimension header for FINCH output.*
- void [print2file\\_time\\_header](#) (FILE \*Output, [FINCH\\_DATA](#) \*dat)  
*Function will print out a time header for FINCH output.*
- void [print2file\\_result\\_old](#) (FILE \*Output, [FINCH\\_DATA](#) \*dat)  
*Function will print out the old results to the variable u.*
- void [print2file\\_result\\_new](#) (FILE \*Output, [FINCH\\_DATA](#) \*dat)  
*Function will print out the new results to the variable u.*
- void [print2file\\_newline](#) (FILE \*Output, [FINCH\\_DATA](#) \*dat)  
*Function will force print out a blank line.*
- void [print2file\\_tab](#) (FILE \*Output, [FINCH\\_DATA](#) \*dat)  
*Function will force print out a tab.*
- int [default\\_execution](#) (const void \*user\_data)  
*Default executioner function for FINCH.*
- int [default\\_ic](#) (const void \*user\_data)  
*Default initial conditions function for FINCH.*
- int [default\\_timestep](#) (const void \*user\_data)  
*Default time step function for FINCH.*
- int [default\\_preprocess](#) (const void \*user\_data)  
*Default preprocesses function for FINCH.*
- int [default\\_solve](#) (const void \*user\_data)  
*Default solve function for FINCH.*
- int [default\\_params](#) (const void \*user\_data)  
*Default params function for FINCH.*
- int [minmod\\_discretization](#) (const void \*user\_data)  
*Minmod Discretization function for FINCH.*
- int [vanAlbada\\_discretization](#) (const void \*user\_data)  
*Van Albada Discretization function for FINCH.*
- int [ospre\\_discretization](#) (const void \*user\_data)  
*Ospre Discretization function for FINCH.*
- int [default\\_bcs](#) (const void \*user\_data)  
*Default boundary conditions function for FINCH.*
- int [default\\_res](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &res, const void \*user\_data)  
*Default residual function for FINCH.*
- int [default\\_precon](#) (const [Matrix](#)< double > &b, [Matrix](#)< double > &p, const void \*user\_data)  
*Default preconditioning function for FINCH.*
- int [default\\_postprocess](#) (const void \*user\_data)
- int [default\\_reset](#) (const void \*user\_data)  
*Default reset function for FINCH.*
- int [FINCH\\_TESTS](#) ()  
*Function runs a particular FINCH test.*



### 6.5.1 Detailed Description

Flux-limiting Implicit Non-oscillatory Conservative High-resolution scheme. finch.cpp

This is a conservative finite differences scheme based on the Kurganov and Tadmor (2000) MUSCL scheme for non-linear conservation laws. It can solve 1-D conservation law problems in three different coordinate systems: (i) Cartesian - axial, (ii) Cylindrical - radial, and (iii) Spherical - radial. It is the backbone algorithm behind all 1-D PDE problems in the ecosystem software.

The form of the general conservation law problem that FINCH solves is...

$$z^{\wedge}d*R*du/dt = d/dz(z^{\wedge}d*D*du/dz) - d/dz(z^{\wedge}d*v*u) - z^{\wedge}d*k*u + z^{\wedge}d*S$$

where R, D, v, k, and S are the parameters of the problem and d, z, and u are the coordinates, spatial dimension, and conserved quantities, respectively. The parameter R is a retardation coefficient, D is a diffusion coefficient, v is a velocity, k is a reaction coefficient, and S is a forcing function or source/sink term.

FINCH supports the use of both Dirichlet and Neuman boundary conditions as the input/inlet condition and uses the No Flux (or Natural) boundary condition for the output/outlet of the domain. For radial problems, the outlet is always taken to the the center of the cylindrical or spherical particle. This enforces the symmetry of the problem. For axial problems, the outlet is determined by the sign of the velocity term and is therefore choosen by the routine based on the actual flow direction in the domain.

Parameters of the problem can be coupled to the variable u and also be functions of space and time. The coupling of the parameters with the variable forces the problem to become non-linear, which requires iteration to solve. The default iterative method is a built-in Picard's method. This method is equivalent to an inexact Newton method, because we use the Linear Solve of this system as a weak approximation to the non-linear solve. Generally, this method is sufficient and is the most efficient. However, if a problem is particularly difficult to solve, then we can call some of the non-linear solvers developed in LARK. If PJFNK is used, then the Linear Solve for the FINCH problem is used as the Preconditioner for the Linear Solve in PJFNK.

This algorithm comes packaged with three different slope limiter functions to stabilize the velocity term for highly advectively dominate problems. The available slope limiters are: (i) minmod, (ii) van Albada, and (iii) ospre. By default, the FINCH setup function will set the slope limiter to ospre, because this method provides a reasonable compromise between accuracy and efficiency.

#### Slope Limiter Stats:

minmod -> Highest Accuracy, Lowest Efficiency

van Albada -> Lowest Accuracy, Highest Efficiency

ospre -> Average Accuracy, Average Efficiency

#### Author

Austin Ladshaw

#### Date

01/29/2015

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### 6.5.2 Enumeration Type Documentation

#### 6.5.2.1 enum finch\_solve\_type

List of enum options to define the solver type in FINCH.

Enumerator

***FINCH\_Picard***

***LARK\_Picard***

***LARK\_PJFNK***

### 6.5.2.2 enum finch\_coord\_type

List of enum options to define the coordinate system in FINCH.

Enumerator

***Cartesian***

***Cylindrical***

***Spherical***

### 6.5.3 Function Documentation

#### 6.5.3.1 double max ( std::vector< double > & values )

Function returns the maximum in a list of values.

#### 6.5.3.2 double min ( std::vector< double > & values )

Function returns the minimum in a list of values.

#### 6.5.3.3 double minmod ( std::vector< double > & values )

Function returns the result of the minmod function acting on a list of values.

#### 6.5.3.4 int uTotal ( FINCH\_DATA \* dat )

Function integrates the conserved quantity to return it's total in the domain.

#### 6.5.3.5 int uAverage ( FINCH\_DATA \* dat )

Function integrates the conserved quantity to return it's average in the domain.

#### 6.5.3.6 int check\_Mass ( FINCH\_DATA \* dat )

Function checks the unp1 vector for negative values and will adjust if needed.

This function can be turned off or on in the [FINCH\\_DATA](#) structure. Typically, you will want to leave this on so that the routine does not return negative values for u. However, if you want to get negative values of u, then turn this option off.

#### 6.5.3.7 int l\_direct ( FINCH\_DATA \* dat )

Function solves the discretized FINCH problem directly by assuming it is linear.

#### 6.5.3.8 int lark\_picard\_step ( const Matrix< double > & x, Matrix< double > & G, const void \* data )

Function to perform the necessary LARK Picard iterative method (not typically used)

#### 6.5.3.9 int nl\_picard ( FINCH\_DATA \* dat )

Function to solve the discretized FINCH problem iteratively by assuming it is non-linear.

## Note

If the problem is actually linear, then this will solve it in one iteration. So it may be best to always assume the problem is non-linear.

**6.5.3.10** `int setup_FINCH_DATA ( int (*)(const void *user_data) user_callroutine, int (*)(const void *user_data) user_setic, int (*)(const void *user_data) user_timestep, int (*)(const void *user_data) user_preprocess, int (*)(const void *user_data) user_solve, int (*)(const void *user_data) user_setparams, int (*)(const void *user_data) user_discretize, int (*)(const void *user_data) user_bcs, int (*)(const Matrix< double > &x, Matrix< double > &res, const void *user_data) user_res, int (*)(const Matrix< double > &b, Matrix< double > &p, const void *user_data) user_precon, int (*)(const void *user_data) user_postprocess, int (*)(const void *user_data) user_reset, FINCH_DATA * dat, const void * param_data )`

Function to setup memory and set user defined functions into the FINCH object.

This function MUST be called prior to running any FINCH based simulation. However, you are only every required to provide this function with the [FINCH\\_DATA](#) pointer. It is recommended, however, that you do provide the `user_setparams` and `param_data` pointers, as these will likely vary significantly from problem to problem.

After the problem is setup in memory, you do not technically have to have FINCH call all of it's own functions. You can write your own executioner, initial conditions, and other functions and decided how and when everything is called. Then just call the solve function in [FINCH\\_DATA](#) when you want to use the FINCH solver. This is how FINCH is used in SKUA, SCOPSOWL, DOGFISH, and MONKFISH.

## Parameters

<code>user_callroutine</code>	function pointer the the call routine function
<code>user_setic</code>	function pointer to set initial conditions for problem
<code>user_timestep</code>	function pointer to set the next time step
<code>user_preprocess</code>	function pointer to setup a preprocess operation
<code>user_solve</code>	function pointer to solve the system of equations
<code>user_setparams</code>	function pointer to set the parameters in the problem (always override this)
<code>user_discretize</code>	function pointer to select discretization scheme for the problem
<code>user_bcs</code>	function pointer to evaluate boundary conditions for the problem
<code>user_res</code>	function pointer to evaluate non-linear residuals for the problem
<code>user_precon</code>	function pointer to perform a linear preconditioning operation
<code>user_postprocess</code>	function pointer to setup a postprocess operation
<code>user_reset</code>	function pointer to reset stateful data for next simulation
<code>dat</code>	pointer to the <a href="#">FINCH_DATA</a> structure
<code>param_data</code>	user supplied pointer to a data structure needed in <code>user_setparams</code>

**6.5.3.11** `void print2file_dim_header ( FILE * Output, FINCH_DATA * dat )`

Function will print out a dimension header for FINCH output.

**6.5.3.12** `void print2file_time_header ( FILE * Output, FINCH_DATA * dat )`

Function will print out a time header for FINCH output.

**6.5.3.13** `void print2file_result_old ( FILE * Output, FINCH_DATA * dat )`

Function will print out the old results to the variable u.

**6.5.3.14** `void print2file_result_new ( FILE * Output, FINCH_DATA * dat )`

Function will print out the new results to the variable u.

6.5.3.15 void print2file\_newline ( FILE \* *Output*, FINCH\_DATA \* *dat* )

Function will force print out a blank line.

6.5.3.16 void print2file\_tab ( FILE \* *Output*, FINCH\_DATA \* *dat* )

Function will force print out a tab.

6.5.3.17 int default\_execution ( const void \* *user\_data* )

Default executioner function for FINCH.

The default executioner function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and calls the preprocesses, solve, postprocesses, checkMass, uTotal, and uAverage functions in that order.

6.5.3.18 int default\_ic ( const void \* *user\_data* )

Default initial conditions function for FINCH.

The default initial condition function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and sets the initial values of all system parameters according to the given constants in that structure.

6.5.3.19 int default\_timestep ( const void \* *user\_data* )

Default time step function for FINCH.

The default time step function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and sets the time step to 1/2 the mesh size or bases the time step off of the CFL condition if the problem is not being solved iteratively and involves an advective portion.

6.5.3.20 int default\_preprocess ( const void \* *user\_data* )

Default preprocesses function for FINCH.

The default preprocesses function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and does nothing.

6.5.3.21 int default\_solve ( const void \* *user\_data* )

Default solve function for FINCH.

The default solve function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and calls the corresponding solution method depending on the users conditions.

6.5.3.22 int default\_params ( const void \* *user\_data* )

Default params function for FINCH.

The default params function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and sets the values of all parameters at all nodes equal to the values of those parameters at the boundaries.

6.5.3.23 int minmod\_discretization ( const void \* *user\_data* )

Minmod Discretization function for FINCH.

The minmod discretization function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and discretizes the time and space portion of the problem with 2nd order finite differences and uses the minmod slope limiter function to stabilize the advective physics.

6.5.3.24 int vanAlbada\_discretization ( const void \* *user\_data* )

Van Albada Discretization function for FINCH.

The van Albada discretization function for FINCH assumes the *user\_data* parameter is the [FINCH\\_DATA](#) structure and discretizes the time and space portion of the problem with 2nd order finite differences and uses the van Albada

slope limiter function to stabilize the advective physics.

**6.5.3.25** `int ospre_discretization ( const void * user_data )`

Ospre Discretization function for FINCH.

The ospre discretization function for FINCH assumes the user\_data parameter is the [FINCH\\_DATA](#) structure and discretizes the time and space portion of the problem with 2nd order finite differences and uses the ospre slope limiter function to stabilize the advective physics. This is the default discretization function.

**6.5.3.26** `int default_bcs ( const void * user_data )`

Default boundary conditions function for FINCH.

The default boundary conditions function for FINCH assumes the user\_data parameter is the [FINCH\\_DATA](#) structure and sets the boundary conditions according to the type of problem requested. The input BCs will always be either Neumann or Dirichlet and the output BC will always be a zero flux Neumann BC.

**6.5.3.27** `int default_res ( const Matrix< double > & x, Matrix< double > & res, const void * user_data )`

Default residual function for FINCH.

The default residual function for FINCH assumes the user\_data parameter is the [FINCH\\_DATA](#) structure and calls the setparams function (passing the param\_data structure), the discretization function, and the set BCs functions, in that order. It then forms the implicit and explicit side residuals that go into the iterative solver.

**6.5.3.28** `int default_precon ( const Matrix< double > & b, Matrix< double > & p, const void * user_data )`

Default preconditioning function for FINCH.

The default preconditioning function for FINCH assumes the user\_data parameter is the [FINCH\\_DATA](#) structure and performs a tridiagonal linear solve using a Modified Thomas Algorithm. This preconditioner will solve the linear problem exactly if there is no advective portion of the physics. Additionally, this preconditioner is also used as the basis for forming the default FINCH non-linear iterations and is sufficient for solving most problems.

**6.5.3.29** `int default_postprocess ( const void * user_data )`

The default postprocesses function for FINCH assumes the user\_data parameter is the [FINCH\\_DATA](#) structure and does nothing.

**6.5.3.30** `int default_reset ( const void * user_data )`

Default reset function for FINCH.

The default reset function for FINCH assumes the user\_data parameter is the [FINCH\\_DATA](#) structure and sets all old state parameters and variables to the new state.

**6.5.3.31** `int FINCH_TESTS ( )`

Function runs a particular FINCH test.

The FINCH\_TESTS function is used to exercise and test out the FINCH algorithms for correctness, efficiency, and accuracy. This test should never report a failure.

## 6.6 flock.h File Reference

Fundamental Off-gas Collection of Kernels.

```
#include "macaw.h"
#include "egret.h"
#include "finch.h"
#include "lark.h"
#include "skua.h"
#include "scopsowl.h"
#include "gsta_opt.h"
#include "magpie.h"
#include "skua_opt.h"
#include "scopsowl_opt.h"
#include "yaml_wrapper.h"
```

### 6.6.1 Detailed Description

Fundamental Off-gas Collection of Kernels. This is just a .h file that holds all the includes necessary to develop and run simulations for adsorption and/or mass/energy transfer problems for gaseous systems. Include this file into any other project or source code that needs the methods below.

#### Files Included in FLOCK

[macaw.h](#) [egret.h](#) [finch.h](#) [lark.h](#) [skua.h](#) [scopsowl.h](#) [gsta\\_opt.h](#) [magpie.h](#) [skua\\_opt.h](#) [scopsowl\\_opt.h](#) [yaml\\_wrapper.h](#)

#### Author

Austin Ladshaw

#### Date

04/28/2014

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## 6.7 gsta\_opt.h File Reference

Generalized Statistical Thermodynamic Adsorption (GSTA) Optimization Routine.

```
#include "lmcurve.h"
#include <stdio.h>
#include <math.h>
#include <iostream>
#include <fstream>
#include <stdlib.h>
#include <vector>
#include <time.h>
#include <float.h>
#include <string>
#include "error.h"
```

#### Classes

- struct [GSTA\\_OPT\\_DATA](#)

*Data structure used in the GSTA optimization routines.*

## Macros

- `#define Po 100.0`  
*Standard State Pressure - Units: kPa.*
- `#define R 8.3144621`  
*Gas Constant - Units: J/(K\*mol) = kB \* Na.*
- `#define Na 6.0221413E+23`  
*Avagadro's Number - Units: molecules/mol.*

## Functions

- `int roundIt (double d)`  
*Function rounds a double to an integer.*
- `int twoFifths (int m)`  
*Function returns the rounded two-fifths result of int m.*
- `int orderMag (double x)`  
*Function returns the order of magnitude for the parameter x.*
- `int minValue (std::vector< int > &array)`  
*Function returns the minimum integer in an array of integers.*
- `int minIndex (std::vector< double > &array)`  
*Function returns the index of the minimum integer in an array of integers.*
- `int avgPar (std::vector< int > &array)`  
*Function returns the average integer value in an array of integers.*
- `double avgValue (std::vector< double > &array)`  
*Function returns an average in an array of doubles.*
- `double weightedAvg (double *enorm, double *x, int n)`  
*Function returns a weighted average in an array.*
- `double rSq (double *x, double *y, double slope, double vint, int m_dat)`  
*Function calculates the Coefficient of Determination (R Squared) for the temperature regression.*
- `bool isSmooth (double *par, void *data)`  
*Function looks at the list of parameters to check if they are smoothly changing.*
- `void orthoLinReg (double *x, double *y, double *par, int m_dat, int n_par)`  
*Function performs an Orthogonal Linear Regression on a set of data.*
- `void eduGuess (double *P, double *q, double *par, int k, int m_dat, void *data)`  
*Function will formed an educated guess for the next set of parameters in the GSTA analysis.*
- `double gstaFunc (double p, const double *K, double qmax, int n_par)`  
*Function evaluates the result of the GSTA isotherm model.*
- `double gstaObjFunc (double *t, double *y, double *par, int m_dat, void *data)`  
*Function to evaluate the GSTA objective function value.*
- `void eval_GSTA (const double *par, int m_dat, const void *data, double *fvec, int *info)`  
*Function to evaluate the GSTA model and feed into the Imfit routine.*
- `int gsta_optimize (const char *fileName)`  
*Function to perform the GSTA optimization routine.*

### 6.7.1 Detailed Description

Generalized Statistical Thermodynamic Adsorption (GSTA) Optimization Routine. gsta\_opt.cpp

Optimization routine developed for the GSTA isotherm and data analysis. This algorithm was the primary subject of a publication made in Fluid Phase Equilibria. Please refer to the below paper for technical information about the algorithms.

Reference: Ladshaw, Yiacoumi, Tsouris, and DePaoli, Fluid Phase Equilibria, 388, 169-181, 2015.

The GSTA model was first introduced by Llano-Restrepo and Mosquera (2009). Please refer to the below reference for theoretical information about the model.

Reference: Llano-Restrepo and Mosquera, Fluid Phase Equilibria, 283, 73-88, 2009.

#### Author

Austin Ladshaw

#### Date

12/17/2013

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### 6.7.2 Macro Definition Documentation

#### 6.7.2.1 #define Po 100.0

Standard State Pressure - Units: kPa.

#### 6.7.2.2 #define R 8.3144621

Gas Constant - Units: J/(K\*mol) = kB \* Na.

#### 6.7.2.3 #define Na 6.0221413E+23

Avagadro's Number - Units: molecules/mol.

### 6.7.3 Function Documentation

#### 6.7.3.1 int roundIt ( double d )

Function rounds a double to an integer.

This function returns a rounded value of d. Rounding up for any decimal larger than 0.5 and down for all else.

#### 6.7.3.2 int twoFifths ( int m )

Function returns the rounded two-fifths result of int m.

This function is used to determine what the maximum number of parameters should be based on the number of data points m. It is designed to prevent the algorithms from "over fitting" the data.

#### 6.7.3.3 int orderMag ( double x )

Function returns the order of magnitude for the parameter x.



This function is used to help create initial guesses for the new GSTA parameters that are being optimized for. In order to make sure that those parameters are considered relevant in the optimization routine, we need to make the initial guesses to be around the same order of magnitude of the other GSTA parameters.

#### 6.7.3.4 int minValue ( std::vector< int > & array )

Function returns the minimum integer in an array of integers.

This function is used to determine the minimum number of GSTA parameters that were required to adequately fit the isotherm data.

#### 6.7.3.5 int minIndex ( std::vector< double > & array )

Function returns the index of the minimum integer in an array of integers.

This function identifies the index of the minimum number of parameters needed for the GSTA model to fit the data. This index is common for all vectors in the [GSTA\\_OPT\\_DATA](#) structure and is used to identify the most suitable solution.

#### 6.7.3.6 int avgPar ( std::vector< int > & array )

Function returns the average integer value in an array of integers.

This function is used to identify the average number of parameters that all the data fitting needed for each GSTA analysis.

#### 6.7.3.7 double avgValue ( std::vector< double > & array )

Function returns an average in an array of doubles.

#### 6.7.3.8 double weightedAvg ( double \* enorm, double \* x, int n )

Function returns a weighted average in an array.

This averaging scheme is used to approximate the qmax parameter for the GSTA isotherm model, if that value is unknown. The weighting is based on the euclidean norms of all the fits of the data. Smaller norms are more heavily weighted since they represent a better fit of the data. Once averaging is complete and we have an estimate for qmax, the entire algorithm is re-run holding that qmax constant.

##### Parameters

<i>enorm</i>	array of euclidean norms from the fitting of the data
<i>x</i>	array of optimum qmax values to be averaged
<i>n</i>	the number of enorm and x values in the array

#### 6.7.3.9 double rSq ( double \* x, double \* y, double slope, double vint, int m\_dat )

Function calculates the Coefficient of Determination (R Squared) for the temperature regression.

This function is used to determine the "fitness" of the linear regression performed on the temperature independent parameters of the GSTA isotherm. A good linear regression should return a value between 1.0 and 0.9.

##### Parameters

<i>x</i>	observations in the x-axis
<i>y</i>	observations in the y-axis
<i>slope</i>	slope of the linear regression
<i>vint</i>	intercept of the linear regression
<i>m_dat</i>	number of data points used in the linear regression

#### 6.7.3.10 bool isSmooth ( double \* *par*, void \* *data* )

Function looks at the list of parameters to check if they are smoothly changing.

This function takes the parameter array *par* and [GSTA\\_OPT\\_DATA](#) structure and checks to see if those parameters are changing smoothly. If they are erratic or non-smooth, then it could be an indication of "over fitting" of the data.

#### 6.7.3.11 void orthoLinReg ( double \* *x*, double \* *y*, double \* *par*, int *m\_dat*, int *n\_par* )

Function performs an Orthogonal Linear Regression on a set of data.

This function takes an array of *x* and *y* observations and performs an orthogonal linear regression on that information to find optimum parameters for slope and intercept.

##### Parameters

<i>x</i>	array of x-axis observations
<i>y</i>	array of y-axis observations
<i>par</i>	array of parameter results after regression
<i>m_dat</i>	number of data points or observations
<i>n_par</i>	number of parameters to seek (if <i>n_par</i> != 1 or 2, then <i>par</i> [0] = intercept and <i>par</i> [1] = slope)

#### 6.7.3.12 void eduGuess ( double \* *P*, double \* *q*, double \* *par*, int *k*, int *m\_dat*, void \* *data* )

Function will formed an educated guess for the next set of parameters in the GSTA analysis.

This function takes partial pressure and adsorption observations, *P* and *q*, and tries to give a decent initial guess to what the GSTA parameters, *par*, will be for the next iteration.

##### Parameters

<i>P</i>	partial pressure observations in the data (kPa)
<i>q</i>	adsorption observations in the data (any units)
<i>par</i>	parameter array for the GSTA isotherm
<i>k</i>	index of the current number of parameters being considered
<i>m_dat</i>	number of pressure-adsorption observations in the isotherm
<i>data</i>	pointer to the <a href="#">GSTA_OPT_DATA</a> data structure

#### 6.7.3.13 double gstaFunc ( double *p*, const double \* *K*, double *qmax*, int *n\_par* )

Function evaluates the result of the GSTA isotherm model.

This function will evaluate the GSTA model and return the adsorbed amount given the current partial pressure *p* and the equilibrium parameters *K*.

##### Parameters

<i>p</i>	current partial pressure (kPa)
<i>K</i>	array of equilibrium parameters ( $1/\text{kPa}^n$ )
<i>qmax</i>	the theoretical maximum capacity for the isotherm
<i>n_par</i>	the number of equilibrium parameters

#### 6.7.3.14 double gstaObjFunc ( double \* *t*, double \* *y*, double \* *par*, int *m\_dat*, void \* *data* )

Function to evaluate the GSTA objective function value.

The objective function seeks to penalize the relative fitness of the model based on the number of parameters it took to minimize the euclidean norms. By penalizing the fitness of the model in this fashion, we can find the best solution to the system that required the least number of equilibrium parameters.

6.7.3.15 void eval.GSTA ( const double \* *par*, int *m\_dat*, const void \* *data*, double \* *fvec*, int \* *info* )

Function to evaluate the GSTA model and feed into the Imfit routine.

This function will formulate the residuals that go into the Levenberg-Marquardt's Algorithm for non-linear least squares regression. The form of this function is specific to how we interface with the Imfit routines.

6.7.3.16 int gsta\_optimize ( const char \* *fileName* )

Function to perform the GSTA optimization routine.

This function is callable from the UI and is used to find the optimum parameters of the GSTA isotherm model given a particular set of isotherm data for single-component adsorption equilibria.

#### Parameters

<i>fileName</i>	name of the input file that holds the isotherm data
-----------------	---

#### Note

The input file for the GSTA optimization routine is a text file holding the necessary information and data needed to run the routine. That input file has a very specific format that is detailed below.

Number of Isotherm Curves

Theoretical Maximum Adsorption Capacity (if unknown, provide 0)

Temperature of the ith Isotherm (K)

Number of Data points for the ith Isotherm

Partial Pressure (kPa) [tab] Corresponding Adsorbed Amount (any units)

(2nd Line down is repeated for all isotherms you are optimizing on...)

#### Example:

```
2
21.0
298.15
4
0.000165483 2.77
0.000306379 2.75
0.00044922 5.00
0.000939259 10.40
313.15
4
0.000589636 2.75
0.001063584 3.70
0.001351836 4.2
0.001543464 4.6
```

The above example would be for 2 sets of isotherms at 298.15 and 313.15 K, respectively. Maximum adsorption capacity is given as 21 (which in this has units of wt%). Each isotherm has 4 data points, which are given in a list as p (kPa) and q (wt%) pairs. Units of adsorption don't matter as long as they are consistent. If you give maximum capacity in mol/kg, then the q's in the lists must also be in mol/kg.

## 6.8 lark.h File Reference

Linear Algebra Residual Kernels.

```
#include "macaw.h"
#include <float.h>
```

### Classes

- struct [ARNOLDI\\_DATA](#)  
*Data structure for the construction of the Krylov subspaces for a linear system.*
- struct [GMRESLP\\_DATA](#)  
*Data structure for implementation of the Restarted GMRES algorithm with Left Preconditioning.*
- struct [GMRESRP\\_DATA](#)  
*Data structure for the Restarted GMRES algorithm with Right Preconditioning.*
- struct [PCG\\_DATA](#)  
*Data structure for implementation of the PCG algorithms for symmetric linear systems.*
- struct [BiCGSTAB\\_DATA](#)  
*Data structure for the implementation of the BiCGSTAB algorithm for non-symmetric linear systems.*
- struct [CGS\\_DATA](#)  
*Data structure for the implementation of the CGS algorithm for non-symmetric linear systems.*
- struct [OPTRANS\\_DATA](#)  
*Data structure for implementation of linear operator transposition.*
- struct [GCR\\_DATA](#)  
*Data structure for the implementation of the GCR algorithm for non-symmetric linear systems.*
- struct [GMRESR\\_DATA](#)  
*Data structure for the implementation of GCR with Nested GMRES preconditioning (i.e., GMRESR)*
- struct [KMS\\_DATA](#)  
*Data structure for the implemenation of the Krylov Multi-Space (KMS) Method.*
- struct [PICARD\\_DATA](#)  
*Data structure for the implementation of a Picard or Fixed-Point iteration for non-linear systems.*
- struct [BACKTRACK\\_DATA](#)  
*Data structure for the implementation of Backtracking Linesearch.*
- struct [PJFNK\\_DATA](#)  
*Data structure for the implementation of the PJFNK algorithm for non-linear systems.*
- struct [NUM\\_JAC\\_DATA](#)  
*Data structure to form a numerical jacobian matrix with finite differences.*

### Macros

- #define [MIN\\_TOL](#) 1e-15  
*Minimum Allowable Tolerance for linear and non-linear problems.*

### Enumerations

- enum [krylov\\_method](#) {  
    [GMRESLP](#), [PCG](#), [BiCGSTAB](#), [CGS](#),  
    [FOM](#), [GMRESRP](#), [GCR](#), [GMRESR](#),  
    [KMS](#) }  
*Enum of definitions for linear solver types in PJFNK.*

## Functions

- int [update\\_arnoldi\\_solution](#) (Matrix< double > &x, Matrix< double > &x0, ARNOLDI\_DATA \*arnoldi\_dat)  
*Function to update the linear vector  $x$  based on the Arnoldi Krylov subspace.*
- int [arnoldi](#) (int(\*matvec)(const Matrix< double > &v, Matrix< double > &w, const void \*data), int(\*precon)(const Matrix< double > &b, Matrix< double > &p, const void \*data), Matrix< double > &r0, ARNOLDI\_DATA \*arnoldi\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to factor a linear operator into an orthonormal basis and upper Hessenberg matrix.*
- int [gmresLeftPreconditioned](#) (int(\*matvec)(const Matrix< double > &v, Matrix< double > &w, const void \*data), int(\*precon)(const Matrix< double > &b, Matrix< double > &p, const void \*data), Matrix< double > &b, GMRESLP\_DATA \*gmreslp\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to iteratively solve a non-symmetric, indefinite linear system with GMRESLP.*
- int [fom](#) (int(\*matvec)(const Matrix< double > &v, Matrix< double > &w, const void \*data), int(\*precon)(const Matrix< double > &b, Matrix< double > &p, const void \*data), Matrix< double > &b, GMRESLP\_DATA \*gmreslp\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to directly solve a non-symmetric, indefinite linear system with FOM.*
- int [gmresRightPreconditioned](#) (int(\*matvec)(const Matrix< double > &v, Matrix< double > &w, const void \*data), int(\*precon)(const Matrix< double > &b, Matrix< double > &p, const void \*data), Matrix< double > &b, GMRESRP\_DATA \*gmresrp\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to iteratively solve a non-symmetric, indefinite linear system with GMRESRP.*
- int [pcg](#) (int(\*matvec)(const Matrix< double > &p, Matrix< double > &Ap, const void \*data), int(\*precon)(const Matrix< double > &r, Matrix< double > &z, const void \*data), Matrix< double > &b, PCG\_DATA \*pcg\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to iteratively solve a symmetric, definite linear system with PCG.*
- int [bicgstab](#) (int(\*matvec)(const Matrix< double > &p, Matrix< double > &Ap, const void \*data), int(\*precon)(const Matrix< double > &r, Matrix< double > &z, const void \*data), Matrix< double > &b, BICGSTAB\_DATA \*bicgstab\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to iteratively solve a non-symmetric, definite linear system with BiCGSTAB.*
- int [cgs](#) (int(\*matvec)(const Matrix< double > &p, Matrix< double > &Ap, const void \*data), int(\*precon)(const Matrix< double > &r, Matrix< double > &z, const void \*data), Matrix< double > &b, CGS\_DATA \*cgs\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to iteratively solve a non-symmetric, definite linear system with CGS.*
- int [operatorTranspose](#) (int(\*matvec)(const Matrix< double > &v, Matrix< double > &Av, const void \*data), Matrix< double > &r, Matrix< double > &u, OPTRANS\_DATA \*transpose\_dat, const void \*matvec\_data)  
*Function that is used to perform transposition of a linear operator and results in a new vector  $A^T r = u$ .*
- int [gcr](#) (int(\*matvec)(const Matrix< double > &x, Matrix< double > &Ax, const void \*data), int(\*precon)(const Matrix< double > &r, Matrix< double > &Mr, const void \*data), Matrix< double > &b, GCR\_DATA \*gcr\_dat, const void \*matvec\_data, const void \*precon\_data)  
*Function to iteratively solve a non-symmetric, definite linear system with GCR.*
- int [gmresrPreconditioner](#) (const Matrix< double > &r, Matrix< double > &Mr, const void \*data)  
*Function used in conjunction with GMRESR to apply GMRESRP iterations as a preconditioner.*
- int [gmresr](#) (int(\*matvec)(const Matrix< double > &x, Matrix< double > &Ax, const void \*data), int(\*terminal\_precon)(const Matrix< double > &r, Matrix< double > &Mr, const void \*data), Matrix< double > &b, GMRESR\_DATA \*gmresr\_dat, const void \*matvec\_data, const void \*term\_precon\_data)  
*Function to iteratively solve a non-symmetric, indefinite linear system with GMRESR.*
- int [kmsPreconditioner](#) (const Matrix< double > &r, Matrix< double > &Mr, const void \*data)  
*Preconditioner function for the Krylov Multi-Space.*
- int [krylovMultiSpace](#) (int(\*matvec)(const Matrix< double > &x, Matrix< double > &Ax, const void \*data), int(\*terminal\_precon)(const Matrix< double > &r, Matrix< double > &Mr, const void \*data), Matrix< double > &b, KMS\_DATA \*kms\_dat, const void \*matvec\_data, const void \*term\_precon\_data)  
*Function to iteratively solve a non-symmetric, indefinite linear system with KMS.*
- int [picard](#) (int(\*res)(const Matrix< double > &x, Matrix< double > &r, const void \*data), int(\*evalx)(const Matrix< double > &x0, Matrix< double > &x, const void \*data), Matrix< double > &x, PICARD\_DATA \*picard\_dat, const void \*res\_data, const void \*evalx\_data)

*Function to iteratively solve a non-linear system using the Picard or Fixed-Point method.*

- int `javec` (const `Matrix< double >` &v, `Matrix< double >` &Jv, const void \*data)

*Function to form a linear operator of a Jacobian matrix used along with the PJFNK method.*

- int `backtrackLineSearch` (int(\*feval)(const `Matrix< double >` &x, `Matrix< double >` &F, const void \*data), `Matrix< double >` &Fkp1, `Matrix< double >` &xkp1, `Matrix< double >` &pk, double normFk, `BACKTRACK_DATA` \*backtrack\_dat, const void \*feval\_data)

*Function to perform a Backtracking Line Search operation to smooth out convergence of PJFNK.*

- int `pjfnk` (int(\*res)(const `Matrix< double >` &x, `Matrix< double >` &F, const void \*data), int(\*precon)(const `Matrix< double >` &r, `Matrix< double >` &p, const void \*data), `Matrix< double >` &x, `PJFNK_DATA` \*pjfnk\_dat, const void \*res\_data, const void \*precon\_data)

*Function to perform the PJFNK algorithm to solve a non-linear system of equations.*

- int `NumericalJacobian` (int(\*Func)(const `Matrix< double >` &x, `Matrix< double >` &F, const void \*user\_data), const `Matrix< double >` &x, `Matrix< double >` &J, int Nx, int Nf, `NUM_JAC_DATA` \*jac\_dat, const void \*user\_data)

*Function to form a full numerical Jacobian matrix from a given non-linear function.*

- int `LARK_TESTS` ()

*Function that runs a variety of tests on all the functions in LARK.*

### 6.8.1 Detailed Description

Linear Algebra Residual Kernels. `lark.cpp`

The functions contained within are designed to solve generic linear and non-linear square systems of equations given a function argument and data from the user. Optionally, the user can also provide a function to return a preconditioning result that will be applied to the system.

Having the user define how the preconditioning is carried out provides two major advantages: (1) we do not need to store and large, sparse preconditioning matrices and instead only store the preconditioned vector result and (2) this allows the user to use any kind of preconditioner they see fit for their problem.

The Arnoldi function is typically not called by the user, but can be if desired. It accepts the function arguments and a residual vector to form an orthonormal basis of the Krylov subspace using the Modified Gram-Schmidt process (aka Arnoldi Iteration). This function is called by GMRES to iteratively solve a linear system of equations. Note that you can use this function to directly solve the linear system as long as that system is not too large. Construction of the basis is expensive, which is why this is used as a sub-function of an iterative method.

The Restarted GMRES function will accept function arguments for a linear system and attempt to solve said system iteratively by constructing an orthonormal basis from the Krylov function. Note that this GMRES function does support restarting and will use restarting by default if the linear system is too large.

Also included is a GMRES algorithm without restarting. This will directly solve the linear system within residual tolerance using a Full Orthogonal basis set of that system. It is equivalent to calling the Krylov method with the `k` parameter equal to `N` (i.e. the number of equations). This method is nick-named the Full Orthogonalization Method (FOM), although the true FOM algorithm in literature is slightly different.

The PJFNK function will accept function arguments for a square, non-linear system of equations and attempt to solve it iteratively using both the GMRES and Krylov functions with Newton's method to convert the non-linear system into a linear system.

Also built here is a PCG implementation for solving symmetric linear systems. Can also be called by PJFNK if we know that the linear system (i.e. the Jacobian) is symmetric. This algorithm is significantly more efficient than GMRES, but is only valid if the system of equations is symmetric.

Other linear solvers implemented in this work are the BiCGSTAB and CGS algorithms for non-symmetric, positive definite matrices. These algorithms are significantly more computationally efficient than GMRES or FOM. However, they can both break down if the linear system is poorly conditioned. In general, you only want to use these methods if you have preconditioning available and your linear system is very, very large. Otherwise, you will be better suited to using GMRES or FOM.

There is also an implementation of the Generalized Conjugate Residual (GCR) method with and without restarting. This is a GMRES-like method that should give the exact solution within `N` iterations, where `N` is the original size of

the matrix. Built on top of the GCR method is a GMRESR (or GMRES Recursive) algorithm that uses GCR as the base method and performs GMRESR iterations as a preconditioner at each iteration of GCR. This is the only linear solver that has built-in preconditioning. As a result, it may be slower than other algorithms for simple problems, but generally will have much better convergence behavior and will almost always give better residual reduction, even for hard to solve problems.

We have also developed a novel/experimental iterative method based on the idea of recursively preconditioning a Krylov Subspace with more Krylov Subspaces. We have called with algorithm the Krylov Multi-Space (KMS) method. This algorithm is based on publications from Vorst and Vuk (1991) and Saad (1993). The idea is to use the FGMRES algorithm developed by Saad (1993) and precondition it with more FGMRES steps, i.e., nesting the iterations as Vorst and Vuk (1991) had proposed. In this way, we have created a generalized Krylov Subspace method that has its own variable preconditioner that can be adjusted depending on the user's desired complexity and convergence rate. If the levels of recursion requested is zero, then this algorithm is exactly equal to GMRES with right preconditioning. If the level is one, then it is FGMRES with a GMRES preconditioner. However, we allow the levels of recursion to reach up to 5, thus allowing us to precondition the preconditioners with more GMRES steps. This can result in significantly faster convergence rates, but is typically only necessary for very large or difficult to solve problems.

NOTE: There are three GMRES implementations: (i) gmresLP, (ii) fom, and (iii) gmresRP. GMRESLP is a restarted GMRES implementation that is left preconditioned and only checks the residual on the outer loops. This may be less efficient than GMRESRP, which can check both outer and inner loop residuals. However, GMRESRP has to use right preconditioning, which also slightly changes the convergence behavior of the linear system. GMRES with left preconditioning and without restarting will just build the full subspace by default, thus solving the system exactly, but may require too much memory. You can do a GMRESRP un restarted by specifying that the restart parameter be equal to the size of the problem.

#### Basic Implementation Details:

Linear Solvers -> Solve  $Ax=b$  for  $x$

Non-Linear Solvers -> Solve  $F(x)=0$  for  $x$

All implementations require system size to be 2 or greater

#### Author

Austin Ladshaw

#### Date

10/14/2014

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This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

### 6.8.2 Macro Definition Documentation

#### 6.8.2.1 #define MIN\_TOL 1e-15

Minimum Allowable Tolerance for linear and non-linear problems.

### 6.8.3 Enumeration Type Documentation

#### 6.8.3.1 enum krylov\_method

Enum of definitions for linear solver types in PJFNK.

Enum delineates the available Krylov Subspace methods that can be used to solve the linear sub-problem at each non-linear iteration in a Newton method.

## Enumerator

**GMRESLP**  
**PCG**  
**BiCGSTAB**  
**CGS**  
**FOM**  
**GMRESRP**  
**GCR**  
**GMRESR**  
**KMS**

## 6.8.4 Function Documentation

6.8.4.1 `int update_arnoldi_solution ( Matrix< double > & x, Matrix< double > & x0, ARNOLDI_DATA * arnoldi_dat )`

Function to update the linear vector x based on the Arnoldi Krylov subspace.

This function will update a solution vector x based on the previous solution x0 given the orthonormal basis and upper Hessenberg matrix formed in the Arnoldi algorithm. Updating is automatically called by the GMRESLP function. It is expected that the Arnoldi algorithm has already been called prior to calling this function.

## Parameters

<i>x</i>	matrix that will hold the new updated solution to the linear system
<i>x0</i>	matrix that holds the previous solution to the linear system
<i>arnoldi_dat</i>	pointer to the <a href="#">ARNOLDI_DATA</a> data structure

6.8.4.2 `int arnoldi ( int (*)(const Matrix< double > &v, Matrix< double > &w, const void *data) matvec, int (*)(const Matrix< double > &b, Matrix< double > &p, const void *data) precon, Matrix< double > & r0, ARNOLDI_DATA * arnoldi_dat, const void * matvec_data, const void * precon_data )`

Function to factor a linear operator into an orthonormal basis and upper Hessenberg matrix.

This function performs the Arnoldi algorithm to factor a linear operator into an orthonormal basis and upper Hessenberg matrix. Each orthonormal vector is formed using a Modified Gram-Schmidt procedure. When used in conjunction with GMRESLP, user may supply a preconditioning operator to improve convergence of the linear system. However, this function can be used by itself to factor the user's linear operator.

## Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>r0</i>	user supplied vector to serve as the first basis vector in the orthonormal basis
<i>arnoldi_dat</i>	pointer to the <a href="#">ARNOLDI_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

## Note

`int (*)(const Matrix<double> & v, Matrix<double> &Av, const void *data)`

-----  
 This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.  
 -----



---

```
int (*precon) (const Matrix<double> &b, Matrix<double> &Mb, const void *data)
```

---

This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.3** `int gmresLeftPreconditioned ( int(*) (const Matrix<double> &v, Matrix<double> &w, const void *data) matvec, int(*) (const Matrix<double> &b, Matrix<double> &p, const void *data) precon, Matrix<double> &b, GMRESLP\_DATA * gmreslp_dat, const void * matvec_data, const void * precon_data )`

Function to iteratively solve a non-symmetric, indefinite linear system with GMRESLP.

This function iteratively solves a non-symmetric, indefinite linear system using the Generalized Minimum RESidual method with Left Preconditioning (GMRESLP). It calls the Arnoldi algorithm to factor a linear operator into an orthonormal basis and upper Hessenberg matrix, then uses that factorization to form an approximation to the linear system. Because this algorithm uses left-side preconditioning, it can only check the linear residuals at the outer iterations.

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system Ax=b
<i>gmreslp_dat</i>	pointer to the <a href="#">GMRESLP_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

#### Note

---

```
int (*matvec) (const Matrix<double> &v, Matrix<double> &Av, const void *data)
```

---

This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

---



---

```
int (*precon) (const Matrix<double> &b, Matrix<double> &Mb, const void *data)
```

---

This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.4** `int fom ( int(*) (const Matrix<double> &v, Matrix<double> &w, const void *data) matvec, int(*) (const Matrix<double> &b, Matrix<double> &p, const void *data) precon, Matrix<double> &b, GMRESLP\_DATA * gmreslp_dat, const void * matvec_data, const void * precon_data )`

Function to directly solve a non-symmetric, indefinite linear system with FOM.

This function directly solves a non-symmetric, indefinite linear system using the Full Orthogonalization Method (FOM). This algorithm is exactly equivalent to GMRESLP without restarting. Therefore, it uses the [GMRESLP\\_DATA](#) structure and calls the GMRESLP algorithm without using restarts. As a result, it never checks linear residuals. However, this should give the exact solution upon completion, assuming the linear operator is not singular.

## Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system $Ax=b$
<i>gmreslp_dat</i>	pointer to the <a href="#">GMRESLP_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

## Note

int (\*matvec) (const [Matrix<double>](#) & v, [Matrix<double>](#) &Av, const void \*data)

-----  
 This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

int (\*precon) (const [Matrix<double>](#) & b, [Matrix<double>](#) &Mb, const void \*data)

-----  
 This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

**6.8.4.5** int gmresRightPreconditioned ( int(\*) (const [Matrix<double>](#) &v, [Matrix<double>](#) &w, const void \*data) *matvec*, int(\*) (const [Matrix<double>](#) &b, [Matrix<double>](#) &p, const void \*data) *precon*, [Matrix<double>](#) & b, [GMRESRP\\_DATA](#) \* *gmresrp\_dat*, const void \* *matvec\_data*, const void \* *precon\_data* )

Function to iteratively solve a non-symmetric, indefinite linear system with GMRESRP.

This function iteratively solves a non-symmetric, indefinite linear system using the Generalized Minimum RESidual method with Right Preconditioning (GMRESRP). Because this algorithm uses right preconditioning, it is able to check the linear residuals at both the outer and inner iterations. This may be much for efficient compared to GMRESLP. In order to check inner residuals, this algorithm has to perform it's own internal Modified Gram-Schmidt procedure and will not call the Arnoldi algorithm.

## Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system $Ax=b$
<i>gmresrp_dat</i>	pointer to the <a href="#">GMRESRP_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

## Note

int (\*matvec) (const [Matrix<double>](#) & v, [Matrix<double>](#) &Av, const void \*data)

-----  
 This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

int (\*precon) (const [Matrix<double>](#) & b, [Matrix<double>](#) &Mb, const void \*data)

This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.6** `int pcg ( int(*)(const Matrix< double > &p, Matrix< double > &Ap, const void *data) matvec, int(*)(const Matrix< double > &r, Matrix< double > &z, const void *data) precon, Matrix< double > &b, PCG_DATA * pcg_dat, const void * matvec_data, const void * precon_data )`

Function to iteratively solve a symmetric, definite linear system with PCG.

This function iteratively solves a symmetric, definite linear system using the Preconditioned Conjugate Gradient (PCG) method. The PCG algorithm is optimal in terms of efficiency and residual reduction, but only if the linear system is symmetric. PCG will fail if the linear operator is non-symmetric!

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system $Ax=b$
<i>pcg_dat</i>	pointer to the <a href="#">PCG_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

#### Note

`int (*matvec) (const Matrix<double> &v, Matrix<double> &Av, const void *data)`

---

This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

---

`int (*precon) (const Matrix<double> &b, Matrix<double> &Mb, const void *data)`

---

This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.7** `int bicgstab ( int(*)(const Matrix< double > &p, Matrix< double > &Ap, const void *data) matvec, int(*)(const Matrix< double > &r, Matrix< double > &z, const void *data) precon, Matrix< double > &b, BiCGSTAB_DATA * bicg_dat, const void * matvec_data, const void * precon_data )`

Function to iteratively solve a non-symmetric, definite linear system with BiCGSTAB.

This function iteratively solves a non-symmetric, definite linear system using the Bi-Conjugate Gradient STABILized (BiCGSTAB) method. This is a highly efficient algorithm for solving non-symmetric problems, but will occasionally breakdown and fail. Most common failures are caused by poor preconditioning. Works very well for grid-based linear systems.

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function

<i>b</i>	matrix of boundary conditions in the linear system $Ax=b$
<i>bicg_dat</i>	pointer to the <a href="#">BiCGSTAB_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

**Note**

int (\*matvec) (const [Matrix<double>](#) &v, [Matrix<double>](#) &Av, const void \*data)

-----  
This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

int (\*precon) (const [Matrix<double>](#) &b, [Matrix<double>](#) &Mb, const void \*data)

-----  
This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

6.8.4.8 int cgs ( int(\*) (const [Matrix<double>](#) &p, [Matrix<double>](#) &Ap, const void \*data) matvec, int(\*) (const [Matrix<double>](#) &r, [Matrix<double>](#) &z, const void \*data) precon, [Matrix<double>](#) &b, [CGS\\_DATA](#) \* cgs\_dat, const void \* matvec\_data, const void \* precon\_data )

Function to iteratively solve a non-symmetric, definite linear system with CGS.

This function iteratively solves a non-symmetric, definite linear system using the Conjugate Gradient Squared (CGS) method. This is an extremely efficient algorithm for solving non-symmetric problems, but will often breakdown and fail. Most common failures are caused by poor or no preconditioning. Works very well for grid-based linear systems.

**Parameters**

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system $Ax=b$
<i>cgs_dat</i>	pointer to the <a href="#">CGS_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

**Note**

int (\*matvec) (const [Matrix<double>](#) &v, [Matrix<double>](#) &Av, const void \*data)

-----  
This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

int (\*precon) (const [Matrix<double>](#) &b, [Matrix<double>](#) &Mb, const void \*data)

-----  
This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

```
6.8.4.9 int operatorTranspose ( int (*)(const Matrix< double > &v, Matrix< double > &Av, const void *data) matvec,
                               Matrix< double > &r, Matrix< double > &u, OPTRANS_DATA * transpose_dat, const void * matvec_data )
```

Function that is used to perform transposition of a linear operator and results in a new vector  $A^T r = u$ .

This function takes a user supplied linear operator and forms the result of that operator transposed and multiplied by a given vector  $r$  ( $A^T r = u$ ). Transposition is accomplished by reordering the transpose operator and multiplying the non-transposed operator by a complete set of orthonormal vectors. The end result gives the  $i$ th component of the vector  $u$  for each operation ( $u_i = r^T A \cdot i$ ). Here,  $i$  is a vector made from the  $i$ th column of the identity matrix. If the linear system is sufficiently large, then this operation may take some time.

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>r</i>	vector to be multiplied by the transpose of the operator
<i>u</i>	vector to store the result of the operator transposition ( $u = A^T r$ )
<i>transpose_dat</i>	pointer to the <a href="#">OPTRANS_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator

#### Note

```
int (*matvec) (const Matrix<double> &v, Matrix<double> &Av, const void *data)
```

---

This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix  $v$  that will act on the linear operator a modified the matrix entries of  $Av$  to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

---

```
6.8.4.10 int gcr ( int (*)(const Matrix< double > &x, Matrix< double > &Ax, const void *data) matvec, int (*)(const
                  Matrix< double > &r, Matrix< double > &Mr, const void *data) precon, Matrix< double > &b, GCR_DATA *
                  gcr_dat, const void * matvec_data, const void * precon_data )
```

Function to iteratively solve a non-symmetric, definite linear system with GCR.

This function iteratively solves a non-symmetric, definite linear system using the Generalized Conjugate Residual (GCR) method. Similar to GMRESRP, this algorithm will construct a growing orthonormal basis set that will eventually form the exact solution to the linear system. However, this algorithm is less efficient than GMRESRP and can suffer breakdowns if the linear system is indefinite.

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system $Ax=b$
<i>gcr_dat</i>	pointer to the <a href="#">GCR_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

#### Note

```
int (*matvec) (const Matrix<double> &v, Matrix<double> &Av, const void *data)
```

---

This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix  $v$  that will act on the linear operator a modified the matrix entries of  $Av$  to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

---

```
int (*precon) (const Matrix<double> &b, Matrix<double> &Mb, const void *data)
```

---

This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.11** `int gmresrPreconditioner ( const Matrix< double > &r, Matrix< double > &Mr, const void * data )`

Function used in conjunction with GMRESR to apply GMRESRP iterations as a preconditioner.

This function is required to take the form of the user supplied preconditioning functions for other iterative methods. However, it cannot be used in conjunction with any other Krylov method. It is only called by the GMRESR function when the preconditioner needs to be applied.

#### Parameters

<i>r</i>	vector supplied to the preconditioner to operate on
<i>Mr</i>	vector to hold the result of the preconditioning operation
<i>data</i>	void pointer to the <a href="#">GMRESR_DATA</a> data structure

**6.8.4.12** `int gmresr ( int(*) (const Matrix< double > &x, Matrix< double > &Ax, const void *data) matvec, int(*) (const Matrix< double > &r, Matrix< double > &Mr, const void *data) terminal_precon, Matrix< double > &b, GMRESR\_DATA * gmresr_dat, const void * matvec_data, const void * term_precon_data )`

Function to iteratively solve a non-symmetric, indefinite linear system with GMRESR.

This function iteratively solves a non-symmetric, indefinite linear system using the Generalized Minimum RESidual Recursive (GMRESR) method. This algorithm actually uses GCR at the outer iterations, but stabilizes GCR with GMRESRP inner iterations to implicitly form a variable preconditioner to the linear system. As such, this is one of only two methods that inherently includes preconditioning (the other is KMS), without any user supplied preconditioning operator. However, this algorithm is significantly more computationally expensive than GCR or GMRESRP separately. It should only be used for solving very large or very hard to solve linear systems.

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>terminal_precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system Ax=b
<i>gmresr_dat</i>	pointer to the <a href="#">GMRESR_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>term_precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

#### Note

```
int (*matvec) (const Matrix<double> &v, Matrix<double> &Av, const void *data)
```

---

This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

---

```
int (*terminal_precon) (const Matrix<double> &b, Matrix<double> &Mb, const void *data)
```

---

This is a user supplied function for a preconditioning operator. It has the same form as the above linear

operator function and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.13** `int kmsPreconditioner ( const Matrix< double > & r, Matrix< double > & Mr, const void * data )`

Preconditioner function for the Krylov Multi-Space.

This function is required to take the form of the user supplied preconditioning functions for other iterative methods. However, it cannot be used in conjunction with any other Krylov method. It is only called by the KMS function when the preconditioner needs to be applied.

#### Parameters

<i>r</i>	vector supplied to the preconditioner to operate on
<i>Mr</i>	vector to hold the result of the preconditioning operation
<i>data</i>	void pointer to the <a href="#">KMS_DATA</a> data structure

**6.8.4.14** `int krylovMultiSpace ( int(*) (const Matrix< double > &x, Matrix< double > &Ax, const void *data) matvec, int(*) (const Matrix< double > &r, Matrix< double > &Mr, const void *data) terminal_precon, Matrix< double > &b, KMS_DATA * kms_dat, const void * matvec_data, const void * term_precon_data )`

Function to iteratively solve a non-symmetric, indefinite linear system with KMS.

This function iteratively solves a non-symmetric, indefinite linear system using the Krylov Multi-Space (KMS) method. This algorithm uses GMRESRP at both outer and inner iterations to implicitly form a variable preconditioner to the linear system. As such, this is one of only two methods that inherently includes preconditioning, without any user supplied preconditioning operator (the other being GMRESR). The advantage to this method over GMRESR is that this method is GMRES at its core, and will therefore never breakdown or need to be stabilized. Additionally, you can call this method and set its max\_level parameter (see [KMS\\_DATA](#)) to 0, which will make this algorithm exactly equal to GMRESRP. If the max\_level is set to 1, then this algorithm is exactly FGMRES (Saad, 1993) with the GMRES algorithm as a preconditioner. However, you can set max\_level higher to precondition the preconditioners with more preconditioners. Thus creating a method with any desired complexity or rate of convergence.

#### Parameters

<i>matvec</i>	user supplied linear operator given as an int function
<i>terminal_precon</i>	user supplied preconditioning operator given as an int function
<i>b</i>	matrix of boundary conditions in the linear system Ax=b
<i>kms_dat</i>	pointer to the <a href="#">KMS_DATA</a> data structure
<i>matvec_data</i>	user supplied void pointer to a data structure needed for the linear operator
<i>term_precon_data</i>	user supplied void pointer to a data structure needed for the preconditioning operator

#### Note

`int (*matvec) (const Matrix<double> & v, Matrix<double> &Av, const void *data)`

---

This is a user supplied function for a linear operator. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix v that will act on the linear operator a modified the matrix entries of Av to form the result of a matrix-vector product. Void pointer data is used to pass any user data structure that the function may need in order to perform the linear operation.

---

`int (*terminal_precon) (const Matrix<double> & b, Matrix<double> &Mb, const void *data)`

---

This is a user supplied function for a preconditioning operator. It has the same form as the above linear operator function and should have all the same properties. The only difference is that this function must form



an approximate matrix inversion on the original linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

---

**6.8.4.15** `int picard ( int(*) (const Matrix< double > &x, Matrix< double > &r, const void *data) res, int(*) (const Matrix< double > &x0, Matrix< double > &x, const void *data) evalx, Matrix< double > &x, PICARD_DATA * picard_dat, const void * res_data, const void * evalx_data )`

Function to iteratively solve a non-linear system using the Picard or Fixed-Point method.

This function iteratively solves a non-linear system using the Picard method. User supplies a residual function and a weak solution form function. The weak form function is used to approximate the next solution vector for the non-linear system and the residual function is used to determine convergence. User also supplies an initial guess to the non-linear system as a matrix x, which will also be used to store the solution. This algorithm is very simple and may not be sufficient to solve complex non-linear systems.

#### Parameters

<i>res</i>	user supplied function for the non-linear residuals of the system
<i>evalx</i>	user supplied function for the weak form to estimate the next solution
<i>x</i>	user supplied matrix holding the initial guess to the non-linear system
<i>picard_dat</i>	pointer to the <a href="#">PICARD_DATA</a> data structure
<i>res_data</i>	user supplied void pointer to a data structure used for residual evaluations
<i>evalx_data</i>	user supplied void pointer to a data structure used for evaluation of weak form

#### Note

`int (*res) (const Matrix<double> &x, Matrix<double> &F, const void *data)`

---

This is a user supplied function for the non-linear residuals. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix x representing the current non-linear variables. Those variables are used to evaluate the users functions and return the residuals in the matrix F. The void pointer data is a data structure provided by the user to hold information the function may need in order to form the residuals.

---

`int (*evalx) (const Matrix<double> &x0, Matrix<double> &x, const void *data)`

---

This is a user supplied function to approximate the next solution vector x based on the previous solution vector x0. The x0 matrix is passed to this function and must be used to edit the entries of x based on the weak form of the problem. The user is free to define any weak form approximation. Void pointer data is the users data structure that may be used to pass additional information into this function in order to evaluate the weak form.

Example Residual:  $F(x) = x^2 + x - 1$  Goal is to make this function equal zero

Example Weak Form:  $x = 1 - x^2$  Rearrange residual to form a weak solution

---

**6.8.4.16** `int jacvec ( const Matrix< double > &v, Matrix< double > &Jv, const void * data )`

Function to form a linear operator of a Jacobian matrix used along with the PJFNK method.

This function is used in conjunction with the PJFNK routine to form a linear operator that a Krylov method can operate on. This linear operator is formed from the current residual vector of the non-linear iteration in PJFNK using a finite difference approximation.

Jacobian Linear Operator:  $J*v = ( F(x_k + \text{eps}*v) - F(x_k) ) / \text{eps}$



## Parameters

<i>v</i>	vector to be multiplied by the Jacobian matrix
<i>Jv</i>	storage vector for the result of the Jacobi-vector product
<i>data</i>	void pointer to the <a href="#">PJFNK_DATA</a> data structure holding solver information

**6.8.4.17** `int backtrackLineSearch ( int(*) (const Matrix< double > &x, Matrix< double > &F, const void *data) feval, Matrix< double > &Fkp1, Matrix< double > &xkp1, Matrix< double > &pk, double normFk, BACKTRACK_DATA * backtrack_dat, const void * feval_data )`

Function to perform a Backtracking Line Search operation to smooth out convergence of PJFNK.

This function performs a simple backtracking line search operation on the residuals from the PJFNK method. The step size of the non-linear iteration is checked against a level of tolerance for residual reduction, then adjusted down if necessary. This method always starts out with the maximum allowable step size. If the largest step size is fine, then the algorithm does nothing. Otherwise, it iteratively adjusts the step size down, until a suitable step is found. In the case that no suitable step is found, this algorithm will report failure to the PJFNK method and PJFNK will decide whether to continue trying to find a global minimum or report that it is stuck in a local minimum.

## Parameters

<i>feval</i>	user supplied residual function for the non-linear system
<i>Fkp1</i>	vector holding the residuals for the next non-linear step
<i>xkp1</i>	vector holding the solution for the next non-linear step
<i>pk</i>	vector holding the current non-linear search direction
<i>normFk</i>	value of the current non-linear residual
<i>backtrack_dat</i>	pointer to the <a href="#">BACKTRACK_DATA</a> data structure
<i>feval_data</i>	user supplied void pointer to the data structure needed for residual evaluation

## Note

`int (*feval) (const Matrix<double> &x, Matrix<double> &F, const void *data)`

-----  
This is a user supplied function for the non-linear residuals. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix x representing the current non-linear variables. Those variables are used to evaluate the users functions and return the residuals in the matrix F. The void pointer data is a data structure provided by the user to hold information the function may need in order to form the residuals.  
-----

**6.8.4.18** `int pjfnk ( int(*) (const Matrix< double > &x, Matrix< double > &F, const void *data) res, int(*) (const Matrix< double > &r, Matrix< double > &p, const void *data) precon, Matrix< double > &x, PJFNK_DATA * pjfnk_dat, const void * res_data, const void * precon_data )`

Function to perform the PJFNK algorithm to solve a non-linear system of equations.

This function solves a non-linear system of equations using the Preconditioned Jacobian- Free Newton-Krylov (PJFNK) algorithm. Each non-linear step of this method results in a linear sub-problem that is solved iteratively with one of the Krylov methods in the krylov\_method enum. User must supplied a residual function that computes the non-linear residuals of the system given the current state of the variables x. Additionally, the user must also supplied an initial guess to the non-linear system. Optionally, the user may supply a preconditioning function for the linear sub-problem.

Basic Steps: (i) Calc  $F(x_k)$ , (ii) Solve  $J(x_k)s_k = -F(x_k)$  for  $s_k$ , (iii) Form  $x_{kp1} = x_k + s_k$

## Parameters

<i>res</i>	user supplied residual function for the non-linear system
<i>precon</i>	user supplied preconditioning function for the linear sub-problems
<i>x</i>	user supplied initial guess and storage location of the solution

<i>pjfnk_dat</i>	pointer to the <a href="#">PJFNK_DATA</a> data structure
<i>res_data</i>	user supplied void pointer to data structure used in residual function
<i>precon_data</i>	user supplied void pointer to data structure used in preconditioning function

**Note**

int (\*res) (const [Matrix<double>](#) &x, [Matrix<double>](#) &F, const void \*data)

-----

This is a user supplied function for the non-linear residuals. User's function must return an int of 0 upon success and anything else denotes a failure. The function accepts a matrix x representing the current non-linear variables. Those variables are used to evaluate the users functions and return the residuals in the matrix F. The void pointer data is a data structure provided by the user to hold information the function may need in order to form the residuals.

-----

int (\*precon) (const [Matrix<double>](#) &b, [Matrix<double>](#) &Mb, const void \*data)

-----

This is a user supplied function for a preconditioning operator. It has the same form as the linear operators from the Krylov methods and should have all the same properties. The only difference is that this function must form an approximate matrix inversion on the jacvec linear operator and modify the entries of Mb to represent the result of that approximate matrix inversion. The matrix b is given as the vector that this operator is acting on and the void pointer data is for any user data structure that the operator may need.

6.8.4.19 int NumericalJacobian ( int(\*) (const [Matrix< double >](#) &x, [Matrix< double >](#) &F, const void \*user\_data) *Func*, const [Matrix< double >](#) &x, [Matrix< double >](#) &J, int *Nx*, int *Nf*, [NUM\\_JAC\\_DATA](#) \* *jac\_dat*, const void \* *user\_data* )

Function to form a full numerical Jacobian matrix from a given non-linear function.

This function uses finite differences to form a full rank Jacobian matrix for a user supplied non-linear function. The Jacobian matrix will be formed at the current state of the non-linear variables x and stored in a full matrix J. Integers Nx and Nf are used to determine the size of the Jacobian matrix.

**Parameters**

<i>Func</i>	user supplied function for evaluation of the non-linear system
<i>x</i>	matrix holding the current value of the non-linear variables
<i>J</i>	matrix that will store the numerical Jacobian result
<i>Nx</i>	number of non-linear variables in the system
<i>Nf</i>	number of non-linear functions in the system
<i>jac_dat</i>	pointer to the <a href="#">NUM_JAC_DATA</a> data structure
<i>user_data</i>	user supplied void pointer to a data structure used in the non-linear function

6.8.4.20 int LARK\_TESTS ( )

Function that runs a variety of tests on all the functions in LARK.

This function runs a variety of tests on the linear and non-linear methods developed in LARK. It can be called from the UI.

**6.9 macaw.h File Reference**

MAtrix CAlculation Workspace.

```
#include <stdio.h>
#include <math.h>
#include <iostream>
#include <fstream>
#include <stdlib.h>
#include <vector>
#include <time.h>
#include <float.h>
#include <string>
#include <exception>
#include "error.h"
```

## Classes

- class [Matrix< T >](#)  
*Templated C++ [Matrix](#) Class Object (click [Matrix](#) to go to function definitions)*

## Macros

- `#define M_PI 3.14159265358979323846264338327950288`  
*Value of PI with double precision.*

## Functions

- int [MACAW\\_TESTS](#) ()  
*Function to run the MACAW tests.*

### 6.9.1 Detailed Description

MATrix CAlculation Workspace. `macaw.cpp`

This is a small C++ library that facilitates the use and construction of real matrices using vector objects. The [Matrix](#) class is templated so that users are able to work with matrices of any type including, but not limited to: (i) doubles, (ii) ints, (iii) floats, and (iv) even other matrices! Routines and functions are defined for Dense matrix operations. As a result, we typically only use Column Matrices (or Vectors) when doing any actual simulations. However, the development of this class was integral to the development and testing of the Sparse matrix operators in [lark.h](#).

While the primary goal of this object was to define how to operate on real matrices, we could extend this idea to complex matrices as well. For this, we could develop objects that represent imaginary and complex numbers and then create a [Matrix](#) of those objects. For this reason, the matrix operations here are all templated to abstract away the specificity of the type of matrix being operated on.

## Author

Austin Ladshaw

## Date

01/07/2014

## Copyright

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

## 6.9.2 Macro Definition Documentation

## 6.9.2.1 #define M\_PI 3.14159265358979323846264338327950288

Value of PI with double precision.

## 6.9.3 Function Documentation

## 6.9.3.1 int MACAW\_TESTS ( )

Function to run the MACAW tests.

This function is callable from the UI and is used to run several algorithm tests for the [Matrix](#) objects. This test should never report any errors.

## 6.10 magpie.h File Reference

Multicomponent Adsorption Generalized Procedure for Isothermal Equilibria.

```
#include "lmcurve.h"
#include <stdio.h>
#include <math.h>
#include <iostream>
#include <fstream>
#include <stdlib.h>
#include <vector>
#include <time.h>
#include <float.h>
#include <string>
#include "error.h"
```

## Classes

- struct [GSTA\\_DATA](#)  
*GSTA Data Structure.*
- struct [mSPD\\_DATA](#)  
*MSPD Data Structure.*
- struct [GPAST\\_DATA](#)  
*GPAST Data Structure.*
- struct [SYSTEM\\_DATA](#)  
*System Data Structure.*
- struct [MAGPIE\\_DATA](#)  
*MAGPIE Data Structure.*

## Macros

- #define [DBL\\_EPSILON](#) 2.2204460492503131e-016  
*Machine precision value used for approximating gradients.*
- #define [Z](#) 10.0  
*Surface coordination number used in the MSPD activity model.*
- #define [A](#) 3.13E+09  
*Corresponding van der Waals standard area for our coordination number (cm<sup>2</sup>/mol)*
- #define [V](#) 18.92

- Corresponding van der Waals standard volume for our coordination number ( $\text{cm}^3/\text{mol}$ )
- #define **Po** 100.0
- Standard State Pressure - Units: kPa.
- #define **R** 8.3144621
- Gas Constant - Units:  $\text{J}/(\text{K}\cdot\text{mol}) = k_B \cdot N_A$ .
- #define **Na** 6.0221413E+23
- Avagadro's Number - Units: molecules/mol.
- #define **kB** 1.3806488E-23
- Boltzmann's Constant - Units: J/K.
- #define **shapeFactor**(v\_i) ( ( (Z - 2) \* v\_i ) / ( Z \* V ) ) + ( 2 / Z )
- This macro replaces all instances of shapeFactor(#) with the following single line calculation.
- #define **lnKo**(H, S, T) -( H / ( R \* T ) ) + ( S / R )
- This macro calculates the natural log of the dimensionless isotherm parameter.
- #define **He**(qm, K1, m) ( qm \* K1 ) / ( m \* Po )
- This macro calculates the Henry's Coefficient for the ith component.

## Functions

- double **qo** (double po, const void \*data, int i)
- Function computes the result of the GSTA isotherm for the ith species.
- double **dq\_dp** (double p, const void \*data, int i)
- Function computes the derivative of the GSTA model with respect to partial pressure.
- double **q\_p** (double p, const void \*data, int i)
- Function computes the ratio between the adsorbed amount and partial pressure for the GSTA isotherm.
- double **PI** (double po, const void \*data, int i)
- Function computes the spreading pressure integral of the ith species.
- double **Qst** (double po, const void \*data, int i)
- Function computes the heat of adsorption based on the ith species GSTA parameters.
- double **eMax** (const void \*data, int i)
- Function to approximate the maximum lateral energy term for the ith species.
- double **lnact\_mSPD** (const double \*par, const void \*data, int i, volatile double PI)
- Function to evaluate the MSPD activity coefficient for the ith species.
- double **grad\_mSPD** (const double \*par, const void \*data, int i)
- Function to approximate the derivative of the MSPD activity model with spreading pressure.
- double **qT** (const double \*par, const void \*data)
- Function to calculate the total adsorbed amount (mol/kg) for the mixed surface phase.
- void **initialGuess\_mSPD** (double \*par, const void \*data)
- Function to provide an initial guess to the unknown parameters being solved for in GPAST.
- void **eval\_po\_PI** (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)
- Function used with Imfit to evaluate the reference state pressure of a species based on spreading pressure.
- void **eval\_po\_qo** (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)
- Function used with Imfit to evaluate the reference state pressure of a species based on that species isotherm.
- void **eval\_po** (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)
- Function used with Imfit to evaluate the reference state pressure of a species based on a sub-system.
- void **eval\_eta** (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)
- Function used with Imfit to evaluate the binary interaction parameters for each unique species pair.
- void **eval\_GPAST** (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)
- Function used with Imfit to solve the GPAST system of equations.
- int **MAGPIE** (const void \*data)
- Function to call all sub-routines to solve a MAGPIE/GPAST problem at a given temperature and pressure.
- int **MAGPIE\_SCENARIOS** (const char \*inputFileName, const char \*sceneFileName)
- Function to perform a series of MAGPIE simulations based on given input files.

### 6.10.1 Detailed Description

Multicomponent Adsorption Generalized Procedure for Isothermal Equilibria. magpie.cpp

This file contains all functions and routines associated with predicting isothermal adsorption equilibria from only single component isotherm information. The basis of the model is the Adsorbed Solution Theory developed by Myers and Prausnitz (1965). Added to that base model is a procedure by which we can predict the non-idealities present at the surface phase by solving a closed system of equations involving the activity model.

For more details on this procedure, check out our publication in AIChE where we give a fully feature explanation of our Generalized Predictive Adsorbed Solution Theory (GPAST).

Reference: Ladshaw, A., Yiaccoumi, S., and Tsouris, C., "A generalized procedure for the prediction of multicomponent adsorption equilibria", AIChE J., vol. 61, No. 8, p. 2600-2610, 2015.

MAGPIE represents a special case of the more general GPAST procedure, wherein the isotherm for each species is represented by the GSTA isotherm (see [gsta\\_opt.h](#)) and the activity model for non-ideality at the adsorbent surface is a Modified Spreading Pressure Dependent (MSPD) model. See the above paper reference for more details.

#### Author

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#### Date

12/17/2013

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### 6.10.2 Macro Definition Documentation

#### 6.10.2.1 #define DBL\_EPSILON 2.2204460492503131e-016

Machine precision value used for approximating gradients.

#### 6.10.2.2 #define Z 10.0

Surface coordination number used in the MSPD activity model.

#### 6.10.2.3 #define A 3.13E+09

Corresponding van der Waals standard area for our coordination number ( $\text{cm}^2/\text{mol}$ )

#### 6.10.2.4 #define V 18.92

Corresponding van der Waals standard volume for our coordination number ( $\text{cm}^3/\text{mol}$ )

#### 6.10.2.5 #define Po 100.0

Standard State Pressure - Units: kPa.

#### 6.10.2.6 #define R 8.3144621

Gas Constant - Units:  $\text{J}/(\text{K} \cdot \text{mol}) = \text{kJ} \cdot \text{mol}^{-1} \cdot \text{K}^{-1}$ .

#### 6.10.2.7 #define Na 6.0221413E+23

Avagadro's Number - Units: molecules/mol.

6.10.2.8 `#define kB 1.3806488E-23`

Boltzmann's Constant - Units: J/K.

6.10.2.9 `#define shapeFactor( v,i ) ( ( (Z - 2) * v.i ) / ( Z * V ) ) + ( 2 / Z )`

This macro replaces all instances of shapeFactor(#) with the following single line calculation.

6.10.2.10 `#define lnKo( H, S, T ) -( H / ( R * T ) ) + ( S / R )`

This macro calculates the natural log of the dimensionless isotherm parameter.

6.10.2.11 `#define He( qm, K1, m ) ( qm * K1 ) / ( m * Po )`

This macro calculates the Henry's Coefficient for the ith component.

### 6.10.3 Function Documentation

6.10.3.1 `double qo ( double po, const void * data, int i )`

Function computes the result of the GSTA isotherm for the ith species.

This function just computes the result of the GSTA isotherm model for the ith species given the partial pressure po.

#### Parameters

<i>po</i>	partial pressure in kPa at which to evaluate the GSTA model
<i>data</i>	void pointer to the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	index of the gas species for which the GSTA model is being evaluated

6.10.3.2 `double dq.dp ( double p, const void * data, int i )`

Function computes the derivative of the GSTA model with respect to partial pressure.

This function just computes the result of the derivative of GSTA isotherm model for the ith species at the given the partial pressure p.

#### Parameters

<i>p</i>	partial pressure in kPa at which to evaluate the GSTA model
<i>data</i>	void pointer to the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	index of the gas species for which the GSTA model is being evaluated

6.10.3.3 `double q.p ( double p, const void * data, int i )`

Function computes the ratio between the adsorbed amount and partial pressure for the GSTA isotherm.

This function just computes the ratio between the adsorbed amount q (mol/kg) and the partial pressure p (kPa) at the given partial pressure. If p == 0, then this function returns the Henry's Law constant for the isotherm of the ith species.

#### Parameters

<i>p</i>	partial pressure in kPa at which to evaluate the GSTA model
<i>data</i>	void pointer to the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	index of the gas species for which the GSTA model is being evaluated

6.10.3.4 `double PI ( double po, const void * data, int i )`

Function computes the spreading pressure integral of the ith species.

This function uses an analytical solution to the spreading pressure integral with the GSTA isotherm to evaluate and return the value computed by that integral equation.

#### Parameters

<i>po</i>	partial pressure in kPa at which to evaluate the lumped spreading pressure
<i>data</i>	void pointer to the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	index of the gas species for which the GSTA model is being evaluated

#### 6.10.3.5 double Qst ( double *po*, const void \* *data*, int *i* )

Function computes the heat of adsorption based on the *i*th species GSTA parameters.

This function computes the isosteric heat of adsorption (J/mol) for the GSTA parameters of the *i*th species.

#### Parameters

<i>po</i>	partial pressure in kPa at which to evaluate the heat of adsorption
<i>data</i>	void pointer to the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	index of the gas species for which the GSTA model is being evaluated

#### 6.10.3.6 double eMax ( const void \* *data*, int *i* )

Function to approximate the maximum lateral energy term for the *i*th species.

The function attempts to approximate the maximum lateral energy term for the *i*th species. This is not a true maximum, but a cheaper estimate. Value being computed is used to shift the geometric mean and formulate the average cross-lateral energy term between species *i* and *j*.

#### 6.10.3.7 double lnact\_mSPD ( const double \* *par*, const void \* *data*, int *i*, volatile double *PI* )

Function to evaluate the MSPD activity coefficient for the *i*th species.

This function will return the natural log of the *i*th species activity coefficient using the Modified Spreading Pressure Dependent (MSPD) activity model. The *par* argument holds the variable values being solved for by GPAST and their contents will change depending on whether we are doing a forward or reverse evaluation. This function should not be called by the user and will only be called when needed in the GPAST routine.

#### Parameters

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	<i>i</i> th species that we want to calculate the activity coefficient for
<i>PI</i>	lumped spreading pressure term used in gradient estimations

#### 6.10.3.8 double grad\_mSPD ( const double \* *par*, const void \* *data*, int *i* )

Function to approximate the derivative of the MSPD activity model with spreading pressure.

This function returns a 2nd order, finite different approximation of the derivative of the MSPD activity model with the spreading pressure. The *par* argument will either hold the current iterates estimate of spreading pressure or should be passed as null. User does not need to call this function. GPAST will call automatically when needed.

#### Parameters

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>i</i>	<i>i</i> th species for which we will approximate the activity model gradient



**6.10.3.9 double qT ( const double \* par, const void \* data )**

Function to calculate the total adsorbed amount (mol/kg) for the mixed surface phase.

This function will use the obtained system parameters from par and estimate the total amount of gases adsorbed to the surface in mol/kg. The user does not need to call this function, since this result will be stored in the [SYSTEM\\_DATA](#) structure.

**Parameters**

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure

**6.10.3.10 void initialGuess\_mSPD ( double \* par, const void \* data )**

Function to provide an initial guess to the unknown parameters being solved for in GPAST.

This function intends to provide an initial guess for the unknown values being solved for in the GPAST system. Depending on what type of solve is requested, this algorithm will provide a guess for the adsorbed or gas phase composition.

**Parameters**

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure

**6.10.3.11 void eval\_po\_PI ( const double \* par, int m\_dat, const void \* data, double \* fvec, int \* info )**

Function used with Imfit to evaluate the reference state pressure of a species based on spreading pressure.

This function is used inside of the MSPD activity model to calculate the reference state pressure of a particular species at a given spreading pressure for the system. User does not need to call this function. GPAST will call automatically when needed.

**Parameters**

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>m_dat</i>	number of functions/variables in the GPAST system of equations
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>fvec</i>	list of residuals formed by the functions in GPAST
<i>info</i>	integer flag variable used in the Imfit routine

**6.10.3.12 void eval\_po\_qo ( const double \* par, int m\_dat, const void \* data, double \* fvec, int \* info )**

Function used with Imfit to evaluate the reference state pressure of a species based on that species isotherm.

This function is used to evaluate the partial pressure or reference state pressure for a particular species given single-component adsorbed amount. User does not need to call this function. GPAST will call automatically when needed.

**Parameters**

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>m_dat</i>	number of functions/variables in the GPAST system of equations
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>fvec</i>	list of residuals formed by the functions in GPAST
<i>info</i>	integer flag variable used in the Imfit routine

6.10.3.13 void eval\_po ( const double \* *par*, int *m\_dat*, const void \* *data*, double \* *fvec*, int \* *info* )

Function used with Imfit to evaluate the reference state pressure of a species based on a sub-system.

This function is used to approximate reference state pressures based on the spreading pressure of a sub-system in GPAST. The sub-system will be one of the unique binary systems that exist in the overall mixed gas system. User does not need to call this function. GPAST will call automatically when needed.

#### Parameters

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>m_dat</i>	number of functions/variables in the GPAST system of equations
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>fvec</i>	list of residuals formed by the functions in GPAST
<i>info</i>	integer flag variable used in the Imfit routine

6.10.3.14 void eval\_eta ( const double \* *par*, int *m\_dat*, const void \* *data*, double \* *fvec*, int \* *info* )

Function used with Imfit to evaluate the binary interaction parameters for each unique species pair.

This function is used to estimate the binary interaction parameters for all species pairs in a given sub-system. Those parameters are then stored for later used when evaluating the activity coefficients for the overall mixture. User does not need to call this function. GPAST will call automatically when needed.

#### Parameters

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>m_dat</i>	number of functions/variables in the GPAST system of equations
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>fvec</i>	list of residuals formed by the functions in GPAST
<i>info</i>	integer flag variable used in the Imfit routine

6.10.3.15 void eval\_GPAST ( const double \* *par*, int *m\_dat*, const void \* *data*, double \* *fvec*, int \* *info* )

Function used with Imfit to solve the GPAST system of equations.

This function is used after having calculated and stored all necessary information to solve a closed form GPAST system of equations. User does not need to call this function. GPAST will call automatically when needed.

#### Parameters

<i>par</i>	list of parameters representing variables to be solved for in GPAST
<i>m_dat</i>	number of functions/variables in the GPAST system of equations
<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure
<i>fvec</i>	list of residuals formed by the functions in GPAST
<i>info</i>	integer flag variable used in the Imfit routine

6.10.3.16 int MAGPIE ( const void \* *data* )

Function to call all sub-routines to solve a MAGPIE/GPAST problem at a given temperature and pressure.

This is the function that a typical user will want to incorporate into their own codes when evaluating adsorption of a gas mixture. Prior to calling this function, all required structures and information in the [MAGPIE\\_DATA](#) structure must have been properly initialized. After this function has completed it's operations, it will return an integer used to denote a success or failure of the routine. Integers 0, 1, 2, and 3 all denote success. Anything else is considered a failure.

To setup the [MAGPIE\\_DATA](#) structure correctly, you must reserve space for all vector objects based on the number of gas species in the mixture. In general, you only need to reserve space for the adsorbing species. However, you can also reserve space for non-adsorbing species, but you MUST give a gas/adsorbed mole fraction of the non-adsorbing species 0.0 so that the routine knows to ignore them (very important)!

After setting up the memory for the vector objects, you can initialize information specific to the simulation you want to request. The number of species (N), total pressure (PT) and gas temperature (T) must always be given. You can neglect the non-idealities of the surface phase by setting the Ideal bool to true. This will result in faster calculations, because MAGPIE will just revert down to the Ideal Adsorbed Solution Theory (IAST).

The Recover bool will denote whether we are doing a forward or reverse GPAST evaluation. Forward evaluation is for solving for the composition of the adsorbed phase given the composition of the gas phase (Recover = false). Reverse evaluation is for solve for the composition of the gas phase given the composition of the adsorbed phase (Recover = true).

For a reverse evaluation (Recover = true) you will also need to stipulate whether or not there is a carrier gas (Carrier = true or false). A carrier gas is considered any non-adsorbing species that may be present in the gas phase and contributing to the total pressure in the system.

The parameters that must be initialized for all species include all [GSTA\\_DATA](#) parameters and the van der Waals volume parameter (v) in the [mspd\\_DATA](#) structure. For non-adsorbing species, you can ignore these parameters, but need to set the sites (m) from [GSTA\\_DATA](#) to 1. GPAST cannot run any evaluations without these parameters being set properly AND set in the same order for all species (i.e., make sure that `gpast_dat[i].qmax` corresponds to `mspd_dat[i].v` and so on).

Lastly, you need to give either the gas phase or adsorbed phase mole fractions, depending on whether you are going to run a forward or reverse evaluation, respectively. For a forward evaluation, provide the gas mole fractions (y) in [GPAST\\_DATA](#) for each species (non-adsorbing species should have this value set to 0.0). For a reverse evaluation, provide the adsorbed mole fractions (x) in [GPAST\\_DATA](#) for each species, as well as the total adsorbed amount (qT) in [SYSTEM\\_DATA](#). Again, non-adsorbing species should have their respective phase mole fractions set to 0.0 to exclude them from the simulation. Additionally, if there are non-adsorbing species present, then the Carrier bool in [SYSTEM\\_DATA](#) must be set to true.

#### Parameters

<i>data</i>	void pointer for the <a href="#">MAGPIE_DATA</a> data structure holding all necessary information
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#### 6.10.3.17 int MAGPIE\_SCENARIOS ( const char \* *inputFileName*, const char \* *sceneFileName* )

Function to perform a series of MAGPIE simulations based on given input files.

This function is callable from the UI and is used to perform a series of isothermal equilibria evaluations using the MAGPIE routines. There are two input files that must be provided: (i) *inputFileName* - containing parameter information for the species and (ii) *sceneFileName* - containing information for each MAGPIE simulation. Each of these files have a specific structure (see below). NOTE: this may change in future versions.

##### *inputFileName* Text File Structure:

Integer for Number of Adsorbing Species

van der Waals Volume ( $\text{cm}^3/\text{mol}$ ) of *ith* species

GSTA adsorption capacity ( $\text{mol/kg}$ ) of *ith* species

Number of GSTA parameters of *ith* species

Enthalpy ( $\text{J/mol}$ ) of *nth* site [tab] Entropy of *nth* site ( $\text{J/K/mol}$ ) of *ith* species

(repeat above for all *n* sites in species *i*)

(repeat above for all species *i*)

##### Example Input File:

5

17.1

5.8797

1

-20351.9 -81.8369

16.2

5.14934

1

-16662.7 -74.4766

19.7

9.27339

4

-46597.5 -53.6994

-125024 -221.073

-193619 -356.728

-272228 -567.459

13.25

4.59144

1

-13418.5 -84.888

18.0

10.0348

1

-20640.4 -72.6119

(The above input file gives the parameter information for 5 adsorbing species)

#### sceneFileName Text File Structure:

Integer Flag to mark Forward (0) or { Reverse (1) evaluations }

Number of Simulations to Run

Total Pressure (kPa) [tab] Temperature (K) { [tab] Total Adsorption (mol/kg) [tab] Carrier Gas Flag (0=false, 1=true) }

Gas/Adsorbed Mole Fractions for each species in the order given in prior file (tab separated)

(repeat above for all simulations desired)

NOTE: only provide the Total Adsorption and Carrier Flag if doing Reverse evaluations!

#### Example Scenario File 1:

0

4

0.65 303.15

0.364 0.318 0.318

3.25 303.15

0.371 0.32 0.309

6.85 303.15

0.388 0.299 0.313

13.42 303.15

0.349 0.326 0.325

(The above scenario file is for 4 forward evaluations/simulations for a 3-adsorbing species system)

Example Scenario File 2:

1

4

0.65 303.15 5.4 0

0.364 0.318 0.318

3.25 303.15 7.7 0

0.371 0.32 0.309

6.85 303.15 9.8 0

0.388 0.299 0.313

13.42 303.15 10.4 0

0.349 0.326 0.325

(The above scenario file is for 4 reverse evaluations/simulations for a 3-adsorbing species system and no carrier gas)

## 6.11 mola.h File Reference

[Molecule](#) Object Library from Atoms.

```
#include <ctype.h>
#include "eel.h"
```

### Classes

- class [Molecule](#)  
*C++ [Molecule](#) Object built from [Atom](#) Objects (click [Molecule](#) to go to function definitions)*

### Enumerations

- enum [valid\\_phase](#) {  
    [SOLID](#), [LIQUID](#), [AQUEOUS](#), [GAS](#),  
    [PLASMA](#), [OTHER](#) }

### Functions

- int [MOLA\\_TESTS](#) ()  
*Function to run the MOLA tests.*

#### 6.11.1 Detailed Description

[Molecule](#) Object Library from Atoms. mola.cpp

This file contains a C++ Class for creating [Molecule](#) objects from the [Atom](#) objects that were defined in [eel.h](#). Molecules can be created and registered from basic information or can be registered from a growing list of pre-registered molecules that are accessible by name/formula.

Registered Molecules are known and defined prior to runtime. They have a charge, energy characteristics, phase, name, and formula that they are recognized by. The formula is used to create the atoms that they are made from. If some information is incomplete, it must be specified as to what information is missing (i.e. denote whether the formation energies are known).

Formation energies are used to determine stability/dissociation/acidity equilibrium constants during runtime. If the formation energies are unknown, then the equilibrium constants must be given to a reaction object on when it is initialized.

The molecule formula's are given as strings which are parsed in the constructor to determine what atoms from the EEL files will be registered and used. Note, you will be able to build molecules from an input file, but the library molecules here are ready to be used in applications and require no more input other than the molecule's formula.

#### List of Currently Registered Molecules

Ag (s)  
Ag + (aq)  
AgBr (s)  
AgCl (s)  
AgI (s)  
Ag<sub>2</sub>S (s)  
AgOH (aq)  
Ag(OH)<sub>2</sub> - (aq)  
AgCl (aq)  
AgCl<sub>2</sub> - (aq)  
Al (s)  
Al<sup>3+</sup> (aq)  
AlOH<sub>2</sub><sup>+</sup> (aq)  
Al(OH)<sub>2</sub><sup>+</sup> (aq)  
Al(OH)<sub>3</sub> (aq)  
Al(OH)<sub>4</sub><sup>-</sup> (aq)  
Al<sub>2</sub>O<sub>3</sub> (s)  
AlOOH (s)  
Al(OH)<sub>3</sub> (s)  
Al<sub>2</sub>Si<sub>2</sub>(OH)<sub>4</sub> (s)  
As (s)  
AsO<sub>4</sub><sup>3-</sup> (aq)  
Ba<sup>2+</sup> (aq)  
BaSO<sub>4</sub> (s)  
BaCO<sub>3</sub> (s)  
Be<sup>2+</sup> (aq)  
Be(OH)<sub>2</sub> (s)  
Be<sub>3</sub>(OH)<sub>3</sub><sup>3+</sup> (aq)  
B(OH)<sub>4</sub><sup>-</sup> (aq)  
Br<sub>2</sub> (l)

Br<sub>2</sub> (aq)  
Br - (aq)  
BrO - (aq)  
CO<sub>3</sub><sup>2-</sup> (aq)  
Cl - (aq)  
CaCl<sub>2</sub> (aq)  
CaAl<sub>2</sub>Si<sub>2</sub>O<sub>8</sub> (s)  
C (s)  
CO<sub>2</sub> (g)  
CH<sub>4</sub> (g)  
CH<sub>4</sub> (aq)  
CH<sub>3</sub>OH (aq)  
CN - (aq)  
CH<sub>3</sub>COOH (aq)  
CH<sub>3</sub>COO - (aq)  
C<sub>2</sub>H<sub>5</sub>OH (aq)  
Ca<sup>2+</sup> (aq)  
CaOH + (aq)  
Ca(OH)<sub>2</sub> (aq)  
Ca(OH)<sub>2</sub> (s)  
CaCO<sub>3</sub> (s)  
CaMg(CO<sub>3</sub>)<sub>2</sub> (s)  
CaSiO<sub>3</sub> (s)  
CaSO<sub>4</sub> (s)  
CaSO<sub>4</sub>(H<sub>2</sub>O)<sub>2</sub> (s)  
Ca<sub>5</sub>(PO<sub>4</sub>)<sub>3</sub>OH (s)  
Cd<sup>2+</sup> (aq)  
Cd(OH) + (aq)  
Cd(OH)<sub>3</sub> - (aq)  
Cd(OH)<sub>4</sub><sup>2-</sup> (aq)  
Cd(OH)<sub>2</sub> (aq)  
CdO (s)  
Cd(OH)<sub>2</sub> (s)  
CdCl + (aq)  
CdCl<sub>2</sub> (aq)  
CdCl<sub>3</sub> - (aq)  
CdCO<sub>3</sub> (s)  
Cl<sub>2</sub> (g)  
Cl<sub>2</sub> (aq)  
ClO - (aq)

ClO2 (aq)  
ClO2 - (aq)  
ClO3 - (aq)  
ClO4 (aq)  
Co (s)  
Co 2+ (aq)  
Co 3+ (aq)  
CoOH + (aq)  
Co(OH)2 (aq)  
Co(OH)3 - (aq)  
Co(OH)2 (s)  
CoO (s)  
Co3O4 (s)  
Cr (s)  
Cr 2+ (aq)  
Cr 3+ (aq)  
CrOH 2+ (aq)  
Cr(OH)2 + (aq)  
Cr(OH)3 (aq)  
Cr(OH)4 - (aq)  
Cr2O3 (s)  
CrO4 2- (aq)  
Cr2O7 2- (aq)  
Cu (s)  
Cu + (aq)  
Cu 2+ (aq)  
CuOH + (aq)  
Cu(OH)2 (aq)  
Cu(OH)3 - (aq)  
Cu(OH)4 2- (aq)  
CuS (s)  
Cu2S (s)  
CuO (s)  
CuCO3Cu(OH)2 (s)  
(CuCO3)2Cu(OH)2 (s)  
F2 (g)  
F - (aq)  
Fe (s)  
Fe 2+ (aq)  
FeOH + (aq)



Fe(OH)2 (aq)  
Fe(OH)3 - (aq)  
Fe 3+ (aq)  
FeOH 2+ (aq)  
Fe(OH)2 + (aq)  
Fe(OH)3 (aq)  
Fe(OH)4 - (aq)  
Fe2(OH)2 4+ (aq)  
FeS2 (s)  
FeO (s)  
Fe(OH)2 (s)  
Fe2O3 (s)  
Fe3O4 (s)  
FeOOH (s)  
Fe(OH)3 (s)  
FeCO3 (s)  
Fe2SiO4 (s)  
H2O (l)  
H + (aq)  
H2CO3 (aq)  
HCO3 - (aq)  
HNO3 (aq)  
HCl (aq)  
H3AsO4 (aq)  
H2AsO4 - (aq)  
HAsO4 2- (aq)  
H2AsO3 - (aq)  
H3BO3 (aq)  
HBrO (aq)  
HCOOH (aq)  
HCOO - (aq)  
HCN (aq)  
HClO (aq)  
HCoO2 - (aq)  
HCrO4 - (aq)  
HCuO2 - (aq)  
HF (aq)  
HF2 - (aq)  
H2 (g)  
H2 (aq)

H<sub>2</sub>O<sub>2</sub> (aq)  
HO<sub>2</sub> - (aq)  
H<sub>2</sub>O (g)  
Hg (l)  
Hg<sup>2+</sup> (aq)  
Hg<sup>2+</sup> (aq)  
HgOH + (aq)  
Hg(OH)<sub>2</sub> (aq)  
Hg(OH)<sub>3</sub> - (aq)  
Hg<sub>2</sub>Cl<sub>2</sub> (s)  
HgO (s)  
HgS (s)  
HgI<sub>2</sub> (s)  
HgCl + (aq)  
HgCl<sub>2</sub> (aq)  
HgCl<sub>3</sub> - (aq)  
HgCl<sub>4</sub> <sup>2-</sup> (aq)  
HgOH + (aq)  
Hg(OH)<sub>2</sub> (aq)  
HgO<sub>2</sub> - (aq)  
HIO (aq)  
HIO<sub>3</sub> (aq)  
HNO<sub>2</sub> (aq)  
HPO<sub>4</sub> <sup>2-</sup> (aq)  
H<sub>2</sub>PO<sub>4</sub> - (aq)  
H<sub>3</sub>PO<sub>4</sub> (aq)  
H<sub>2</sub>S (g)  
H<sub>2</sub>S (aq)  
HS - (aq)  
HSO<sub>3</sub> - (aq)  
H<sub>2</sub>SO<sub>3</sub> (aq)  
HSO<sub>4</sub> - (aq)  
H<sub>2</sub>SO<sub>4</sub> (aq)  
HSeO<sub>3</sub> - (aq)  
H<sub>2</sub>SeO<sub>3</sub> (aq)  
HSeO<sub>4</sub> - (aq)  
H<sub>4</sub>SiO<sub>4</sub> (aq)  
HV<sub>2</sub>O<sub>5</sub> - (aq)  
H<sub>4</sub>VO<sub>4</sub> + (aq)  
H<sub>3</sub>VO<sub>4</sub> (aq)

H<sub>2</sub>VO<sub>4</sub> - (aq)  
HVO<sub>4</sub> 2- (aq)  
H<sub>4</sub>VO<sub>4</sub>(C<sub>2</sub>O<sub>4</sub>)<sub>2</sub> 3- (aq)  
H<sub>4</sub>VO<sub>4</sub>C<sub>2</sub>O<sub>4</sub> - (aq)  
H<sub>2</sub>V<sub>10</sub>O<sub>28</sub> 4- (aq)  
HV<sub>10</sub>O<sub>28</sub> 5- (aq)  
HV<sub>2</sub>O<sub>7</sub> 3- (aq)  
I<sub>2</sub> (s)  
I<sub>2</sub> (aq)  
I - (aq)  
I<sub>3</sub> - (aq)  
IO - (aq)  
IO<sub>3</sub> - (aq)  
KAl<sub>3</sub>Si<sub>3</sub>O<sub>10</sub>(OH)<sub>2</sub> (s)  
K + (aq)  
Mg(OH)<sub>2</sub> (aq)  
Mg<sub>5</sub>Al<sub>2</sub>Si<sub>3</sub>O<sub>10</sub>(OH)<sub>8</sub> (s)  
Mg (s)  
Mg 2+ (aq)  
MgOH + (aq)  
Mg(OH)<sub>2</sub> (s)  
Mn (s)  
Mn 2+ (aq)  
Mn(OH)<sub>2</sub> (s)  
Mn<sub>3</sub>O<sub>4</sub> (s)  
MnOOH (s)  
MnO<sub>2</sub> (s)  
MnCO<sub>3</sub> (s)  
MnS (s)  
MnSiO<sub>3</sub> (s)  
NaHCO<sub>3</sub> (aq)  
NaCO<sub>3</sub> - (aq)  
Na + (aq)  
NaCl (aq)  
NaOH (aq)  
NO<sub>3</sub> - (aq)  
NH<sub>3</sub> (aq)  
NaAlSiO<sub>3</sub>O<sub>8</sub> (s)  
NH<sub>2</sub>CH<sub>2</sub>COOH (aq)  
NH<sub>2</sub>CH<sub>2</sub>COO - (aq)

N2 (g)  
N2O (g)  
NH3 (g)  
NH4 + (aq)  
NO2 - (aq)  
Ni 2+ (aq)  
NiOH + (aq)  
Ni(OH)2 (aq)  
Ni(OH)3 - (aq)  
NiO (s)  
NiS (s)  
OH - (aq)  
O2 (g)  
O2 (aq)  
O3 (g)  
P (s)  
PO4 3- (aq)  
Pb (s)  
Pb 2+ (aq)  
PbOH + (aq)  
Pb(OH)2 (aq)  
Pb(OH)3 - (aq)  
Pb(OH)4 2- (aq)  
Pb(OH)2 (s)  
PbO (s)  
PbO2 (s)  
Pb3O4 (s)  
PbS (s)  
PbSO4 (s)  
PbCO3 (s)  
S (s)  
SO2 (g)  
SO3 (g)  
S 2- (aq)  
SO3 2- (aq)  
SO4 2- (aq)  
Se (s)  
SeO3 2- (aq)  
SeO4 2- (aq)  
Si (s)

SiO2 (s)  
Sr 2+ (aq)  
SrOH + (aq)  
SrCO3 (s)  
SrSO4 (s)  
UO2 2+ (aq)  
UO2NO3 + (aq)  
UO2(NO3)2 (aq)  
UO2OH + (aq)  
UO2(OH)2 (aq)  
UO2(OH)3 - (aq)  
UO2(OH)4 2- (aq)  
(UO2)2OH 3+ (aq)  
(UO2)2(OH)2 2+ (aq)  
(UO2)3(OH)4 2+ (aq)  
(UO2)3(OH)5 + (aq)  
(UO2)3(OH)7 - (aq)  
(UO2)4(OH)7 + (aq)  
UO2CO3 (aq)  
UO2(CO3)2 2- (aq)  
UO2(CO3)3 4- (aq)  
UO2Cl + (aq)  
UO2Cl2 (aq)  
UO2Cl3 - (aq)  
UO2SO4 (aq)  
UO2(SO4)2 2- (aq)  
VO 2+ (aq)  
VOOH + (aq)  
VO(OH)2 (s)  
V2O4 (s)  
(VO)2(OH)2 + (aq)  
VOF + (aq)  
VOF2 (aq)  
VOF3 - (aq)  
VOF4 2- (aq)  
VOCl + (aq)  
VOSO4 (aq)  
VO(C2O4)2 2- (aq)  
VOOHC2O4 - (aq)  
VOCH3COO + (aq)

VO(CH<sub>3</sub>COO)<sub>2</sub> (aq)

VOCO<sub>3</sub> (aq)

VOOHCO<sub>3</sub> - (aq)

V<sub>4</sub>O<sub>9</sub> 2- (aq)

VO<sub>2</sub> + (aq)

VO<sub>4</sub> 3- (aq)

V<sub>2</sub>O<sub>5</sub> (s)

V<sub>10</sub>O<sub>28</sub> 6- (aq)

V<sub>2</sub>O<sub>7</sub> 4- (aq)

V<sub>4</sub>O<sub>12</sub> 4- (aq)

VO<sub>2</sub>SO<sub>4</sub> - (aq)

VO<sub>2</sub>OHCO<sub>3</sub> 2- (aq)

VO<sub>2</sub>(CO<sub>3</sub>)<sub>2</sub> 3- (aq)

Zn (s)

Zn 2+ (aq)

ZnOH + (aq)

Zn(OH)<sub>2</sub> (aq)

Zn(OH)<sub>3</sub> - (aq)

Zn(OH)<sub>4</sub> 2- (aq)

Zn(OH)<sub>2</sub> (s)

ZnCl + (aq)

ZnCl<sub>2</sub> (aq)

ZnCl<sub>3</sub> - (aq)

ZnCl<sub>4</sub> 2- (aq)

ZnCO<sub>3</sub> (s)

Those registered molecules follow a strict naming convention by which they can be recognized (see below)...

#### Naming Convention

Plus (+) and minus (-) charges are denoted by the numeric value of the charge followed by a + or - sign, respectively ( e.g. UO<sub>2</sub>(CO<sub>3</sub>)<sub>3</sub> 4- (aq) )

The phase is always denoted last and will be marked as (l) for liquid, (s) for solid, (aq) for aqueous, and (g) for gas (see above).

When registering a molecule that is not in the library, you must also provide a linear formula during construction or registration. This is needed so that the string parsing is easier to handle when the molecule subsequently registers the necessary atoms. (e.g. UO<sub>2</sub>(CO<sub>3</sub>)<sub>3</sub> = UO<sub>2</sub>C<sub>3</sub>O<sub>9</sub> or UO<sub>11</sub>C<sub>3</sub>).

#### Author

Austin Ladshaw

#### Date

02/24/2014

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### 6.11.2 Enumeration Type Documentation

#### 6.11.2.1 enum valid\_phase

##### Enumerator

**SOLID**  
**LIQUID**  
**AQUEOUS**  
**GAS**  
**PLASMA**  
**OTHER**

### 6.11.3 Function Documentation

#### 6.11.3.1 int MOLA.TESTS ( )

Function to run the MOLA tests.

This function is callable from the UI and is used to run several algorithm tests for the [Molecule](#) objects. This test should never report any errors.

## 6.12 monkfish.h File Reference

Multi-fiber wOven Nest Kernel For Interparticle Sorption History.

```
#include "dogfish.h"
```

### Classes

- struct [MONKFISH\\_PARAM](#)  
*Data structure for species specific information and parameters.*
- struct [MONKFISH\\_DATA](#)  
*Primary data structure for running MONKFISH.*

### Functions

- double [default\\_porosity](#) (int i, int l, const void \*user\_data)  
*Default porosity function for MONKFISH.*
- double [default\\_density](#) (int i, int l, const void \*user\_data)  
*Default density function for MONKFISH.*
- double [default\\_interparticle\\_diffusion](#) (int i, int l, const void \*user\_data)  
*Default interparticle diffusion function.*
- double [default\\_monk\\_adsorption](#) (int i, int l, const void \*user\_data)  
*Default adsorption strength function.*
- double [default\\_monk\\_equilibrium](#) (int i, int l, const void \*user\_data)  
*Default equilibrium adsorption function in mg/g.*

- double [default\\_monkfish\\_retardation](#) (int i, int l, const void \*user\_data)  
*Default retardation coefficient function.*
- double [default\\_exterior\\_concentration](#) (int i, const void \*user\_data)  
*Default exterior concentration function.*
- double [default\\_film\\_transfer](#) (int i, const void \*user\_data)  
*Default film mass transfer function.*
- int [setup\\_MONKFISH\\_DATA](#) (FILE \*file, double(\*eval\_porosity)(int i, int l, const void \*user\_data), double(\*eval\_density)(int i, int l, const void \*user\_data), double(\*eval\_ext\_diff)(int i, int l, const void \*user\_data), double(\*eval\_adsorb)(int i, int l, const void \*user\_data), double(\*eval\_retard)(int i, int l, const void \*user\_data), double(\*eval\_ext\_conc)(int i, const void \*user\_data), double(\*eval\_ext\_film)(int i, const void \*user\_data), double(\*dog\_diffusion)(int i, int l, const void \*user\_data), double(\*dog\_ext\_film)(int i, const void \*user\_data), double(\*dog\_surf\_conc)(int i, const void \*user\_data), const void \*user\_data, [MONKFISH\\_DATA](#) \*monk\_dat)  
*Setup function to allocate memory and setup function pointers for the MONKFISH simulation.*
- int [MONKFISH\\_TESTS](#) ()  
*Function to run tests on the MONKFISH algorithms.*

### 6.12.1 Detailed Description

Multi-fiber wOven Nest Kernel For Interparticle Sorption History. monkfish.cpp

This file contains structures and functions associated with modeling the sorption characteristics of woven fiber bundles used to recover uranium from seawater. It is coupled with the DOGFISH kernel that determines the sorption of individual fibers. This kernel will resolve the interparticle diffusion between bundles of individual fibers in a woven ball-like domain.

#### Warning

Functions and methods in this file are still under construction.

#### Author

Austin Ladshaw

#### Date

04/14/2015

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### 6.12.2 Function Documentation

#### 6.12.2.1 double default\_porosity ( int i, int l, const void \* user\_data )

Default porosity function for MONKFISH.

This function assumes a linear relationship between the maximum porosity at the center of the woven fibers and the minimum porosity at the edge of the woven fiber bundle.

#### Parameters

<i>i</i>	index for the ith adsorbing species
<i>l</i>	index for the lth node in the domain
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure



**6.12.2.2 double default\_density ( int *i*, int *l*, const void \* *user\_data* )**

Default density function for MONKFISH.

This function calls the porosity function and uses the single fiber density to provide an estimate of the bulk fiber density locally in the woven fiber bundle.

**Parameters**

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

**6.12.2.3 double default\_interparticle\_diffusion ( int *i*, int *l*, const void \* *user\_data* )**

Default interparticle diffusion function.

This function assumes that the interparticle diffusivity is a constant and returns that diffusivity multiplied by the domain porosity to form the effective diffusion coefficient in the domain.

**Parameters**

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

**6.12.2.4 double default\_monk\_adsorption ( int *i*, int *l*, const void \* *user\_data* )**

Default adsorption strength function.

This function will either use the default equilibrium function or the DOGFISH simulation result to produce the approximate adsorption strength using perturbation theory.

**Parameters**

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

**6.12.2.5 double default\_monk\_equilibrium ( int *i*, int *l*, const void \* *user\_data* )**

Default equilibrium adsorption function in mg/g.

This function uses the exterior species' concentration (mol/L), the species' molecular weight (g/mol), and the bulk fiber density (g/L) to calculate the adsorption equilibrium in mg/g. It assumes that the exterior concentration represents the moles of species per liter of solution that is being sorbed.

**Parameters**

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

**6.12.2.6 double default\_monkfish\_retardation ( int *i*, int *l*, const void \* *user\_data* )**

Default retardation coefficient function.

This function calls the porosity, density, and adsorption functions to evaluate the retardation coefficient of the diffusing material.

## Parameters

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>l</i>	index for the <i>l</i> th node in the domain
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

6.12.2.7 double default\_exterior\_concentration ( int *i*, const void \* *user\_data* )

Default exterior concentratio function.

This function assumes that the exterior concentration for sorption is just equal to the value of exterior\_concentration given in [MONKFISH\\_PARAM](#).

## Parameters

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

6.12.2.8 double default\_film\_transfer ( int *i*, const void \* *user\_data* )

Default film mass transfer function.

This function assumes that the film mass transfer coefficient is just equal to the value of the film\_transfer\_coeff in [MONKFISH\\_PARAM](#).

## Parameters

<i>i</i>	index for the <i>i</i> th adsorbing species
<i>user_data</i>	pointer to the <a href="#">MONKFISH_DATA</a> structure

6.12.2.9 int setup\_MONKFISH\_DATA ( FILE \* *file*, double(\*)(int *i*, int *l*, const void \**user\_data*) *eval\_porosity*, double(\*)(int *i*, int *l*, const void \**user\_data*) *eval\_density*, double(\*)(int *i*, int *l*, const void \**user\_data*) *eval\_ext\_diff*, double(\*)(int *i*, int *l*, const void \**user\_data*) *eval\_adsorb*, double(\*)(int *i*, int *l*, const void \**user\_data*) *eval\_retard*, double(\*)(int *i*, const void \**user\_data*) *eval\_ext\_conc*, double(\*)(int *i*, const void \**user\_data*) *eval\_ext\_film*, double(\*)(int *i*, int *l*, const void \**user\_data*) *dog\_diffusion*, double(\*)(int *i*, const void \**user\_data*) *dog\_ext\_film*, double(\*)(int *i*, const void \**user\_data*) *dog\_surf\_conc*, const void \* *user\_data*, [MONKFISH\\_DATA](#) \* *monk\_dat* )

Setup function to allocate memory and setup function pointers for the MONKFISH simulation.

This function will allocate memory and setup the MONKFISH problem. To specify use of the default functions in MONKFISH, pass NULL args for all function pointers and the user\_data data structure. Otherwise, pass in your own custom arguments. The [MONKFISH\\_DATA](#) pointer must always be passed to this function.

## Parameters

<i>file</i>	pointer to the output file to print out results
<i>eval_porosity</i>	function pointer for the bulk domain porosity function
<i>eval_density</i>	function pointer for the bulk domain density function
<i>eval_ext_diff</i>	function pointer for the interparticle diffusion function
<i>eval_adsorb</i>	function pointer for the adsorption strength function
<i>eval_retard</i>	function pointer for the retardation coefficient function
<i>eval_ext_conc</i>	function pointer for the external concentration function
<i>eval_ext_film</i>	function pointer for the external film mass transfer function
<i>dog_diffusion</i>	function pointer for the DOGFISH diffusion function (see <a href="#">dogfish.h</a> )
<i>dog_ext_film</i>	function pointer for the DOGFISH film mass transfer (see <a href="#">dogfish.h</a> )
<i>dog_surf_conc</i>	function pointer for the DOGFISH surface concentration (see <a href="#">dogfish.h</a> )
<i>user_data</i>	pointer for the user's own data structure (only if using custom functions)
<i>monk_dat</i>	pointer for the <a href="#">MONKFISH_DATA</a> structure

#### 6.12.2.10 int MONKFISH\_TESTS ( )

Function to run tests on the MONKFISH algorithms.

This function currently does nothing and is not callable from the UI.

### 6.13 sandbox.h File Reference

Coding Test Area.

```
#include "flock.h"
#include "school.h"
```

#### Functions

- int [RUN\\_SANDBOX](#) ()  
*Function to run the methods implemented in the Sandbox.*

#### 6.13.1 Detailed Description

Coding Test Area. sandbox.cpp

This file contains a series of simple tests for routines used in other files and algorithms. Before any code or methods are used, they are tested here to make sure that they are useful. The tests in the sandbox are callable from the UI to make it easier to alter existing sandbox code and run tests on new proposed methods or algorithms.

#### Warning

Functions and methods in this file are not meant to be used anywhere else.

#### Author

Austin Ladshaw

#### Date

04/11/2015

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#### 6.13.2 Function Documentation

##### 6.13.2.1 int RUN\_SANDBOX ( )

Function to run the methods implemented in the Sandbox.

This function is callable from the UI and is used to observe results from the tests of newly developed algorithms. Edit header and source files here to test out your own routines or functions. Then you can run those functions by rebuilding the Ecosystem executable and running the sandbox tests.

## 6.14 school.h File Reference

Seawater Codes from a Highly Object-Oriented Library.

```
#include "eel.h"
#include "mola.h"
#include "shark.h"
#include "dogfish.h"
#include "monkfish.h"
#include "yaml_wrapper.h"
```

### 6.14.1 Detailed Description

Seawater Codes from a Highly Object-Oriented Library. This file contains include statements for all files used in the aqueous adsorption problems, primarily targeted at Seawater simulations. Include this file into any other project or source code that needs the methods below.

Files Included in SCHOOL

[eel.h](#) [mola.h](#) [shark.h](#) [dogfish.h](#) [monkfish.h](#) [yaml\\_wrapper.h](#)

Note

- (1) [shark.h](#) also includes methods from [macaw.h](#) and [lark.h](#)
- (2) [dogfish.h](#) also includes methods from [finch.h](#)

Author

Austin Ladshaw

Date

02/23/2015

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## 6.15 scopsowl.h File Reference

Simultaneously Coupled Objects for Pore and Surface diffusion Operations With Linear systems.

```
#include "egret.h"
#include "skua.h"
```

Classes

- struct [SCOPSOWL\\_PARAM\\_DATA](#)  
*Data structure for the species' parameters in SCOPSOWL.*
- struct [SCOPSOWL\\_DATA](#)  
*Primary data structure for SCOPSOWL simulations.*

## Macros

- #define `SCOPSOWL_HPP_`
- #define `Dp`(Dm, ep) (ep\*ep\*Dm)  
*Estimate of Pore Diffusivity (cm<sup>2</sup>/s)*
- #define `Dk`(rp, T, MW) (9700.0\*rp\*pow((T/MW),0.5))  
*Estimate of Knudsen Diffusivity (cm<sup>2</sup>/s)*
- #define `avgDp`(Dp, Dk) (pow(((1/Dp)+(1/Dk)), -1.0))  
*Estimate of Average Pore Diffusion (cm<sup>2</sup>/s)*

## Functions

- void `print2file_species_header` (FILE \*Output, `SCOPSOWL_DATA` \*owl\_dat, int i)  
*Function to print out the main header for the output file.*
- void `print2file_SCOPSOWL_time_header` (FILE \*Output, `SCOPSOWL_DATA` \*owl\_dat, int i)  
*Function to print out the time and space header for the output file.*
- void `print2file_SCOPSOWL_header` (`SCOPSOWL_DATA` \*owl\_dat)  
*Function to call the species and time header functions.*
- void `print2file_SCOPSOWL_result_old` (`SCOPSOWL_DATA` \*owl\_dat)  
*Function to print out the old time results to the output file.*
- void `print2file_SCOPSOWL_result_new` (`SCOPSOWL_DATA` \*owl\_dat)  
*Function to print out the new time results to the output file.*
- double `default_adsorption` (int i, int l, const void \*user\_data)  
*Default function for evaluating adsorption and adsorption strength.*
- double `default_retardation` (int i, int l, const void \*user\_data)  
*Default function for evaluating retardation coefficient.*
- double `default_pore_diffusion` (int i, int l, const void \*user\_data)  
*Default function for evaluating pore diffusivity.*
- double `default_surf_diffusion` (int i, int l, const void \*user\_data)  
*Default function for evaluating surface diffusion for HOMOGENEOUS pellets.*
- double `default_effective_diffusion` (int i, int l, const void \*user\_data)  
*Default function for evaluating effective diffusivity for HOMOGENEOUS pellets.*
- double `const_pore_diffusion` (int i, int l, const void \*user\_data)  
*Constant pore diffusion function for homogeneous or heterogeneous pellets.*
- double `default_filmMassTransfer` (int i, const void \*user\_data)  
*Default function for evaluating the film mass transfer coefficient.*
- double `const_filmMassTransfer` (int i, const void \*user\_data)  
*Constant film mass transfer coefficient function.*
- int `setup_SCOPSOWL_DATA` (FILE \*file, double(\*eval\_sorption)(int i, int l, const void \*user\_data), double(\*eval\_retardation)(int i, int l, const void \*user\_data), double(\*eval\_pore\_diff)(int i, int l, const void \*user\_data), double(\*eval\_filmMT)(int i, const void \*user\_data), double(\*eval\_surface\_diff)(int i, int l, const void \*user\_data), const void \*user\_data, `MIXED_GAS` \*gas\_data, `SCOPSOWL_DATA` \*owl\_dat)  
*Setup function to allocate memory and setup function pointers for the SCOPSOWL simulation.*
- int `SCOPSOWL_Executioner` (`SCOPSOWL_DATA` \*owl\_dat)  
*SCOPSOWL executioner function to solve a time step.*
- int `set_SCOPSOWL_ICs` (`SCOPSOWL_DATA` \*owl\_dat)  
*Function to set the initial conditions for a SCOPSOWL simulation.*
- int `set_SCOPSOWL_timestep` (`SCOPSOWL_DATA` \*owl\_dat)  
*Function to set the timestep of the SCOPSOWL simulation.*
- int `SCOPSOWL_preprocesses` (`SCOPSOWL_DATA` \*owl\_dat)  
*Function to perform all preprocess SCOPSOWL operations.*

- int [set\\_SCOPSOWL\\_params](#) (const void \*user\_data)  
*Function to set the values of all non-linear system parameters during simulation.*
- int [SCOPSOWL\\_postprocesses](#) ([SCOPSOWL\\_DATA](#) \*owl\_dat)  
*Function to perform all postprocess SCOPSOWL operations.*
- int [SCOPSOWL\\_reset](#) ([SCOPSOWL\\_DATA](#) \*owl\_dat)  
*Function to reset all stateful information to prepare for next simulation.*
- int [SCOPSOWL](#) ([SCOPSOWL\\_DATA](#) \*owl\_dat)  
*Function to progress the SCOPSOWL simulation through time till complete.*
- int [SCOPSOWL\\_SCENARIOS](#) (const char \*scene, const char \*sorbent, const char \*comp, const char \*sorbate)  
*Function to perform a SCOPSOWL simulation based on a set of parameters given in input files.*
- int [SCOPSOWL\\_TESTS](#) ()  
*Function to run a SCOPSOWL test simulation.*

### 6.15.1 Detailed Description

Simultaneously Coupled Objects for Pore and Surface diffusion Operations With Linear systems. `scopsowl.cpp`

This file contains structures and functions associated with modeling adsorption in commercial, bi-porous adsorbents such as zeolites and mordenites. The pore diffusion and mass transfer equations are coupled with adsorption and surface diffusion through smaller crystals embedded in a binder matrix. However, you can also direct this simulation to treat the adsorbent as homogeneous (instead of heterogeneous) in order to model an even greater variety of gaseous adsorption kinetic problems. This object is coupled with either MAGPIE, SKUA, or BOTH depending on the type of simulation requested.

#### Author

Austin Ladshaw

#### Date

01/29/2015

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### 6.15.2 Macro Definition Documentation

#### 6.15.2.1 `#define SCOPSOWL_HPP_`

#### 6.15.2.2 `#define Dp( Dm, ep )(ep*ep*Dm)`

Estimate of Pore Diffusivity ( $\text{cm}^2/\text{s}$ )

#### 6.15.2.3 `#define Dk( rp, T, MW )(9700.0*rp*pow((T/MW),0.5))`

Estimate of Knudsen Diffusivity ( $\text{cm}^2/\text{s}$ )

#### 6.15.2.4 `#define avgDp( Dp, Dk )(pow(((1/Dp)+(1/Dk)), -1.0))`

Estimate of Average Pore Diffusion ( $\text{cm}^2/\text{s}$ )

## 6.15.3 Function Documentation

6.15.3.1 void print2file\_species\_header ( FILE \* *Output*, SCOPSOWL\_DATA \* *owl\_dat*, int *i* )

Function to print out the main header for the output file.

6.15.3.2 void print2file\_SCOPSOWL\_time\_header ( FILE \* *Output*, SCOPSOWL\_DATA \* *owl\_dat*, int *i* )

Function to print out the time and space header for the output file.

6.15.3.3 void print2file\_SCOPSOWL\_header ( SCOPSOWL\_DATA \* *owl\_dat* )

Function to call the species and time header functions.

6.15.3.4 void print2file\_SCOPSOWL\_result\_old ( SCOPSOWL\_DATA \* *owl\_dat* )

Function to print out the old time results to the output file.

6.15.3.5 void print2file\_SCOPSOWL\_result\_new ( SCOPSOWL\_DATA \* *owl\_dat* )

Function to print out the new time results to the output file.

6.15.3.6 double default\_adsorption ( int *i*, int *l*, const void \* *user\_data* )

Default function for evaluating adsorption and adsorption strength.

This function is called in the preprocesses and postprocesses to estimate the strength of adsorption in the macro-scale problem from perturbations. It will use perturbations in either the MAGPIE simulation or SKUA simulation, depending on the type of problem the user is solving.

## Parameters

<i>i</i>	index for the <i>i</i> th species in the system
<i>l</i>	index for the <i>l</i> th node in the macro-scale domain
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

6.15.3.7 double default\_retardation ( int *i*, int *l*, const void \* *user\_data* )

Default function for evaluating retardation coefficient.

This function is called in the preprocesses and postprocesses to estimate the retardation coefficient for the simulation. It is recalculated at every time step to keep track of all changing conditions in the simulation.

## Parameters

<i>i</i>	index for the <i>i</i> th species in the system
<i>l</i>	index for the <i>l</i> th node in the macro-scale domain
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

6.15.3.8 double default\_pore\_diffusion ( int *i*, int *l*, const void \* *user\_data* )

Default function for evaluating pore diffusivity.

This function is called during the evaluation of non-linear residuals to more accurately represent non-linearities in the pore diffusion behavior. The pore diffusion is calculated based on kinetic theory of gases (see [egret.h](#)) and is adjusted according to the Knudsen Diffusion model and the porosity of the binder material.

## Parameters

<i>i</i>	index for the <i>i</i> th species in the system
<i>l</i>	index for the <i>l</i> th node in the macro-scale domain
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

**6.15.3.9 double default\_surf\_diffusion ( int *i*, int *l*, const void \* *user\_data* )**

Default function for evaluating surface diffusion for HOMOGENEOUS pellets.

This function is ONLY used if the pellet is determined to be homogeneous. Otherwise, this is replaced by the surface diffusion function for the SKUA simulation. The diffusivity is calculated based on the Arrhenius rate expression and then adjusted by the outside partial pressure of the adsorbing species.

**Parameters**

<i>i</i>	index for the <i>i</i> th species in the system
<i>l</i>	index for the <i>l</i> th node in the macro-scale domain
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

**6.15.3.10 double default\_effective\_diffusion ( int *i*, int *l*, const void \* *user\_data* )**

Default function for evaluating effective diffusivity for HOMOGENEOUS pellets.

This function is ONLY used if the pellet is determined to be homogeneous. Otherwise, this is replaced by the pore diffusion function. The effective diffusivity is determined by the combination of pore diffusivity and surface diffusivity with adsorption strength in an homogeneous pellet.

**Parameters**

<i>i</i>	index for the <i>i</i> th species in the system
<i>l</i>	index for the <i>l</i> th node in the macro-scale domain
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

**6.15.3.11 double const\_pore\_diffusion ( int *i*, int *l*, const void \* *user\_data* )**

Constant pore diffusion function for homogeneous or heterogeneous pellets.

This function should be used if the user wants to specify a constant pore diffusivity. The value of pore diffusion is then set equal to the value of pore\_diffusion in the SCOPSOWL\_PARAM\_DATA structure.

**Parameters**

<i>i</i>	index for the <i>i</i> th species in the system
<i>l</i>	index for the <i>l</i> th node in the macro-scale domain
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

**6.15.3.12 double default\_filmMassTransfer ( int *i*, const void \* *user\_data* )**

Default function for evaluating the film mass transfer coefficient.

This function is called during the setup of the boundary conditions and is used to estimate the film mass transfer coefficient for the macro-scale problem. The coefficient is calculated according to the kinetic theory of gases (see [egret.h](#)).

**Parameters**

<i>i</i>	index for the <i>i</i> th species in the system
<i>user_data</i>	pointer for the SCOSPOWL_DATA structure

**6.15.3.13 double const\_filmMassTransfer ( int *i*, const void \* *user\_data* )**

Constant film mass transfer coefficient function.

This function is used when the user wants to specify a constant value for film mass transfer. The value of that coefficient is then set equal to the value of film\_transfer in the SCOPSOWL\_PARAM\_DATA structure.



## Parameters

<i>i</i>	index for the <i>i</i> th species in the system
<i>user_data</i>	pointer for the SCOPSOWL_DATA structure

6.15.3.14 `int setup_SCOPSOWL_DATA ( FILE * file, double(*)(int i, int l, const void *user_data) eval_sorption, double(*)(int i, int l, const void *user_data) eval_retardation, double(*)(int i, int l, const void *user_data) eval_pore_diff, double(*)(int i, const void *user_data) eval_filmMT, double(*)(int i, int l, const void *user_data) eval_surface_diff, const void * user_data, MIXED_GAS * gas_data, SCOPSOWL_DATA * owl_data )`

Setup function to allocate memory and setup function pointers for the SCOPSOWL simulation.

This function sets up the memory and function pointers used in SCOPSOWL simulations. User can provide NULL in place of functions for the function pointers and the setup will automatically use just the default settings. However, the user is required to pass the necessary data structure pointers for [MIXED\\_GAS](#) and [SCOPSOWL\\_DATA](#).

## Parameters

<i>file</i>	pointer to the output file to print out results
<i>eval_sorption</i>	pointer to the adsorption evaluation function
<i>eval_retardation</i>	pointer to the retardation evaluation function
<i>eval_pore_diff</i>	pointer to the pore diffusion function
<i>eval_filmMT</i>	pointer to the film mass transfer function
<i>eval_surface_diff</i>	pointer to the surface diffusion function (required)
<i>user_data</i>	pointer to the user's data structure used for the parameter functions
<i>gas_data</i>	pointer to the <a href="#">MIXED_GAS</a> structure used to evaluate kinetic gas theory
<i>owl_data</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure

6.15.3.15 `int SCOPSOWL_Executioner ( SCOPSOWL_DATA * owl_dat )`

SCOPSOWL executioner function to solve a time step.

This function will call the preprocess, solver, and postprocess functions to evaluate a single time step in a simulation. All simulation conditions must be set prior to calling this function. This function will typically be the one called from other simulations that will involve a SCOPSOWL evaluation to resolve kinetic coupling.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

6.15.3.16 `int set_SCOPSOWL_ICs ( SCOPSOWL_DATA * owl_dat )`

Function to set the initial conditions for a SCOPSOWL simulation.

This function will setup the initial conditions of the simulation based on the initial temperature, pressure, and adsorbed molefractions. It assumes that the initial conditions are constant throughout the domain of the problem. This function should only be called once during a simulation.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

6.15.3.17 `int set_SCOPSOWL_timestep ( SCOPSOWL_DATA * owl_dat )`

Function to set the timestep of the SCOPSOWL simulation.

This function is used to set the next time step to be used in the SCOPSOWL simulation. A constant time step based on the size of the pellet discretization will be used. Users may want to use a custom time step to ensure that coupled-multi-scale systems are all in sync.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

## 6.15.3.18 int SCOPSOWL\_preprocesses ( SCOPSOWL\_DATA \* owl\_dat )

Function to perform all preprocess SCOPSOWL operations.

This function will update the boundary conditions and simulation conditions based on the current temperature, pressure, and gas phase composition, which may all vary in time. Since this function is called by the SCOPSOWL\_Executioner, it does not need to be called explicitly by the user.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

## 6.15.3.19 int set\_SCOPSOWL\_params ( const void \* user\_data )

Function to set the values of all non-linear system parameters during simulation.

This is the function override for the FINCH setparams function (see [finch.h](#)). It will update the values of non-linear parameters in the residuals so that all variables in a species' system are fully coupled.

## Parameters

<i>user_data</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
------------------	--

## 6.15.3.20 int SCOPSOWL\_postprocesses ( SCOPSOWL\_DATA \* owl\_dat )

Function to perform all postprocess SCOPSOWL operations.

This function will update the retardation coefficients based on newly obtained simulation results for the current time step and calculate the average and total amount of adsorption of each species in the domain. Additionally, this function will call the print functions to store simulation results in the output file.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

## 6.15.3.21 int SCOPSOWL\_reset ( SCOPSOWL\_DATA \* owl\_dat )

Function to reset all stateful information to prepare for next simulation.

This function will update the stateful information used in SCOPSOWL to prepare the system for the next time step in the simulation. However, because updating the states erases the old state, the user must be absolutely sure that the simulation is ready to be updated. For just running standard simulations, this is not an issue, but in coupling with other simulations it is very important.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

## 6.15.3.22 int SCOPSOWL ( SCOPSOWL\_DATA \* owl\_dat )

Function to progress the SCOPSOWL simulation through time till complete.

This function will call the initial conditions, then progressively call the executioner, time step, and reset functions to propagate the simulation in time. As such, this function is primarily used when running a SCOPSOWL simulation by itself and not when coupling it to an other problem.

## Parameters

<i>owl_dat</i>	pointer to the <a href="#">SCOPSOWL_DATA</a> structure (must be initialized)
----------------	--

6.15.3.23 int SCOPSOWL\_SCENARIOS ( const char \* *scene*, const char \* *sorbent*, const char \* *comp*, const char \* *sorbate* )

Function to perform a SCOPSOWL simulation based on a set of parameters given in input files.

This is the primary function to be called when running a stand-alone SCOPSOWL simulation. Parameters and system information for the simulation are given in a series of input files that come in as character arrays. These inputs are all required to call this function.

## Parameters

<i>scene</i>	Sceneario Input File
<i>sorbent</i>	Adsorbent Input File
<i>comp</i>	Component Input File
<i>sorbate</i>	Adsorbate Input File

## Note

Each input file has a particular format that must be strictly adhered to in order for the simulation to be carried out correctly. The format for each input file, and an example, is provided below...

## Scenario Input Format

System Temperature (K) [tab] Total Pressure (kPa) [tab] Gas Velocity (cm/s)

Simulation Time (hrs) [tab] Print Out Time (hrs)

BC Type (0 = Neumann, 1 = Dirichlet)

Number of Gas Species

Initial Total Adsorption (mol/kg)

Name of ith Species [tab] Adsorbable? (0 = false, 1 = true) [tab] Gas Phase Molefraction [tab] Initial Sorbed Molefraction

(repeat above for all species)

## Example Scenario Input

353.15 101.35 0.36

4.0 0.05

0

5

0.0

N2 0 0.7634 0.0

O2 0 0.2081 0.0

Ar 0 0.009 0.0

CO2 0 0.0004 0.0

H2O 1 0.0191 0.0

Above example is for a 5-component mixture of N2, O2, Ar, CO2, and H2O, but we are only considering the H2O as adsorbable.

## Adsorbent Input File

Heterogeneous Pellet? (0 = false, 1 = true) [tab] Surface Diffusion Included? (0 = false, 1 = true)

Macro Coord. (2 = spherical, 1 = cylindrical) { [tab] Char. Length (cm) (i.e., cylinder length) }

(NOTE: Char. Length is only needed if problem is not spherical)

Pellet Radius (cm) [tab] Pellet Density (kg/L) [tab] Porosity (vol. void / vol. binder) [tab] Pore Radius (cm)

(Below is only needed if pellet is Heterogeneous)

Micro Coord. (2 = spherical, 1 = cylindrical) { [tab] Char. Length (cm) (i.e., cylinder length) }

Crystal Radius (um) [tab] Binder Fraction (vol. binder / vol. pellet)

#### Example Adsorbent Input

1 1

2

0.118 1.69 0.272 3.5E-6

2

2.0 0.175

Above example is for a heterogeneous adsorbent with surface diffusion. The pellet and crystals are both considered spherical. Pellet radius is 0.118 cm, density is 1.69 kg/L, porosity is 0.272, and pore size is 3.5e-6 cm. The pellet is made up of 17.5 % binder material and contains crystals roughly 2.0 um in radius.

#### Component Input File

Molar Weight of ith species (g/mol) [tab] Specific Heat of ith species (J/g/K)

Sutherland Viscosity (g/cm/s) [tab] Sutherland Temperature (K) [tab] Sutherland Constant (K) of ith species

(repeat above for all species in same order they appeared in the Scenario Input File)

#### Example Component Input

28.016 1.04

0.0001781 300.55 111.0

32.0 0.919

0.0002018 292.25 127.0

39.948 0.522

0.0002125 273.11 144.4

44.009 0.846

0.000148 293.15 240.0

18.0 1.97

0.0001043 298.16 784.72

Above example is a continuation of the Scenario Input example wherein each grouping represents parameters that are associated with N2, O2, Ar, CO2, and H2O, respectively. The order is VERY important!

#### Adsorbate Input File

{ Type of Surface Diffusion Function (0 = constant, 1 = simple Darken, 2 = theoretical Darken) }

(NOTE: The above option is only given IF the pellet was specified as Heterogeneous!)

Reference Diffusivity (um<sup>2</sup>/hr) [tab] Activation Energy (J/mol) of ith adsorbable species

Reference Temperature (K) [tab] Affinity Constant (-) of ith adsorbable species

van der Waals Volume (cm<sup>3</sup>/mol) of ith species

GSTA adsorption capacity (mol/kg) of ith species

Number of GSTA parameters of ith species

Enthalpy (J/mol) of nth site [tab] Entropy of nth site (J/K/mol) of ith species

(repeat enthalpy and entropy for all n sites in species i)

(repeat above for all species i)

#### Example Adsorbate Input

```
0
0.8814 0.0
267.999 0.0
13.91
11.67
4
-46597.5 -53.6994
-125024 -221.073
-193619 -356.728
-272228 -567.459
1.28 540.1
374.99 0.01
3.01
1.27
2
-46597.5 -53.6994
-125024 -221.073
```

Above example would be for a simulation involving two adsorbable species using a constant surface diffusion function. Each adsorbable species has it's own set of kinetic and equilibrium parameters that must be given in the same order as the species appeared in the Scenario Input. Note: we do not need to supply this information for non-adsorbable species.

#### 6.15.3.24 int SCOPSOWL\_TESTS ( )

Function to run a SCOPSOWL test simulation.

This function runs a test of the SCOPSOWL physics and prints out results to a text file. It is callable from the UI.

## 6.16 scopsowl\_opt.h File Reference

Optimization Routine for Surface Diffusivities in SCOPSOWL.

```
#include "scopsowl.h"
```

### Classes

- struct [SCOPSOWL\\_OPT\\_DATA](#)

*Data structure for the SCOPSOWL optmization routine.*

## Functions

- int [SCOPSOWL\\_OPT\\_set\\_y](#) ([SCOPSOWL\\_OPT\\_DATA](#) \*owl\_opt)  
*Function to set the rest of the gas phase mole fractions based on current mole fraction of adsorbing gas.*
- int [initial\\_guess\\_SCOPSOWL](#) ([SCOPSOWL\\_OPT\\_DATA](#) \*owl\_opt)  
*Function to set up an initial guess for the surface diffusivity parameter in SCOPSOWL.*
- void [eval\\_SCOPSOWL\\_Uptake](#) (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)  
*Function that works in conjunction with the Imfit routine to minimize the euclidean norm between function and data.*
- int [SCOPSOWL\\_OPTIMIZE](#) (const char \*scene, const char \*sorbent, const char \*comp, const char \*sorbate, const char \*data)  
*Function called to perform the optimization routine given a specific set of information and data.*

## 6.16.1 Detailed Description

## Optimization Routine for Surface Diffusivities in SCOPSOWL. scopsowl\_opt.cpp

This file contains structures and functions associated with performing non-linear least-squares optimization of the SCOPSOWL simulation results against actual kinetic adsorption data. The optimization routine here allows you to run data comparisons and optimizations in three forms: (i) Rough optimizations - cheaper operations, but less accurate, (ii) Exact optimizations - much more expensive, but greater accuracy, and (iii) data/model comparisons - no optimization, just using system parameters to compare simulation results against a set of data.

Depending on the level of optimization desired, this routine could take several minutes or several hours. The optimization/comparisons are printed out in two files: (i) a parameter file, which contains the simulation partial pressures and temperatures and the optimized diffusivities with the euclidean norm of the fitting and (ii) a comparison file that shows the model value and data value at each time step for each kinetic curve.

The optimized diffusion parameters are given for each individual kinetic data curve. Each data curve will have a different pairing of partial pressure and temperature. Because of this, you will get a list of different diffusivities for each data curve. To get the optimum kinetic parameters from this list of diffusivities, you must fit the diffusion parameter values to the following diffusion function model...

$$D_{opt} = D_{ref} * \exp(-E / (R*T)) * \text{pow}(p, (T_{ref}/T) - B)$$

where  $D_{ref}$  is the Reference Diffusivity ( $\mu\text{m}^2/\text{hr}$ ),  $E$  is the activation energy for adsorption (J/mol),  $R$  is the gas law constant (J/K/mol),  $T$  is the system temperature (K),  $p$  is the partial pressure of the adsorbing species (kPa),  $T_{ref}$  is the Reference Temperature (K), and  $B$  is the Affinity constant. This algorithm does not automatically produce these parameters for you, but gives you everything you need to produce them yourself.

This routine allows you to optimize multiple kinetic curves at one time. However, all data must be for the same adsorbent-adsorbate system. In other words, the adsorbent and adsorbate pair must be the same for each kinetic curve analyzed. Also, each experiment must have been done in a thin bed or continuous flow system where the adsorbents were exposed to a nearly constant outside partial pressure for all time steps and the gas velocity of that system is assumed constant for all experiments. This experimental setup is very typical for studying adsorption kinetics for gas-solid systems.

## Author

Austin Ladshaw

## Date

05/14/2015

## Copyright

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

## 6.16.2 Function Documentation

## 6.16.2.1 int SCOPSOWL\_OPT\_set.y ( SCOPSOWL\_OPT\_DATA \* owl\_opt )

Function to set the rest of the gas phase mole fractions based on current mole fraction of adsorbing gas.

This function takes the current mole fraction of the adsorbing gas and calculates the gas mole fractions of the other gases in the system based on the standard inlet gas composition given in the scenario file.

## 6.16.2.2 int initial\_guess\_SCOPSOWL ( SCOPSOWL\_OPT\_DATA \* owl\_opt )

Function to set up an initial guess for the surface diffusivity parameter in SCOPSOWL.

This function performs the Rough optimization on the surface diffusivity based on the idea of reducing or eliminating function bias between data and simulation. A positive function bias means that the simulation curve is "higher" than the data curve and a negative function bias means that the simulation curve is "lower" than the data curve. We use this information to incrementally adjust the rate of surface diffusion until this bias is near zero. When bias is near zero, the simulation is nearly optimized, but further refinement may be necessary to find the true minimum solution.

## 6.16.2.3 void eval.SCOPSOWL.Uptake ( const double \* par, int m\_dat, const void \* data, double \* fvec, int \* info )

Function that works in conjunction with the Imfit routine to minimize the euclidean norm between function and data.

This function will run the SCOPSOWL simulation at a given value of surface diffusivity and produce residuals that feed into the Levenberg-Marquardt's algorithm for non-linear least-squares regression. The form of this function is specific to the format required by the Imfit routine.

## Parameters

<i>par</i>	array of parameters that are to be optimized
<i>m_dat</i>	number of data points or functions to evaluate
<i>data</i>	user supplied data structure holding information necessary to form the residuals
<i>fvec</i>	array of residuals computed at the current parameter values
<i>info</i>	integer pointer denoting whether or not the user requests to end a particular simulation

## 6.16.2.4 int SCOPSOWL\_OPTIMIZE ( const char \* scene, const char \* sorbent, const char \* comp, const char \* sorbate, const char \* data )

Function called to perform the optimization routine given a specific set of information and data.

This is the function that is callable by the UI. The user must provide 5 input files to the routine in order to establish simulation conditions, adsorbent properties, component properties, adsorbate equilibrium parameters, and the set of data that we are comparing the simulations to. Each input file has a very specific structure and order to the information that it contains. The structure here is DIFFERENT than the structure for just running standard SCOPSOWL simulations (see [scopsowl.h](#)).

## Parameters

<i>scene</i>	Scenario Input File
<i>sorbent</i>	Adsorbent Input File
<i>comp</i>	Component Input File
<i>sorbate</i>	Adsorbate Input File
<i>data</i>	Kinetic Adsorption Data File

## Note

Much of the structure of these input files are "similar" to that of the input files used in SCOPSOWL\_SCENARIOS (see [scopsowl.h](#)), but with some notable differences. Below gives the format for each input file with an example. Make sure your input files follow this format before calling this routine from the UI.

**Scenario Input File**

Optimization? (0 = false, 1 = true) [tab] Rough Optimization? (0 = false, 1 = true)

Surf. Diff. (0 = constant, 1 = simple Darken, 2 = theoretical Darken) [tab] BC Type (0 = Neumann, 1 = Dirichlet)

Total Pressure (kPa) [tab] Gas Velocity (cm/s)

Number of Gaseous Species

Initial Adsorption Total (mol/kg)

Name [tab] Adsorbable? (0 = false, 1 = true) [tab] Inlet Gas Mole Fraction [tab] Initial Adsorbed Mole Fraction

(NOTE: The above line is repeated for all species in gas phase. Also, this algorithm only allows you to consider one adsorbable gas component. Inlet gas mole fractions must be non-zero for all non-adsorbing gases and must sum to 1.)

**Example Scenario Input**

```
1 0
0 0
101.35 0.36
5
0.0
N2 0 0.7825 0.0
O2 0 0.2081 0.0
Ar 0 0.009 0.0
CO2 0 0.0004 0.0
H2O 1 0.0 0.0
```

Above example is for running optimizations on data collected with a gas stream at 0.36 cm/s with 5 gas species in the mixture, only H<sub>2</sub>O of which is adsorbing. The "base line" or "inlet gas" without H<sub>2</sub>O has a composition of N<sub>2</sub> at 0.7825, O<sub>2</sub> at 0.2081, Ar at 0.009, and CO<sub>2</sub> at 0.0004.

**Adsorbent Input File**

Heterogeneous Pellet? (0 = false, 1 = true)

Macro Coord. (2 = spherical, 1 = cylindrical) { [tab] Char. Length (cm) (i.e., cylinder length) }

(NOTE: Char. Length is only needed if problem is not spherical)

Pellet Radius (cm) [tab] Pellet Density (kg/L) [tab] Porosity (vol. void / vol. binder) [tab] Pore Radius (cm)

(Below is only needed if pellet is Heterogeneous)

Micro Coord. (2 = spherical, 1 = cylindrical) { [tab] Char. Length (cm) (i.e., cylinder length) }

Crystal Radius (um) [tab] Binder Fraction (vol. binder / vol. pellet)

**Example Adsorbent Input**

```
1
2
0.118 1.69 0.272 3.5E-6
2
2.0 0.175
```

Above example is nearly identical to the file given in the SCOPSOWL\_SCENARIO example (see [scopsowl.h](#)).



However, here we do not give an integer flag denoting whether or not we are considering surface diffusion as a mechanism. This is because we automatically assume that surface diffusion is a mechanism in the system, since that is the unknown parameter that we are performing the optimizations for.

#### Component Input File

Molar Weight of ith species (g/mol) [tab] Specific Heat of ith species (J/g/K)

Sutherland Viscosity (g/cm/s) [tab] Sutherland Temperature (K) [tab] Sutherland Constant (K) of ith species

(repeat above for all species in same order they appeared in the Scenario Input File)

#### Example Component Input

```
28.016 1.04
0.0001781 300.55 111.0
32.0 0.919
0.0002018 292.25 127.0
39.948 0.522
0.0002125 273.11 144.4
44.009 0.846
0.000148 293.15 240.0
18.0 1.97
0.0001043 298.16 784.72
```

Above example is exactly the same as in the SCOPSOWL\_SCENARIO example (see [scopsowl.h](#)). There is no difference in the input file formats for this input. Keep in mind that the order is VERY important! All species information must be in the same order that the species appeared in the Scenario input file.

#### Adsorbate Input File

Reference Diffusivity ( $\text{um}^2/\text{hr}$ ) [tab] Activation Energy (J/mol) of ith adsorbable species

Reference Temperature (K) [tab] Affinity Constant (-) of ith adsorbable species

van der Waals Volume ( $\text{cm}^3/\text{mol}$ ) of ith species

GSTA adsorption capacity (mol/kg) of ith species

Number of GSTA parameters of ith species

Enthalpy (J/mol) of nth site [tab] Entropy of nth site (J/K/mol) of ith species

(repeat enthalpy and entropy for all n sites in species i)

(repeat above for all species i)

#### Example Adsorbate Input

```
0 0
0 0
13.91
11.67
4
-46597.5 -53.6994
-125024 -221.073
-193619 -356.728
```

-272228 -567.459

Above example gives the equilibrium parameters associated with the H<sub>2</sub>O-MS3A single component adsorption system. Note that the kinetic parameters (Ref. Diff., Act. Energy, Ref. Temp., and Affinity) were all given a value of zero. These values are irrelevant if we are running an optimization because they will be replaced with a single estimate for the diffusivity that is being optimization for. However, if we wanted to run this routine with comparisons and not do any optimization, then you would need to provide non-zero values for these parameters (at least for Ref. Diff.).

#### Data Input File

Number of Kinetic Data Curves

Number of data points in the ith curve

Temperature (K) [tab] Partial Pressure (kPa) [tab] Equilibrium Adsorption (mol/kg) all of ith curve

Time point 1 (hrs) [tab] Adsorption 1 (mol/kg) of ith curve

Time point 1 (hrs) [tab] Adsorption 2 (mol/kg) of ith curve

... (Repeat for all time-adsorption data points)

(Repeat above for all curves i)

#### Example Data Input

40

2990

298.15 0.000310922 2.9

0 0

0.166666667 0.001834419

0.333611111 0.004880247

0.5 0.008306803

...

2789

298.15 0.00055189 5

0 0

0.166944444 0.003350185

0.333611111 0.007418267

0.5 0.009930906

0.666666667 0.014597236

0.833611111 0.021377373

....

Above is a partial example for a data set of 40 kinetic curves. The first curve contains 2990 data points and has temperature of 298.15 K, partial pressure of 0.000310922 kPa, and an equilibrium adsorption of 2.9. Each first time point should start from 0 hours and each initial adsorption should correspond to the value of initial adsorption indicated in the Scenario input file. Then, this structure is repeated for all adsorption curves.

## 6.17 shark.h File Reference

Speciation-object Hierarchy for Aqueous [Reaction](#) Kinetics.

```
#include "mola.h"
#include "macaw.h"
#include "lark.h"
#include "yaml_wrapper.h"
#include "dogfish.h"
```

## Classes

- class [MasterSpeciesList](#)  
*Master Species List Object.*
- class [Reaction](#)  
*Reaction Object.*
- class [MassBalance](#)  
*Mass Balance Object.*
- class [UnsteadyReaction](#)  
*Unsteady [Reaction](#) Object (inherits from [Reaction](#))*
- class [AdsorptionReaction](#)  
*Adsorption [Reaction](#) Object.*
- struct [SHARK\\_DATA](#)  
*Data structure for SHARK simulations.*

## Macros

- #define [Rstd](#) 8.3144621  
*Gas Law Constant in J/K/mol (or) L\*kPa/K/mol (Standard Units)*
- #define [Na](#) 6.0221413E+23  
*Avagadro's Number - Units: molecules/mol.*
- #define [kB](#) 1.3806488E-23  
*Boltzmann's Constant - Units: J/K or C\*V/K.*
- #define [e](#) 1.6021766208E-19  
*Elementary Electric Charge - Units: C.*
- #define [Faraday](#) 96485.33289  
*Faraday's Constant - C/mol.*
- #define [VacuumPermittivity](#) 8.8541878176E-12  
*Vacuum Permittivity Constant - F/m or C/V/m.*
- #define [WaterRelPerm](#) 80.1  
*Approximate Relative Permittivity for water - Unitless.*
- #define [AbsPerm](#)(Rel) (Rel\*[VacuumPermittivity](#))  
*Calculation of Absolute Permittivity of a medium - F/m or C/V/m.*

## Typedefs

- typedef struct [SHARK\\_DATA](#) [SHARK\\_DATA](#)  
*Data structure for SHARK simulations.*

## Enumerations

- enum `valid_act` {  
    [IDEAL](#), [DAVIES](#), [DEBYE\\_HUCKEL](#), [SIT](#),  
    [PITZER](#) }  
    Enumeration for the list of valid activity models for non-ideal solutions.
- enum `valid_surf_act` { [IDEAL\\_ADS](#), [FLORY\\_HUGGINS](#) }  
    Enumeration for the list of valid surface activity models for non-ideal adsorption.

## Functions

- void [print2file\\_shark\\_info](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to print out simulation conditions and options to the output file.
- void [print2file\\_shark\\_header](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to print out the head of species and time stamps to the output file.
- void [print2file\\_shark\\_results\\_new](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to print out the simulation results for the current time step.
- void [print2file\\_shark\\_results\\_old](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to print out the simulation results for the previous time step.
- double [calculate\\_ionic\\_strength](#) (const [Matrix](#)< double > &x, [MasterSpeciesList](#) &MasterList)  
    Function to calculate the ionic strength of the solution.
- int [FloryHuggins](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &F, const void \*data)  
    Surface Activity function for simple non-ideal adsorption.
- int [ideal\\_solution](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &F, const void \*data)  
    Activity function for Ideal Solution.
- int [Davies\\_equation](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &F, const void \*data)  
    Activity function for Davies Equation.
- int [DebyeHuckel\\_equation](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &F, const void \*data)  
    Activity function for Debye-Huckel Equation.
- int [Sit\\_equation](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &F, const void \*data)  
    First test of SIT Model.
- int [surf\\_act\\_choice](#) (const std::string &input)  
    Function takes a given string and returns a flag denoting which surface activity model was chosen.
- int [act\\_choice](#) (const std::string &input)  
    Function takes a given string and returns a flag denoting which activity model was chosen.
- bool [linesearch\\_choice](#) (const std::string &input)  
    Function returns a bool to determine the form of line search requested.
- int [linearsolve\\_choice](#) (const std::string &input)  
    Function returns the linear solver flag for the PJFNK method.
- int [Convert2LogConcentration](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &logx)  
    Function to convert the given values of variables (x) to the log of those variables (logx)
- int [Convert2Concentration](#) (const [Matrix](#)< double > &logx, [Matrix](#)< double > &x)  
    Function to convert the given log values of variables (logx) to the values of those variables (x)
- int [read\\_scenario](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to go through the yaml object for the scenario document.
- int [read\\_options](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to go through the yaml object for the solver options document.
- int [read\\_species](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to go through the yaml object for the master species document.
- int [read\\_massbalance](#) ([SHARK\\_DATA](#) \*shark\_dat)  
    Function to go through the yaml object for the mass balance document.

- int [read\\_equilrxn](#) (SHARK\_DATA \*shark\_dat)  
*Function to go through the yaml object for the equilibrium reaction document.*
- int [read\\_unsteadyrxn](#) (SHARK\_DATA \*shark\_dat)  
*Function to go through the yaml object for the unsteady reaction document.*
- int [read\\_adsorbobjects](#) (SHARK\_DATA \*shark\_dat)  
*Function to go through the yaml object for each Adsorption Object.*
- int [setup\\_SHARK\\_DATA](#) (FILE \*file, int(\*residual)(const [Matrix](#)< double > &x, [Matrix](#)< double > &res, const void \*data), int(\*activity)(const [Matrix](#)< double > &x, [Matrix](#)< double > &gamma, const void \*data), int(\*precond)(const [Matrix](#)< double > &r, [Matrix](#)< double > &p, const void \*data), SHARK\_DATA \*dat, const void \*activity\_data, const void \*residual\_data, const void \*precon\_data, const void \*other\_data)  
*Function to setup the memory and pointers for the SHARK\_DATA structure for the current simulation.*
- int [shark\\_add\\_customResidual](#) (int i, double(\*other\_res)(const [Matrix](#)< double > &x, SHARK\_DATA \*shark\_dat, const void \*other\_data), SHARK\_DATA \*shark\_dat)  
*Function to add user defined custom residual functions to the OtherList vector object in SHARK\_DATA.*
- int [shark\\_parameter\\_check](#) (SHARK\_DATA \*shark\_dat)  
*Function to check the [Reaction](#) and [UnsteadyReaction](#) objects for missing info.*
- int [shark\\_energy\\_calculations](#) (SHARK\_DATA \*shark\_dat)  
*Function to calculate all [Reaction](#) and [UnsteadyReaction](#) energies.*
- int [shark\\_temperature\\_calculations](#) (SHARK\_DATA \*shark\_dat)  
*Function to calculate all [Reaction](#) and [UnsteadyReaction](#) parameters as a function of temperature.*
- int [shark\\_ph\\_finder](#) (SHARK\_DATA \*shark\_dat)  
*Function will search [MasterSpeciesList](#) for existence of H + (aq) and OH - (aq) molecules.*
- int [shark\\_guess](#) (SHARK\_DATA \*shark\_dat)  
*Function provides a rough initial guess for the values of all non-linear variables.*
- int [shark\\_initial\\_conditions](#) (SHARK\_DATA \*shark\_dat)  
*Function to establish the initial conditions of the shark simulation.*
- int [shark\\_executioner](#) (SHARK\_DATA \*shark\_dat)  
*Function to execute a shark simulation at a single time step or pH value.*
- int [shark\\_timestep\\_const](#) (SHARK\_DATA \*shark\_dat)  
*Function to set up all time steps in the simulation to a specified constant.*
- int [shark\\_timestep\\_adapt](#) (SHARK\_DATA \*shark\_dat)  
*Function to set up all time steps in the simulation based on success or failure to converge.*
- int [shark\\_preprocesses](#) (SHARK\_DATA \*shark\_dat)  
*Function to call other functions for calculation of parameters and setting of time steps.*
- int [shark\\_solver](#) (SHARK\_DATA \*shark\_dat)  
*Function to call the PJFNK solver routine given the current SHARK\_DATA information.*
- int [shark\\_postprocesses](#) (SHARK\_DATA \*shark\_dat)  
*Function to convert PJFNK solutions to concentration values and print to the output file.*
- int [shark\\_reset](#) (SHARK\_DATA \*shark\_dat)  
*Function to reset the values of all stateful information in SHARK\_DATA.*
- int [shark\\_residual](#) (const [Matrix](#)< double > &x, [Matrix](#)< double > &F, const void \*data)  
*Default residual function for shark evaluations.*
- int [SHARK](#) (SHARK\_DATA \*shark\_dat)  
*Function to call all above functions to perform a shark simulation.*
- int [SHARK\\_SCENARIO](#) (const char \*yaml\_input)  
*Function to perform a shark simulation based on the conditions in a yaml formatted input file.*
- int [SHARK\\_TESTS](#) ()  
*Function to perform a series of shark calculation tests.*

### 6.17.1 Detailed Description

Speciation-object Hierarchy for Aqueous [Reaction](#) Kinetics. `shark.cpp`

This file contains structures and functions associated with solving speciation and kinetic problems in aqueous systems. The primary aim for the development of these algorithms was to solve speciation and adsorption problems for the recovery of uranium resources from seawater. Seawater is an extraordinarily complex medium in which to work, which is why these algorithms are being constructed in a piece-wise, object-oriented fashion. This allows us to displace much of the complexity of the problem by breaking it down into smaller, more manageable pieces.

Each piece of SHARK contributes to a residual function when solving the overall speciation, reaction, kinetic chemical problem. These residuals are then fed into the PJFNK solver function in [lark.h](#). The variables of the system are the  $\log(C)$  concentration values of each species in the system. We solve for  $\log(C)$  concentrations, rather than just  $C$ , because the PJFNK method is an unbounded solution algorithm. So to prevent the algorithm from producing negative values for concentration, we reformulate all residuals in terms of the  $\log(C)$  values. In this way, regardless of the value found for  $\log(C)$ , the concentration  $C$  will always be greater than 0.

Currently, SHARK supports standard aqueous speciation problems with simple kinetic models based on an unsteady form of the standard reaction stoichiometry. As more methods and algorithms are completed, the SHARK simulations will be capable of doing much, much more.

#### Warning

Much of this is still underconstruction and many methods or interfaces may change. Use with caution.

#### Author

Austin Ladshaw

#### Date

05/27/2015

#### Copyright

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

### 6.17.2 Macro Definition Documentation

#### 6.17.2.1 `#define Rstd 8.3144621`

Gas Law Constant in J/K/mol (or) L\*kPa/K/mol (Standard Units)

#### 6.17.2.2 `#define Na 6.0221413E+23`

Avagadro's Number - Units: molecules/mol.

#### 6.17.2.3 `#define kB 1.3806488E-23`

Boltzmann's Constant - Units: J/K or C\*V/K.

#### 6.17.2.4 `#define e 1.6021766208E-19`

Elementary Electric Charge - Units: C.

#### 6.17.2.5 `#define Faraday 96485.33289`

Faraday's Constant - C/mol.

#### 6.17.2.6 #define VacuumPermittivity 8.8541878176E-12

Vacuum Permittivity Constant - F/m or C/V/m.

#### 6.17.2.7 #define WaterRelPerm 80.1

Approximate Relative Permittivity for water - Unitless.

#### 6.17.2.8 #define AbsPerm( Rel ) (Rel\*VacuumPermittivity)

Calculation of Absolute Permittivity of a medium - F/m or C/V/m.

### 6.17.3 Typedef Documentation

#### 6.17.3.1 typedef struct SHARK\_DATA SHARK\_DATA

Data structure for SHARK simulations.

C-style object holding data and function pointers associated with solving aqueous speciation and reaction kinetics. This object couples all other objects available in [shark.h](#) in order to provide residual calculations for each individual function that makes up the overall system model. Those residuals are brought together inside the residual function and fed into the [lark.h](#) PJFNK solver routine. That solver then attempts to find a solution to all non-linear variables simultaneously. Any function or data pointers in this structure can be overridden to change how you interface with and solve the problem. Users may also provide a set of custom residual functions through the "OtherList" vector object. Those residual function must all have the same format.

### 6.17.4 Enumeration Type Documentation

#### 6.17.4.1 enum valid\_act

Enumeration for the list of valid activity models for non-ideal solutions.

##### Note

The SIT and PITZER models are not currently supported.

##### Enumerator

**IDEAL**  
**DAVIES**  
**DEBYE\_HUCKEL**  
**SIT**  
**PITZER**

#### 6.17.4.2 enum valid\_surf\_act

Enumeration for the list of valid surface activity models for non-ideal adsorption.

##### Note

We had to create an IDEAL\_ADS option to replace the IDEAL enum already in use for non-ideal solution or aqueous phases. (ADS => adsorption)

##### Enumerator

**IDEAL\_ADS**  
**FLORY\_HUGGINS**

## 6.17.5 Function Documentation

## 6.17.5.1 void print2file\_shark.info ( SHARK\_DATA \* shark\_dat )

Function to print out simulation conditions and options to the output file.

## 6.17.5.2 void print2file\_shark.header ( SHARK\_DATA \* shark\_dat )

Function to print out the head of species and time stamps to the output file.

## 6.17.5.3 void print2file\_shark.results.new ( SHARK\_DATA \* shark\_dat )

Function to print out the simulation results for the current time step.

## 6.17.5.4 void print2file\_shark.results.old ( SHARK\_DATA \* shark\_dat )

Function to print out the simulation results for the previous time step.

## 6.17.5.5 double calculate\_ionic\_strength ( const Matrix&lt; double &gt; &amp; x, MasterSpeciesList &amp; MasterList )

Function to calculate the ionic strength of the solution.

This function calculates the ionic strength of a system given the concentrations of the species present in solution, as well as any other relevant information from [SHARK\\_DATA](#) such as charge.

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>MasterList</i>	reference to the <a href="#">MasterSpeciesList</a> object holding species information

## 6.17.5.6 int FloryHuggins ( const Matrix&lt; double &gt; &amp; x, Matrix&lt; double &gt; &amp; F, const void \* data )

Surface Activity function for simple non-ideal adsorption.

This is a simple surface activity model to be used with the Adsorption objects to evaluate the non-ideal behavior of the surface phase. The model's only parameters are the shape factors in adsorption and the relative concentrations of each surface species. Therefore, we will pass the Adsorption Object itself as the const void \*data structure.

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>F</i>	matrix of activity coefficients that are to be altered by this function
<i>data</i>	pointer to the <a href="#">AdsorptionReaction</a> object holding parameter information

## 6.17.5.7 int ideal\_solution ( const Matrix&lt; double &gt; &amp; x, Matrix&lt; double &gt; &amp; F, const void \* data )

Activity function for Ideal Solution.

This is one of the default activity models available. It assumes the system behaves ideally and sets the activity coefficients to 1 for all species.

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>F</i>	matrix of activity coefficients that are to be altered by this function
<i>data</i>	pointer to a data structure needed to evaluate the activity model

## 6.17.5.8 int Davies\_equation ( const Matrix&lt; double &gt; &amp; x, Matrix&lt; double &gt; &amp; F, const void \* data )

Activity function for Davies Equation.



This is one of the default activity models available. It uses the Davies semi-empirical model to calculate average activities of each species in solution. This model is typically valid for systems involving high ionic strengths upto 0.5 M (mol/L).

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>F</i>	matrix of activity coefficients that are to be altered by this function
<i>data</i>	pointer to a data structure needed to evaluate the activity model

**6.17.5.9** `int DebyeHuckel_equation ( const Matrix< double > & x, Matrix< double > & F, const void * data )`

Activity function for Debye-Huckel Equation.

This is one of the default activity models available. It uses the Debye-Huckel limiting model to calculate average activities of each species in solution. This model is typically valid for systems involving low ionic strengths and is only good for solutions between 0 and 0.01 M.

## Parameters

<i>x</i>	matrix of the log(C) concentration values at the current non-linear step
<i>F</i>	matrix of activity coefficients that are to be altered by this function
<i>data</i>	pointer to a data structure needed to evaluate the activity model

**6.17.5.10** `int Sit.equation ( const Matrix< double > & x, Matrix< double > & F, const void * data )`

First test of SIT Model.

**6.17.5.11** `int surf.act.choice ( const std::string & input )`

Function takes a given string and returns a flag denoting which surface activity model was choosen.

This function returns an integer flag that will be one of the valid surface activity model flags from the `valid_surf_act` enum. If the input string was not recognized, then it defaults to returning the `IDEAL_ADS` flag.

## Parameters

<i>input</i>	string for the name of the surface activity model
--------------	---

**6.17.5.12** `int act.choice ( const std::string & input )`

Function takes a given string and returns a flag denoting which activity model was choosen.

This function returns an integer flag that will be one of the valid activity model flags from the `valid_act` enum. If the input string was not recognized, then it defaults to returning the `IDEAL` flag.

## Parameters

<i>input</i>	string for the name of the activity model
--------------	---

**6.17.5.13** `bool linesearch.choice ( const std::string & input )`

Function returns a bool to determine the form of line search requested.

This function returns true if the user requests a bouncing line search algorithm and false if the user wants a standard line search. If the input string is unrecognized, then it returns false.

## Parameters

<i>input</i>	string for the line search method option
--------------	--

**6.17.5.14** int linearsolve\_choice ( const std::string & input )

Function returns the linear solver flag for the PJFNK method.

This function takes in a string argument and returns the integer flag for the appropriate linear solver in PJFNK. If the input string was unrecognized, then it returns the GMRESRP flag.

**Parameters**

<i>input</i>	string for the linear solver method option
--------------	--

**6.17.5.15** int Convert2LogConcentration ( const Matrix< double > & x, Matrix< double > & logx )

Function to convert the given values of variables (x) to the log of those variables (logx)

This function returns an integer flag to denote success of failure. It takes a constant matrix argument x and replaces the elements of the matrix logx with the base 10 log of those x values. This is used mainly to convert a set of concentrations (x) to their respective log(C) values (logx).

**Parameters**

<i>x</i>	matrix of values to take the base 10 log of
<i>logx</i>	matrix whose entries are to be changed to base 10 log(x)

**6.17.5.16** int Convert2Concentration ( const Matrix< double > & logx, Matrix< double > & x )

Function to convert the given log values of variables (logx) to the values of those variables (x)

This function returns an integer flag to denote success of failure. It takes a constant matrix argument logx and replaces the elements of the matrix x with  $10^{\log x}$ . This is used mainly to convert a set of log(C) values (logx) to their respective concentration values (x).

**Parameters**

<i>logx</i>	matrix of values to apply as the power of 10 (i.e., $10^{\log x}$ )
<i>x</i>	matrix whose entries are to be changed to the result of $10^{\log x}$

**6.17.5.17** int read\_scenario ( SHARK\_DATA \* shark\_dat )

Function to go through the yaml object for the scenario document.

This function checks the yaml object for the expected keys and values of the scenario document to setup the shark simulation for the input given in the input file.

**6.17.5.18** int read\_options ( SHARK\_DATA \* shark\_dat )

Function to go through the yaml object for the solver options document.

This function checks the yaml object for the expected keys and values of the solver options document to setup the shark simulation for the input given in the input file.

**6.17.5.19** int read\_species ( SHARK\_DATA \* shark\_dat )

Function to go through the yaml object for the master species document.

This function checks the yaml object for the expected keys and values of the master species document to setup the shark simulation for the input given in the input file.

**6.17.5.20** int read\_massbalance ( SHARK\_DATA \* shark\_dat )

Function to go through the yaml object for the mass balance document.

This function checks the yaml object for the expected keys and values of the mass balance document to setup the

shark simulation for the input given in the input file.

**6.17.5.21** `int read_equilrxn ( SHARK_DATA * shark_dat )`

Function to go through the yaml object for the equilibrium reaction document.

This function checks the yaml object for the expected keys and values of the equilibrium reaction document to setup the shark simulation for the input given in the input file.

**6.17.5.22** `int read_unsteadyrxn ( SHARK_DATA * shark_dat )`

Function to go through the yaml object for the unsteady reaction document.

This function checks the yaml object for the expected keys and values of the unsteady reaction document to setup the shark simulation for the input given in the input file.

**6.17.5.23** `int read_adsorbobjects ( SHARK_DATA * shark_dat )`

Function to go through the yaml object for each Adsorption Object.

This function checks the yaml object for the expected keys and values of the adsorption object documents to setup the shark simulation for the input given in the input file.

#### Note

Each adsorption object will have its own document header by the name of that object

**6.17.5.24** `int setup_SHARK_DATA ( FILE * file, int(*) (const Matrix< double > &x, Matrix< double > &res, const void *data) residual, int(*) (const Matrix< double > &x, Matrix< double > &gama, const void *data) activity, int(*) (const Matrix< double > &r, Matrix< double > &p, const void *data) precon, SHARK_DATA * dat, const void * activity_data, const void * residual_data, const void * precon_data, const void * other_data )`

Function to setup the memory and pointers for the [SHARK\\_DATA](#) structure for the current simulation.

This function will be called after reading the scenario file and is used to setup the memory and other pointers for the user requested simulation. This function must be called before running a simulation or trying to read in the remainder of the yaml formatted input file. Options may be overridden manually after calling this function.

#### Parameters

<i>file</i>	pointer for the output file where shark results will be stored
<i>residual</i>	pointer to the residual function that will be fed into the PJFNK solver
<i>activity</i>	pointer to the activity function that will determine the activity coefficients
<i>precond</i>	pointer to the linear preconditioning operation to be applied to the Jacobian
<i>dat</i>	pointer to the <a href="#">SHARK_DATA</a> data structure
<i>activity_data</i>	optional pointer for data needed in activity functions
<i>residual_data</i>	optional pointer for data needed in residual functions
<i>precon_data</i>	optional pointer for data needed in preconditioning functions
<i>other_data</i>	optional pointer for data needed in the evaluation of user defined residual functions

**6.17.5.25** `int shark_add_customResidual ( int i, double(*) (const Matrix< double > &x, SHARK_DATA *shark_dat, const void *other_data) other_res, SHARK_DATA * shark_dat )`

Function to add user defined custom residual functions to the OtherList vector object in [SHARK\\_DATA](#).

This function will need to be used if the user wants to include custom residuals into the system via the OtherList object in [SHARK\\_DATA](#). For each *i* residual you want to add, you must call this function passing your residual function and the [SHARK\\_DATA](#) structure pointer. The order that those functions are executed in are determined by the integer *i*.

## Parameters

<i>i</i>	index that the other_res function will appear at in the OtherList object
<i>other_res</i>	function pointer for the user's custom residual function
<i>shark_dat</i>	pointer to the <a href="#">SHARK_DATA</a> data structure

6.17.5.26 `int shark_parameter_check ( SHARK_DATA * shark_dat )`

Function to check the [Reaction](#) and [UnsteadyReaction](#) objects for missing info.

This function checks the [Reaction](#) and [UnsteadyReaction](#) objects for missing information. If information is missing, this function will return an error that will cause the program to force quit.

6.17.5.27 `int shark_energy_calculations ( SHARK_DATA * shark_dat )`

Function to calculate all [Reaction](#) and [UnsteadyReaction](#) energies.

This function will call the calculate energy functions for [Reaction](#) and [UnsteadyReaction](#) objects.

6.17.5.28 `int shark_temperature_calculations ( SHARK_DATA * shark_dat )`

Function to calculate all [Reaction](#) and [UnsteadyReaction](#) parameters as a function of temperature.

This function will call all temperature dependent functions in [Reaction](#) and [UnsteadyReaction](#) to calculate equilibrium and reaction rate parameters as a function of system temperature.

6.17.5.29 `int shark_pH_finder ( SHARK_DATA * shark_dat )`

Function will search [MasterSpeciesList](#) for existence of H + (aq) and OH - (aq) molecules.

This function searches all molecules in the [MasterSpeciesList](#) object for the H + (aq) and OH - (aq) molecules. If they are found, then it sets the pH\_index and pOH\_index of the [SHARK\\_DATA](#) structure and indicates that the system contains these variables.

6.17.5.30 `int shark_guess ( SHARK_DATA * shark_dat )`

Function provides a rough initial guess for the values of all non-linear variables.

This function constructs an rough initial guess for the values of all non-linear variables in the system. The guess is based primarily off of trying to satisfy all mass balance constraints, initial conditions, and pH constraints if any apply.

6.17.5.31 `int shark_initial_conditions ( SHARK_DATA * shark_dat )`

Function to establish the initial conditions of the shark simulation.

This function will establish the initial conditions for a transient problem by solving the speciation of the system while holding the transient/unsteady variables constant at their respective initial values. However, if the system we are trying to solve is steady, then this function just calls the shark\_guess function.

6.17.5.32 `int shark_executioner ( SHARK_DATA * shark_dat )`

Function to execute a shark simulation at a single time step or pH value.

This function calls the preprocess, solver, and postprocess functions in order. If a particular solve did not converge, then it will retry the solver routine until it runs out of tries or attains convergence.

6.17.5.33 `int shark_timestep_const ( SHARK_DATA * shark_dat )`

Function to set up all time steps in the simulation to a specified constant.

This function will set all time steps for the current simulation to a constant that is specified in the input file. The time step will not be changed unless the simulation fails, then it will be reduced in order to try to get the system to converge.

**6.17.5.34** `int shark_timestep_adapt ( SHARK_DATA * shark_dat )`

Function to set up all time steps in the simulation based on success or failure to converge.

This function will set all time steps for the current simulation based on some factor multiple of the prior time step used and whether or not the previous solution step was successful. If the previous step converged, then the new time step will be 1.5x the old time step. If it failed, then the simulation will be retried with a new time step of 0.5x the old time step.

**6.17.5.35** `int shark_preprocesses ( SHARK_DATA * shark_dat )`

Function to call other functions for calculation of parameters and setting of time steps.

This function will call the `shark_temperature_calculations` function and the appropriate time step function. If the user requests a constant time step, it will call the `shark_timestep_const` function. Otherwise, it calls the `shark_timestep_adapt` function.

**6.17.5.36** `int shark_solver ( SHARK_DATA * shark_dat )`

Function to call the PJFNK solver routine given the current [SHARK\\_DATA](#) information.

This function will perform the necessary steps before and after calling the PJFNK solver routine. Based on the simulation flags, the solver function will perform an initial guess for unsteady variables, call the PJFNK method, and the printout a console message about the performance. If a terminal failure occurs during the solver, it will print out the current state of residuals, variables, and the Jacobian matrix to the console. Analyzing this information could provide clues as to why failure occurred.

**6.17.5.37** `int shark_postprocesses ( SHARK_DATA * shark_dat )`

Function to convert PJFNK solutions to concentration values and print to the output file.

This function will convert the non-linear variables to their respective concentration values, then print the solve information out to the output file.

**6.17.5.38** `int shark_reset ( SHARK_DATA * shark_dat )`

Function to reset the values of all stateful information in [SHARK\\_DATA](#).

This function will reset all stateful matrix data in the [SHARK\\_DATA](#) structure in preparation of the next time step simulation.

**6.17.5.39** `int shark_residual ( const Matrix< double > & x, Matrix< double > & F, const void * data )`

Default residual function for shark evaluations.

This function calls each individual object's residual function to formulate the overall residual function used in the PJFNK solver routine. It will also call the activity function. The order in which these function calls occurs is as follows: (i) activities, (ii) [Reaction](#), (iii) [UnsteadyReaction](#), (iv) [MassBalance](#), (v) [OtherList](#), and (vi) [MasterSpeciesList](#). If a constant pH is specified, then the [MasterSpeciesList](#) residual call is replaced with a constraint on the H + (aq) variable (if one exists).

**6.17.5.40** `int SHARK ( SHARK_DATA * shark_dat )`

Function to call all above functions to perform a shark simulation.

This function is called after reading in all inputs, setting all constants, and calling the setup function. It will call all the necessary functions and subroutines iteratively until the desired simulation is complete.

**6.17.5.41** `int SHARK_SCENARIO ( const char * yaml_input )`

Function to perform a shark simulation based on the conditions in a yaml formatted input file.

This is the primary function used to run shark simulations from the UI. It requires that the user provide one input file that is formatted with yaml keys, symbols, and spacing so that it can be recognized by the parser. This style of

input file is much easier to use and understand than the input files used for SCOPSOWL or SKUA. Below shows an example of a typical input file. Note that the # symbol is used in the input file to comment out lines of text that the parser does not need to read.

#### Example Yaml Input for SHARK

#This will serve as a test input file for shark to demo how to structure the document

#In practice, this section should be listed first, but it doesn't really matter

#DO NOT USE TABS IN THESE INPUT FILES

#— Starts a document ... Ends a document

#All keys must be proceeded by a :

#All lists/header must be preceeded by a -

#Spacing of the keys will indicate which list/header they belong to

Scenario:

—

```

• vars_fun:
  numvar: 25
  num_ssr: 15
  num_mbe: 7
  num_usr: 2
  num_other: 0 #Not required or used in current version

• sys_data:
  act_fun: davies
  const_pH: false
  pH: 7 #Only required if we are specifying a const_pH
  temp: 298.15 #Units must be in Kelvin
  dielec: 78.325 #Units must be in (1/Kelvin)
  rel_perm: 80.1 #Unitless number
  res_alk: 0 #Units must be in mol/L (Residual Alkalinity)
  volume: 1.0 #Units must be in L

• run_time:
  steady: false #NOTE: All time must be represented in hours
  specs_curve: false #Only needed if steady = true, and will default to false
  dt: 0.001 #Only required if steady = false
  time_adapt: true #Only needed if steady = false, and will default to false
  sim_time: 96.0 #Only required if steady = false
  t_out: 0.01 #Only required if steady = false
  ...

```

#The following header is entirely optional, but is used to set solver options

SolverOptions:

—

line\_search: true #Default = true, and is recommended to be true

```
search_type: standard
linear_solve: gmresrp #Note: FOM will be fastest for small problems
restart: 25 #Note: restart only used if using GMRES or GCR type solvers
nl_maxit: 50
nl_abstol: 1e-5
nl_reltol: 1e-8
lin_reltol: 1e-10 #Min Tol = 1e-15
lin_abstol: 1e-10 #Min Tol = 1e-15
nl_print: true
l_print: true
...
#After the Scenario read, shark will call the setup_function, then read info below
MasterSpecies:
—
#Header names are specific
#Keys are chosen by user, but must span numbers 0 through numvar-1
#Keys will denote the ordering of the variables
#Note: Currently, the number of reg molecules is very limited

• reg:
  0: Cl - (aq)
  1: NaHCO3 (aq)
  2: NaCO3 - (aq)
  3: Na + (aq)
  4: HNO3 (aq)
  5: NO3 - (aq)
  6: H2CO3 (aq)
  7: HCO3 - (aq)
  8: CO3 2- (aq)
  9: UO2 2+ (aq)
  10: UO2NO3 + (aq)
  11: UO2(NO3)2 (aq)
  12: UO2OH + (aq)
  13: UO2(OH)3 - (aq)
  14: (UO2)2(OH)2 2+ (aq)
  15: (UO2)3(OH)5 + (aq)
  16: UO2CO3 (aq)
  17: UO2(CO3)2 2- (aq)
  18: UO2(CO3)3 4- (aq)
  19: H2O (l)
  20: OH - (aq)
  21: H + (aq)
```

#Keys for the sub-headers must follow same rules as keys from above

- unreg:
  - 22:
    - formula: [A\(OH\)2](#) (aq)
    - charge: 0
    - enthalpy: 0
    - entropy: 0
    - have\_HS: false
    - energy: 0
    - have\_G: false
    - phase: Aqueous
    - name: Amidoxime
    - lin\_form: none
  - 23:
    - formula: UO2AO2 (aq)
    - charge: 0
    - enthalpy: 0
    - entropy: 0
    - have\_HS: false
    - energy: 0
    - have\_G: false
    - phase: Aqueous
    - name: Uranyl-amidoximate
    - lin\_form: none
  - 24:
    - formula: UO2CO3AO2 2- (aq)
    - charge: -2
    - enthalpy: 0
    - entropy: 0
    - have\_HS: false
    - energy: 0
    - have\_G: false
    - phase: Aqueous
    - name: Uranyl-carbonate-amidoximate
    - lin\_form: none
  - ...

#NOTE: Total concentrations must be given in mol/L

[MassBalance](#):

—

#[Header](#) names under [MassBalance](#) are choosen by the user

#All other keys will be checked

- water:
  - total\_conc: 1
  - delta:
    - "H2O (l)": 1



- carbonate:
  - total\_conc: 0.0004175
  - delta:
    - "NaHCO3 (aq)": 1
    - "NaCO3 - (aq)": 1
    - "H2CO3 (aq)": 1
    - "HCO3 - (aq)": 1
    - "CO3 2- (aq)": 1
    - "UO2CO3 (aq)": 1
    - "UO2(CO3)2 2- (aq)": 2
    - "UO2(CO3)3 4- (aq)": 3
    - "UO2CO3AO2 2- (aq)": 1

#Other mass balances skipped for demo purposes...

...

#Document for equilibrium or steady reactions

EquilRxn:

—

#Headers under EquilRxn separate out each reaction object

#Keys for these headers only factor into the order of the equations

#Stoichiometry follows the convention that products are pos(+) and reactants are neg(-)

#Note: logK is only required if any species in stoichiometry is unregistered

#Example: below represents - {H2O (l)} -> {H + (aq)} + {OH - (aq)}

#Note: a valid reaction statement requires at least 1 stoichiometry args

#Note: You can also provide reaction energies: enthalpy, entropy, and energy

- rxn00:
  - logK: -14
  - stoichiometry:
    - "H2O (l)": -1
    - "OH - (aq)": 1
    - "H + (aq)": 1

- rxn01:
  - logK: -6.35
  - stoichiometry:
    - "H2CO3 (aq)": -1
    - "HCO3 - (aq)": 1
    - "H + (aq)": 1

#Other reactions skipped for demo purposes...

...

#Document for unsteady reactions

UnsteadyRxn:

—

#Same basic standards for this doc as the EquilRxn  
 #Main difference is the inclusion of rate information  
 #You are required to give at least 1 rate  
 #You are also required to denote which variable is unsteady  
 #You must give the initial concentration for the variable in mol/L  
 #Rate units are in (L/mol)<sup>n</sup>/hr  
 #Note: we also have keys for forward\_ref, reverse\_ref,  
 #activation\_energy, and temp\_affinity.  
 #These are optional if forward and/or reverse are given  
 #Note: You can also provide reaction energies: enthalpy, entropy, and energy

- rxn00:
  - unsteady\_var: UO2AO2 (aq)
  - initial\_condition: 0
  - logK: -1.35
  - forward: 4.5e+6
  - reverse: 1.00742e+8
  - stoichiometry:
    - "UO2 2+ (aq)": -1
    - "A(OH)2 (aq)": -1
    - "UO2AO2 (aq)": 1
    - "H + (aq)": 2
- rxn01:
  - unsteady\_var: UO2CO3AO2 2- (aq)
  - initial\_condition: 0
  - logK: 3.45
  - forward: 2.55e+15
  - reverse: 9.04774e+11
  - stoichiometry:
    - "UO2 2+ (aq)": -1
    - "CO3 2- (aq)": -1
    - "A(OH)2 (aq)": -1
    - "UO2CO3AO2 2- (aq)": 1
    - "H + (aq)": 2

...

#### Note

It may be advantageous to look at some other shark input file examples. More input files are provided in the input\_files/SHARK directory of the ecosystem project folder. Please refer to your own source file location for more input file examples for SHARK.

#### 6.17.5.42 int SHARK\_TESTS ( )

Function to perform a series of shark calculation tests.

This function sets up and solves a test problem for shark. It is callable from the UI.

## 6.18 skua.h File Reference

Surface Kinetics for Uptake by Adsorption.

```
#include "finch.h"
#include "magpie.h"
#include "egret.h"
```

### Classes

- struct [SKUA\\_PARAM](#)  
*Data structure for species' parameters in SKUA.*
- struct [SKUA\\_DATA](#)  
*Data structure for all simulation information in SKUA.*

### Macros

- #define [SKUA\\_HPP\\_](#)
- #define [D\\_inf](#)(Dref, Tref, B, p, T) ( Dref \* pow(p+sqrt([DBL\\_EPSILON](#)),(Tref/T)-B) )  
*Empirical correction of diffusivity ( $um^2/hr$ )*
- #define [D\\_o](#)(Diff, E, T) ( Diff \* exp(-E/([Rstd](#)\*T)) )  
*Arrhenius Rate Expression for Diffusivity ( $um^2/hr$ )*
- #define [D\\_c](#)(Diff, phi) ( Diff \* (1.0/((1.0+1.1E-6)-phi)) )  
*Approximate Darken Diffusivity Equation ( $um^2/hr$ )*

### Functions

- void [print2file\\_species\\_header](#) (FILE \*Output, [SKUA\\_DATA](#) \*skua\_dat, int i)  
*Function to print out the species' headers to output file.*
- void [print2file\\_SKUA\\_time\\_header](#) (FILE \*Output, [SKUA\\_DATA](#) \*skua\_dat, int i)  
*Function to print out time and space headers to output file.*
- void [print2file\\_SKUA\\_header](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function calls the other header functions to establish output file structure.*
- void [print2file\\_SKUA\\_results\\_old](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to print out the old time step simulation results to the output file.*
- void [print2file\\_SKUA\\_results\\_new](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to print out the new time step simulation results to the output file.*
- double [default\\_Dc](#) (int i, int l, const void \*data)  
*Default function for surface diffusivity.*
- double [default\\_kf](#) (int i, const void \*data)  
*Default function for film mass transfer coefficient.*
- double [const\\_Dc](#) (int i, int l, const void \*data)  
*Constant surface diffusivity function.*
- double [simple\\_darken\\_Dc](#) (int i, int l, const void \*data)  
*Simple Darken model for surface diffusivity.*
- double [theoretical\\_darken\\_Dc](#) (int i, int l, const void \*data)  
*Theoretical Darken model for surface diffusivity.*
- double [empirical\\_kf](#) (int i, const void \*data)  
*Empirical function for film mass transfer coefficient.*
- double [const\\_kf](#) (int i, const void \*data)  
*Constant function for film mass transfer coefficient.*

- int [molefractionCheck](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to check mole fractions in gas and solid phases for errors.*
- int [setup\\_SKUA\\_DATA](#) (FILE \*file, double(\*eval\_Dc)(int i, int l, const void \*user\_data), double(\*eval\_Kf)(int i, const void \*user\_data), const void \*user\_data, [MIXED\\_GAS](#) \*gas\_data, [SKUA\\_DATA](#) \*skua\_dat)  
*Function to setup the function pointers and vector objects in memory to setup the SKUA simulation.*
- int [SKUA\\_Executioner](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to execute preprocesses, solvers, and postprocesses for a SKUA simulation.*
- int [set\\_SKUA\\_ICs](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to establish the initial conditions of adsorption in the adsorbent.*
- int [set\\_SKUA\\_timestep](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to establish the time step for the current simulation.*
- int [SKUA\\_preprocesses](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to perform the necessary preprocess operations before a solve.*
- int [set\\_SKUA\\_params](#) (const void \*user\_data)  
*Function to call the diffusivity function during the solve.*
- int [SKUA\\_postprocesses](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to perform the necessary postprocess operations after a solve.*
- int [SKUA\\_reset](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to reset the stateful information in SKUA after a simulation.*
- int [SKUA](#) ([SKUA\\_DATA](#) \*skua\_dat)  
*Function to iteratively call all execution steps to evolve a simulation through time.*
- int [SKUA\\_SCENARIOS](#) (const char \*scene, const char \*sorbent, const char \*comp, const char \*sorbate)  
*Function callable from the UI to perform a SKUA simulation based on user supplied input files.*
- int [SKUA\\_TESTS](#) ()  
*Function to perform a test of the SKUA functions and routines.*

#### 6.18.1 Detailed Description

Surface Kinetics for Uptake by Adsorption. skua.cpp

This file contains structures and functions associated with solving the surface diffusion partial differential equations for adsorption kinetics in spherical and/or cylindrical adsorbents. For this system, it is assumed that the pore size is so small that all molecules are confined to movement exclusively on the surface area of the adsorbent. The total amount of adsorption for each species is drive by the MAGPIE model for non-ideal mixed gas adsorption. Spatial and temporal variance in adsorption is caused by a combination of different kinetics between adsorbing species and different adsorption affinities for the surface.

The function for surface diffusion involves four parameters, although not all of these parameters are required to be used. Surface diffusion theoretically varies with temperature according to the Arrhenius rate expression, but we also add in an empirical correction term to account for variations in diffusivity with the partial pressure of the species in the gas phase.

$$D_{\text{surf}} = D_{\text{ref}} * \exp(-E / (R*T)) * \text{pow}(p, (T_{\text{ref}}/T) - B)$$

$D_{\text{ref}}$  is the Reference Diffusivity ( $\text{um}^2/\text{hr}$ ),  $E$  is the activation energy for adsorption ( $\text{J/mol}$ ),  $R$  is the gas law constant ( $\text{J/K/mol}$ ),  $T$  is the system temperature ( $\text{K}$ ),  $p$  is the partial pressure of the adsorbing species ( $\text{kPa}$ ),  $T_{\text{ref}}$  is the Reference Temperature ( $\text{K}$ ), and  $B$  is the Affinity constant.

#### Author

Austin Ladshaw

#### Date

01/26/2015

## Copyright

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

## 6.18.2 Macro Definition Documentation

6.18.2.1 `#define SKUA_HPP_`6.18.2.2 `#define D_inf( Dref, Tref, B, p, T ) ( Dref * pow(p+sqrt(DBL_EPSILON),(Tref/T)-B) )`

Empirical correction of diffusivity ( $\text{um}^2/\text{hr}$ )

6.18.2.3 `#define D_o( Diff, E, T ) ( Diff * exp(-E/(Rstd*T)) )`

Arrhenius Rate Expression for Diffusivity ( $\text{um}^2/\text{hr}$ )

6.18.2.4 `#define D_c( Diff, phi ) ( Diff * (1.0/((1.0+1.1E-6)-phi)) )`

Approximate Darken Diffusivity Equation ( $\text{um}^2/\text{hr}$ )

## 6.18.3 Function Documentation

6.18.3.1 `void print2file_species_header ( FILE * Output, SKUA_DATA * skua_dat, int i )`

Function to print out the species' headers to output file.

6.18.3.2 `void print2file_SKUA_time_header ( FILE * Output, SKUA_DATA * skua_dat, int i )`

Function to print out time and space headers to output file.

6.18.3.3 `void print2file_SKUA_header ( SKUA_DATA * skua_dat )`

Function calls the other header functions to establish output file structure.

6.18.3.4 `void print2file_SKUA_results_old ( SKUA_DATA * skua_dat )`

Function to print out the old time step simulation results to the output file.

6.18.3.5 `void print2file_SKUA_results_new ( SKUA_DATA * skua_dat )`

Function to print out the new time step simulation results to the output file.

6.18.3.6 `double default_Dc ( int i, int l, const void * data )`

Default function for surface diffusivity.

This is the default function provided by SKUA for the calculation of the surface diffusivity parameter. The diffusivity is calculated based on the Arrhenius rate expression, then corrected for using the empirical correction term with the outside partial pressure of the gas species.

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>l</i>	index of the node in the spatial discretization that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.7 `double default_kf ( int i, const void * data )`

Default function for film mass transfer coefficient.

This is the default function provided by SKUA for the calculation of the film mass transfer parameter. By default, we are usually going to couple the SKUA model with a pore diffusion model (see [scopsowl.h](#)). Therefore, the film mass transfer coefficient would be zero, because we would only consider a Dirichlet boundary condition for this sub-problem.

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.8 double const\_Dc ( int *i*, int *l*, const void \* *data* )

Constant surface diffusivity function.

This function allows the user to specify just a single constant value for surface diffusivity. The value of diffusivity applied at all nodes will be the ref\_diffusion parameter in [SKUA\\_PARAM](#).

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>l</i>	index of the node in the spatial discretization that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.9 double simple\_darken\_Dc ( int *i*, int *l*, const void \* *data* )

Simple Darken model for surface diffusivity.

This function uses an approximation to Darken's model for surface diffusion. The approximation is exact if the isotherm for adsorption takes the form of the Langmuir model, but is only approximate if the isotherm is heterogeneous. Forming the approximation in this manner is significantly cheaper than forming the true Darken model expression for the GSTA isotherm.

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>l</i>	index of the node in the spatial discretization that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.10 double theoretical\_darken\_Dc ( int *i*, int *l*, const void \* *data* )

Theoretical Darken model for surface diffusivity.

This function uses the full theoretical expression of the Darken's diffusion model to calculate the surface diffusivity. This calculation involves formulating the reference state pressures for the adsorbed amount at every node, then calculating derivatives of the adsorption isotherm for each species. It is more accurate than the simple Darken model function, but costs significantly more computational time.

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>l</i>	index of the node in the spatial discretization that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.11 double empirical\_kf ( int *i*, const void \* *data* )

Empirical function for film mass transfer coefficient.

This function provides an empirical estimate of the mass transfer coefficient using the gas velocity, molecular diffusivities, and dimensionless numbers (see [egret.h](#)). It is used as the default film mass transfer function IF the boundary condition is specified to be a Neumann type boundary by the user.

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.12 `double const_kf ( int i, const void * data )`

Constant function for film mass transfer coefficient.

This function allows the user to specify a constant value for the film mass transfer coefficient. The value of the film mass transfer coefficient will be the value of `film_transfer` given in the [SKUA\\_PARAM](#) data structure.

## Parameters

<i>i</i>	index of the gas/adsorbed phase species that this function acts on
<i>data</i>	pointer to the <a href="#">SKUA_DATA</a> structure

6.18.3.13 `int molefractionCheck ( SKUA_DATA * skua_dat )`

Function to check mole fractions in gas and solid phases for errors.

This function is called after reading input and before calling the primary solution routines. It will force an error and quit the program if there are inconsistencies in the mole fractions it was given. All mole fractions must sum to 1, otherwise there is missing information.

6.18.3.14 `int setup_SKUA_DATA ( FILE * file, double(*) (int i, int l, const void *user_data) eval_Dc, double(*) (int i, const void *user_data) eval_Kf, const void * user_data, MIXED_GAS * gas_data, SKUA_DATA * skua_dat )`

Function to setup the function pointers and vector objects in memory to setup the SKUA simulation.

This function is called to setup the SKUA problem in memory and set function pointers to either defaults or user specified functions. It must be called prior to calling any other SKUA function and will report an error if the object was not setup properly.

## Parameters

<i>file</i>	pointer to the output file for SKUA simulations
<i>eval_Dc</i>	pointer to the function to evaluate the surface diffusivity
<i>eval_Kf</i>	pointer to the function to evaluate the film mass transfer coefficient
<i>user_data</i>	pointer to a user defined data structure used in the calculation the the parameters
<i>gas_data</i>	pointer to the <a href="#">MIXED_GAS</a> data structure for <a href="#">egret.h</a> calculations
<i>skua_dat</i>	pointer to the <a href="#">SKUA_DATA</a> data structure

6.18.3.15 `int SKUA_Executioner ( SKUA_DATA * skua_dat )`

Function to execute preprocesses, solvers, and postprocesses for a SKUA simulation.

This function calls the preprocess, solver, and postprocess functions to complete a single time step in a SKUA simulation. User's will want to call this function whenever a time step simulation result is needed. This is used primarily when coupling with other models (see [scopsowl.h](#)).

6.18.3.16 `int set_SKUA_ICs ( SKUA_DATA * skua_dat )`

Function to establish the initial conditions of adsorption in the adsorbent.

This function needs to be called before doing any simulation or execution of a time step, but only once per simulation. It sets the value of adsorption for each adsorbable species to the specified initial values given via `qT` and `xIC` in [SKUA\\_DATA](#).

6.18.3.17 `int set_SKUA_timestep ( SKUA_DATA * skua_dat )`

Function to establish the time step for the current simulation.

This function is called to set a time step value for a particular simulation step. By default, the time step is set to (1/4)x space step size. If you need to change the step size, you must do so manually.

#### 6.18.3.18 int SKUA\_preprocesses ( SKUA\_DATA \* skua\_dat )

Function to perform the necessary preprocess operations before a solve.

This function performs preprocess operations prior to calling the solver routine. Those preprocesses include establishing boundary conditions and performing a MAGPIE simulation for the adsorption on the surface (see [magpie.h](#)).

#### 6.18.3.19 int set\_SKUA\_params ( const void \* user\_data )

Function to call the diffusivity function during the solve.

This is the function passed into FINCH to be called during the FINCH solver (see [finch.h](#)). It will call the diffusion functions set by the user in the setup function above. This is not overridable.

#### 6.18.3.20 int SKUA\_postprocesses ( SKUA\_DATA \* skua\_dat )

Function to perform the necessary postprocess operations after a solve.

This function performs postprocess operations after a solve was completed successfully. Those operations include estimating average total adsorption, average adsorbed mole fractions, and heat of adsorption for each species. Results are then printed to the output file.

#### 6.18.3.21 int SKUA\_reset ( SKUA\_DATA \* skua\_dat )

Function to reset the stateful information in SKUA after a simulation.

This function sets all the old state data to the newly formed state data. It needs to be called after a successful execution of the simulation step and before calling for the next time step to be solved. Do not call out of turn, otherwise information will be lost.

#### 6.18.3.22 int SKUA ( SKUA\_DATA \* skua\_dat )

Function to iteratively call all execution steps to evolve a simulation through time.

This function is used in conjunction with the scenario call from the UI to numerically solve the adsorption kinetics problem in time. It will call the initial conditions function once, then iteratively call the reset, time step, and executioner functions for SKUA to push the simulation forward in time. This function will be called from the SKUA\_SCENARIOS function.

#### 6.18.3.23 int SKUA\_SCENARIOS ( const char \* scene, const char \* sorbent, const char \* comp, const char \* sorbate )

Function callable from the UI to perform a SKUA simulation based on user supplied input files.

This is the primary function to be called when running a stand-alone SKUA simulation. Parameters and system information for the simulation are given in a series of input files that come in as character arrays. These inputs are all required to call this function.

##### Parameters

<i>scene</i>	Sceneario Input File
<i>sorbent</i>	Adsorbent Input File
<i>comp</i>	Component Input File
<i>sorbate</i>	Adsorbate Input File

##### Note

Each input file has a particular format that must be strictly adhered to in order for the simulation to be carried out correctly. The format for each input file, and an example, is provided below...



**Scenario Input Format**

System Temperature (K) [tab] Total Pressure (kPa) [tab] Gas Velocity (cm/s)

Simulation Time (hrs) [tab] Print Out Time (hrs)

BC Type (0 = Neumann, 1 = Dirichlet)

Number of Gas Species

Initial Total Adsorption (mol/kg)

Name of ith Species [tab] Adsorbable? (0 = false, 1 = true) [tab] Gas Phase Molefraction [tab] Initial Sorbed Molefraction

(repeat above for all species)

**Example Scenario Input**

353.15 101.35 0.36

4.0 0.05

0

5

0.0

N2 0 0.7634 0.0

O2 0 0.2081 0.0

Ar 0 0.009 0.0

CO2 0 0.0004 0.0

H2O 1 0.0191 0.0

Above example is for a 5-component mixture of N2, O2, Ar, CO2, and H2O, but we are only considering the H2O as adsorbable.

**Adsorbent Input File**

Domain Coord. (2 = spherical, 1 = cylindrical) { [tab] Char. Length (um) (i.e., cylinder length) }

(NOTE: Char. Length is only needed if problem is not spherical)

Pellet Radius (um)

**Example Adsorbent Input**

1 6.0

2.0

Above example is for a cylindrical adsorbent with a length of 5 um and radius of 2 um.

**Component Input File**

Molar Weight of ith species (g/mol) [tab] Specific Heat of ith species (J/g/K)

Sutherland Viscosity (g/cm/s) [tab] Sutherland Temperature (K) [tab] Sutherland Constant (K) of ith species

(repeat above for all species in same order they appeared in the Scenario Input File)

**Example Component Input**

28.016 1.04

0.0001781 300.55 111.0

32.0 0.919  
 0.0002018 292.25 127.0  
 39.948 0.522  
 0.0002125 273.11 144.4  
 44.009 0.846  
 0.000148 293.15 240.0  
 18.0 1.97  
 0.0001043 298.16 784.72

Above example is a continuation of the Scenario Input example wherein each grouping represents parameters that are associated with N<sub>2</sub>, O<sub>2</sub>, Ar, CO<sub>2</sub>, and H<sub>2</sub>O, respectively. The order is VERY important!

#### Adsorbate Input File

Type of Surface Diffusion Function (0 = constant, 1 = simple Darken, 2 = theoretical Darken)

Reference Diffusivity ( $\text{um}^2/\text{hr}$ ) [tab] Activation Energy (J/mol) of ith adsorbable species

Reference Temperature (K) [tab] Affinity Constant (-) of ith adsorbable species

van der Waals Volume ( $\text{cm}^3/\text{mol}$ ) of ith species

GSTA adsorption capacity (mol/kg) of ith species

Number of GSTA parameters of ith species

Enthalpy (J/mol) of nth site [tab] Entropy of nth site (J/K/mol) of ith species

(repeat enthalpy and entropy for all n sites in species i)

(repeat above for all species i)

#### Example Adsorbate Input

0  
 0.8814 0.0  
 267.999 0.0  
 13.91  
 11.67  
 4  
 -46597.5 -53.6994  
 -125024 -221.073  
 -193619 -356.728  
 -272228 -567.459  
 1.28 540.1  
 374.99 0.01  
 3.01  
 1.27  
 2  
 -46597.5 -53.6994  
 -125024 -221.073

Above example would be for a simulation involving two adsorbable species using a constant surface diffusion func-

tion. Each adsorbable species has its own set of kinetic and equilibrium parameters that must be given in the same order as the species appeared in the Scenario Input. Note: we do not need to supply this information for non-adsorbable species.

#### 6.18.3.24 int SKUA\_TESTS ( )

Function to perform a test of the SKUA functions and routines.

This function is callable from the UI and will perform a test simulation of the SKUA system of equations. Results from that test are output into a sub-directory called output and named SKUA\_Test\_Output.txt.

## 6.19 skua\_opt.h File Reference

Optimization Routine for the SKUA Model.

```
#include "skua.h"
```

### Classes

- struct [SKUA\\_OPT\\_DATA](#)  
*Data structure for the SKUA Optimization Routine.*

### Functions

- int [SKUA\\_OPT\\_set\\_y](#) (SKUA\_OPT\_DATA \*skua\_opt)  
*Function to set the rest of the gas phase mole fractions based on current mole fraction of adsorbing gas.*
- int [initial\\_guess\\_SKUA](#) (SKUA\_OPT\_DATA \*skua\_opt)  
*Function to set up an initial guess for the surface diffusivity parameter in SKUA.*
- void [eval\\_SKUA\\_Uptake](#) (const double \*par, int m\_dat, const void \*data, double \*fvec, int \*info)  
*Function that works in conjunction with the Imfit routine to minimize the euclidean norm between function and data.*
- int [SKUA\\_OPTIMIZE](#) (const char \*scene, const char \*sorbent, const char \*comp, const char \*sorbate, const char \*data)  
*Function called to perform the optimization routine given a specific set of information and data.*

#### 6.19.1 Detailed Description

Optimization Routine for the SKUA Model. skua\_opt.cpp

This file contains structures and functions associated with performing non-linear least-squares optimization of the SKUA simulation results against actual kinetic adsorption data. The optimization routine here allows you to run data comparisons and optimizations in three forms: (i) Rough optimizations - cheaper operations, but less accurate, (ii) Exact optimizations - much more expensive, but greater accuracy, and (iii) data/model comparisons - no optimization, just using system parameters to compare simulation results against a set of data.

Depending on the level of optimization desired, this routine could take several minutes or several hours. The optimization/comparisons are printed out in two files: (i) a parameter file, which contains the simulation partial pressures and temperatures and the optimized diffusivities with the euclidean norm of the fitting and (ii) a comparison file that shows the model value and data value at each time step for each kinetic curve.

The optimized diffusion parameters are given for each individual kinetic data curve. Each data curve will have a different pairing of partial pressure and temperature. Because of this, you will get a list of different diffusivities for each data curve. To get the optimum kinetic parameters from this list of diffusivities, you must fit the diffusion parameter values to the following diffusion function model...

$$D_{\text{opt}} = D_{\text{ref}} * \exp(-E / (R*T)) * \text{pow}(p, (T_{\text{ref}}/T) - B)$$

where  $D_{ref}$  is the Reference Diffusivity ( $\mu\text{m}^2/\text{hr}$ ),  $E$  is the activation energy for adsorption ( $\text{J/mol}$ ),  $R$  is the gas law constant ( $\text{J/K/mol}$ ),  $T$  is the system temperature ( $\text{K}$ ),  $p$  is the partial pressure of the adsorbing species ( $\text{kPa}$ ),  $T_{ref}$  is the Reference Temperature ( $\text{K}$ ), and  $B$  is the Affinity constant. This algorithm does not automatically produce these parameters for you, but gives you everything you need to produce them yourself.

This routine allows you to optimize multiple kinetic curves at one time. However, all data must be for the same adsorbent-adsorbate system. In other words, the adsorbent and adsorbate pair must be the same for each kinetic curve analyzed. Also, each experiment must have been done in a thin bed or continuous flow system where the adsorbents were exposed to a nearly constant outside partial pressure for all time steps and the gas velocity of that system is assumed constant for all experiments. This experimental setup is very typical for studying adsorption kinetics for gas-solid systems.

#### Author

Austin Ladshaw

#### Date

05/11/2015

#### Copyright

This software was designed and built at the Georgia Institute of Technology by Austin Ladshaw for PhD research in the area of adsorption and surface science. Copyright (c) 2015, all rights reserved.

### 6.19.2 Function Documentation

#### 6.19.2.1 `int SKUA_OPT_set_y ( SKUA_OPT_DATA * skua_opt )`

Function to set the rest of the gas phase mole fractions based on current mole fraction of adsorbing gas.

This function takes the current mole fraction of the adsorbing gas and calculates the gas mole fractions of the other gases in the sytem based on the standard inlet gas composition given in the scenario file.

#### 6.19.2.2 `int initial_guess_SKUA ( SKUA_OPT_DATA * skua_opt )`

Function to set up an initial guess for the surface diffusivity parameter in SKUA.

This function performs the Rough optimization on the surface diffusivity based on the idea of reducing or eliminating function bias between data and simulation. A positive function bias means that the simulation curve is "higher" than the data curve and a negative function bias means that the simulation curve is "lower" than the data curve. We use this information to incrementally adjust the rate of surface diffusion until this bias is near zero. When bias is near zero, the simulation is nearly optimized, but further refinement may be necessary to find the true minimum solution.

#### 6.19.2.3 `void eval_SKUA_Uptake ( const double * par, int m_dat, const void * data, double * fvec, int * info )`

Function that works in conjunction with the `Imfit` routine to minimize the euclidean norm between function and data.

This function will run the SKUA simulation at a given value of surface diffusivity and produce residuals that feed into the Levenberg-Marquardt's algorithm for non-linear least-squares regression. The form of this function is specific to the format required by the `Imfit` routine.

#### Parameters

<i>par</i>	array of parameters that are to be optimized
<i>m_dat</i>	number of data points or functions to evaluate
<i>data</i>	user supplied data structure holding information necessary to form the residuals
<i>fvec</i>	array of residuals computed at the current parameter values
<i>info</i>	integer pointer denoting whether or not the user requests to end a particular simulation

6.19.2.4 `int SKUA_OPTIMIZE ( const char * scene, const char * sorbent, const char * comp, const char * sorbate, const char * data )`

Function called to perform the optimization routine given a specific set of information and data.

This is the function that is callable by the UI. The user must provide 5 input files to the routine in order to establish simulation conditions, adsorbent properties, component properties, adsorbate equilibrium parameters, and the set of data that we are comparing the simulations to. Each input file has a very specific structure and order to the information that it contains. The structure here is DIFFERENT than the structure for just running standard SKUA simulations (see [skua.h](#)).

#### Parameters

<i>scene</i>	Sceneario Input File
<i>sorbent</i>	Adsorbent Input File
<i>comp</i>	Component Input File
<i>sorbate</i>	Adsorbate Input File
<i>data</i>	Kinetic Adsorption Data File

#### Note

Much of the structure of these input files are "similar" to that of the input files used in SKUA\_SCENARIOS (see [skua.h](#)), but with some notable differences. Below gives the format for each input file with an example. Make sure your input files follow this format before calling this routine from the UI.

#### Scenario Input File

Optimization? (0 = false, 1 = true) [tab] Rough Optimization? (0 = false, 1 = true)

Surf. Diff. (0 = constant, 1 = simple Darken, 2 = theoretical Darken) [tab] BC Type (0 = Neumann, 1 = Dirichlet)

Total Pressure (kPa) [tab] Gas Velocity (cm/s)

Number of Gaseous Species

Initial Adsorption Total (mol/kg)

Name [tab] Adsorbable? (0 = false, 1 = true) [tab] Inlet Gas Mole Fraction [tab] Initial Adsorbed Mole Fraction

(NOTE: The above line is repeated for all species in gas phase. Also, this algorithm only allows you to consider one adsorbable gas component. Inlet gas mole fractions must be non-zero for all non-adsorbing gases and must sum to 1.)

#### Example Scenario Input

```
1 0
0 0
101.35 0.36
5
0.0
N2 0 0.7825 0.0
O2 0 0.2081 0.0
Ar 0 0.009 0.0
CO2 0 0.0004 0.0
H2O 1 0.0 0.0
```

Above example is for running optimizations on data collected with a gas stream at 0.36 cm/s with 5 gas species in the mixture, only H2O of which is adsorbing. The "base line" or "inlet gas" without H2O has a composition of N2 at 0.7825, O2 at 0.2081, Ar at 0.009, and CO2 at 0.0004.

**Adsorbent Input File**

Domain Coord. (2 = spherical, 1 = cylindrical) { [tab] Char. Length (um) (i.e., cylinder length) }

(NOTE: Char. Length is only needed if problem is not spherical)

Pellet Radius (um)

**Example Adsorbent Input**

1 6.0

2.0

Above example is for a cylindrical adsorbent with a length of 5 um and radius of 2 um.

**Component Input File**

Molar Weight of ith species (g/mol) [tab] Specific Heat of ith species (J/g/K)

Sutherland Viscosity (g/cm/s) [tab] Sutherland Temperature (K) [tab] Sutherland Constant (K) of ith species

(repeat above for all species in same order they appeared in the Scenario Input File)

**Example Component Input**

28.016 1.04

0.0001781 300.55 111.0

32.0 0.919

0.0002018 292.25 127.0

39.948 0.522

0.0002125 273.11 144.4

44.009 0.846

0.000148 293.15 240.0

18.0 1.97

0.0001043 298.16 784.72

Above example is exactly the same as in the SCOPSOWL\_SCENARIO example (see [scopsowl.h](#)). There is no difference in the input file formats for this input. Keep in mind that the order is VERY important! All species information must be in the same order that the species appeared in the Scenario input file.

**Adsorbate Input File**

Reference Diffusivity ( $\text{um}^2/\text{hr}$ ) [tab] Activation Energy (J/mol) of ith adsorbable species

Reference Temperature (K) [tab] Affinity Constant (-) of ith adsorbable species

van der Waals Volume ( $\text{cm}^3/\text{mol}$ ) of ith species

GSTA adsorption capacity (mol/kg) of ith species

Number of GSTA parameters of ith species

Enthalpy (J/mol) of nth site [tab] Entropy of nth site (J/K/mol) of ith species

(repeat enthalpy and entropy for all n sites in species i)

(repeat above for all species i)

**Example Adsorbate Input**

0 0

```

0 0
13.91
11.67
4
-46597.5 -53.6994
-125024 -221.073
-193619 -356.728
-272228 -567.459

```

Above example gives the equilibrium parameters associated with the H2O-MS3A single component adsorption system. Note that the kinetic parameters (Ref. Diff., Act. Energy, Ref. Temp., and Affinity) were all given a value of zero. These values are irrelevant if we are running an optimization because they will be replaced with a single estimate for the diffusivity that is being optimization for. However, if we wanted to run this routine with comparisons and not do any optimization, then you would need to provide non-zero values for these parameters (at least for Ref. Diff.).

#### Data Input File

Number of Kinetic Data Curves

Number of data points in the ith curve

Temperature (K) [tab] Partial Pressure (kPa) [tab] Equilibrium Adsorption (mol/kg) all of ith curve

Time point 1 (hrs) [tab] Adsorption 1 (mol/kg) of ith curve

Time point 1 (hrs) [tab] Adsorption 2 (mol/kg) of ith curve

... (Repeat for all time-adsorption data points)

(Repeat above for all curves i)

#### Example Data Input

```

40
2990
298.15 0.000310922 2.9
0 0
0.166666667 0.001834419
0.333611111 0.004880247
0.5 0.008306803
...
2789
298.15 0.00055189 5
0 0
0.166944444 0.003350185
0.333611111 0.007418267
0.5 0.009930906
0.666666667 0.014597236
0.833611111 0.021377373
....

```

Above is a partial example for a data set of 40 kinetic curves. The first curve contains 2990 data points and has temperature of 298.15 K, partial pressure of 0.000310922 kPa, and an equilibrium adsorption of 2.9. Each first time point should start from 0 hours and each initial adsorption should correspond to the value of initial adsorption indicated in the Scenario input file. Then, this structure is repeated for all adsorption curves.

## 6.20 Trajectory.h File Reference

Single Particle Trajectory Analysis for Magnetic Filtration.

```
#include "macaw.h"
#include <random>
#include <chrono>
```

### Classes

- struct [TRAJECTORY\\_DATA](#)

*Data structure holding constants and parameters need in trajectory analysis.*

### Functions

- double [Magnetic\\_R](#) (const [Matrix](#)< double > &dX, const [Matrix](#)< double > &dY, int i, double b, double mu\_0, double chi\_p, double M, double H0, double a)
- double [Magnetic\\_T](#) (const [Matrix](#)< double > &dX, const [Matrix](#)< double > &dY, int i, double b, double mu\_0, double chi\_p, double M, double H0, double a)
- double [Grav\\_R](#) (const [Matrix](#)< double > &dX, int i, double b, double rho\_p, double rho\_f)
- double [Grav\\_T](#) (const [Matrix](#)< double > &dX, int i, double b, double rho\_p, double rho\_f)
- double [Van\\_R](#) (const [Matrix](#)< double > &dX, const [Matrix](#)< double > &dY, int i, double Hamaker, double b, double a)
- double [V\\_RAD](#) (const [Matrix](#)< double > &dX, const [Matrix](#)< double > &dY, int i, double V0, double rho\_f, double a, double eta)
- double [V\\_THETA](#) (const [Matrix](#)< double > &dX, const [Matrix](#)< double > &dY, int i, double V0, double rho\_f, double a, double eta)
- double [Brown\\_RAD](#) (double n\_rand, double m\_rand, double sigma\_n, double sigma\_m)
- double [Brown\\_THETA](#) (double s\_rand, double t\_rand, double sigma\_n, double sigma\_m)
- int [POLAR](#) ([Matrix](#)< double > &POL, const [Matrix](#)< double > &dX, const [Matrix](#)< double > &dY, const void \*data, int i)
- double [RADIAL\\_FORCE](#) (const [Matrix](#)< double > &POL, double eta, double b, double mp, double t, double a)
- double [TANGENTIAL\\_FORCE](#) (const [Matrix](#)< double > &POL, const [Matrix](#)< double > &dY, double eta, double b, double mp, double t, double a, int i)
- int [CARTESIAN](#) (const [Matrix](#)< double > &POL, [Matrix](#)< double > &H, const [Matrix](#)< double > &dY, double i, const void \*data)
- int [DISPLACEMENT](#) ([Matrix](#)< double > &dX, [Matrix](#)< double > &dY, const [Matrix](#)< double > &H, int i)
- int [LOCATION](#) (const [Matrix](#)< double > &dY, const [Matrix](#)< double > &dX, [Matrix](#)< double > &X, [Matrix](#)< double > &Y, int i)
- double [Removal\\_Efficiency](#) (double Sum\_Cap, const void \*data)
- int [Trajectory\\_SetupConstants](#) ([TRAJECTORY\\_DATA](#) \*dat)
- int [Number\\_Generator](#) ([TRAJECTORY\\_DATA](#) \*dat)
- int [Run\\_Trajectory](#) ()

*Main function to run a test of a trajectory analysis.*



## 6.20.1 Detailed Description

Single Particle Trajectory Analysis for Magnetic Filtration. Trajectory.cpp

Alex, Please provide details here... and elsewhere in the file.

## Author

Alex Wiechert

## Date

08/25/2015

## Copyright

This software was designed and built at the Georgia Institute of Technology by Alex Wiechert for PhD research in the area of environmental surface science. Copyright (c) 2015, all rights reserved.

## 6.20.2 Function Documentation

- 6.20.2.1 `double Magnetic_R ( const Matrix< double > & dX, const Matrix< double > & dY, int i, double b, double mu_0, double chi_p, double M, double H0, double a )`
- 6.20.2.2 `double Magnetic_T ( const Matrix< double > & dX, const Matrix< double > & dY, int i, double b, double mu_0, double chi_p, double M, double H0, double a )`
- 6.20.2.3 `double Grav_R ( const Matrix< double > & dX, int i, double b, double rho_p, double rho_f )`
- 6.20.2.4 `double Grav_T ( const Matrix< double > & dX, int i, double b, double rho_p, double rho_f )`
- 6.20.2.5 `double Van_R ( const Matrix< double > & dX, const Matrix< double > & dY, int i, double Hamaker, double b, double a )`
- 6.20.2.6 `double V_RAD ( const Matrix< double > & dX, const Matrix< double > & dY, int i, double V0, double rho_f, double a, double eta )`
- 6.20.2.7 `double V_THETA ( const Matrix< double > & dX, const Matrix< double > & dY, int i, double V0, double rho_f, double a, double eta )`
- 6.20.2.8 `double Brown_RAD ( double n_rand, double m_rand, double sigma_n, double sigma_m )`
- 6.20.2.9 `double Brown_THETA ( double s_rand, double t_rand, double sigma_n, double sigma_m )`
- 6.20.2.10 `int POLAR ( Matrix< double > & POL, const Matrix< double > & dX, const Matrix< double > & dY, const void * data, int i )`
- 6.20.2.11 `double RADIAL_FORCE ( const Matrix< double > & POL, double eta, double b, double mp, double t, double a )`
- 6.20.2.12 `double TANGENTIAL_FORCE ( const Matrix< double > & POL, const Matrix< double > & dY, double eta, double b, double mp, double t, double a, int i )`
- 6.20.2.13 `int CARTESIAN ( const Matrix< double > & POL, Matrix< double > & H, const Matrix< double > & dY, double i, const void * data )`
- 6.20.2.14 `int DISPLACEMENT ( Matrix< double > & dX, Matrix< double > & dY, const Matrix< double > & H, int i )`
- 6.20.2.15 `int LOCATION ( const Matrix< double > & dY, const Matrix< double > & dX, Matrix< double > & X, Matrix< double > & Y, int i )`

6.20.2.16 double Removal\_Efficiency ( double Sum\_Cap, const void \* data )

6.20.2.17 int Trajectory\_SetupConstants ( TRAJECTORY\_DATA \* dat )

6.20.2.18 int Number\_Generator ( TRAJECTORY\_DATA \* dat )

6.20.2.19 int Run\_Trajectory ( )

Main function to run a test of a trajectory analysis.

This is the function called to run a test trajectory analysis for a hard coded set of parameters and conditions. It is callable from only the Advanced UI (see [ui.h](#)) for the time being.

## 6.21 ui.h File Reference

User Interface for Ecosystem.

```
#include <fstream>
#include <string>
#include <iostream>
#include "error.h"
#include "yaml_wrapper.h"
#include "flock.h"
#include "school.h"
#include "sandbox.h"
#include "Trajectory.h"
```

### Classes

- struct [UI\\_DATA](#)  
*Data structure holding the UI arguments.*

### Macros

- #define [UI\\_HPP\\_](#)
- #define [ECO\\_VERSION](#) "0.0 alpha"  
*Macro expansion for executable current version number.*
- #define [ECO\\_EXECUTABLE](#) "eco0"  
*Macro expansion for executable current name.*

### Enumerations

- enum [valid\\_options](#) {  
TEST, EXECUTE, EXIT, CONTINUE,  
HELP, dogfish, eel, egret,  
finch, lark, macaw, mola,  
monkfish, sandbox, scopsowl, shark,  
skua, gsta\_opt, magpie, scops\_opt,  
skua\_opt, trajectory }  
*Valid options available upon execution of the code.*

### Functions

- void [au\\_i\\_help](#) ()

- Function to display help for Advanced User Interface.*

  - void `bui_help` ()
- Function to display help for Basic User Interface.*

  - bool `exit` (const std::string &input)

*Function returns true if user requests exit.*
- bool `help` (const std::string &input)

*Function returns true if the user requests help.*
- bool `version` (const std::string &input)

*Function returns true if user requests to know the executable version.*
- bool `test` (const std::string &input)

*Function returns true if user requests to run a test.*
- bool `exec` (const std::string &input)

*Function returns true if the user requests to run a simulation/executable.*
- bool `path` (const std::string &input)

*Function returns true if the user indicates that input files share a common path.*
- bool `input` (const std::string &input)

*Function returns true if the user indicates that the next arguments are input files.*
- bool `valid_test_string` (const std::string &input, UI\_DATA \*ui\_dat)

*Function returns true if the user gave a valid test option.*
- bool `valid_exec_string` (const std::string &input, UI\_DATA \*ui\_dat)

*Function returns true if the user gave a valid execution option.*
- int `number_files` (UI\_DATA \*ui\_dat)

*Function returns the number of expected input files for the user's run option.*
- bool `valid_addon_options` (UI\_DATA \*ui\_dat)

*Function returns true if the user has chosen a valid additional runtime option.*
- void `display_help` (UI\_DATA \*ui\_dat)

*Function to call the appropriate help menu based on type of interface.*
- void `display_version` (UI\_DATA \*ui\_dat)

*Function to display ecosystem version information to the console.*
- int `invalid_input` (int count, int max)

*Function returns a CONTINUE or EXIT when invalid input is given.*
- bool `valid_input_main` (UI\_DATA \*ui\_dat)

*Function returns true if user gave valid input in Basic UI.*
- bool `valid_input_tests` (UI\_DATA \*ui\_dat)

*Function returns true if user gave a valid test function to run.*
- bool `valid_input_execute` (UI\_DATA \*ui\_dat)

*Function returns true if user gave a valid executable function to run.*
- int `test_loop` (UI\_DATA \*ui\_dat)

*Function that loops the Basic UI until a valid test option was selected.*
- int `exec_loop` (UI\_DATA \*ui\_dat)

*Function that loops the Basic UI until a valid executable option was selected.*
- int `run_test` (UI\_DATA \*ui\_dat)

*Function will call the user requested test function.*
- int `run_exec` (UI\_DATA \*ui\_dat)

*Function will call the user requested executable function.*
- int `run_executable` (int argc, const char \*argv[])

*Function called by the main and runs both user interfaces for the program.*

### 6.21.1 Detailed Description

User Interface for Ecosystem. ui.cpp

These routines define how the user will interface with the software

#### Author

Austin Ladshaw

#### Date

08/25/2015

#### Copyright

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### 6.21.2 Macro Definition Documentation

#### 6.21.2.1 #define UI\_HPP\_

#### 6.21.2.2 #define ECO\_VERSION "0.0 alpha"

Macro expansion for executable current version number.

#### 6.21.2.3 #define ECO\_EXECUTABLE "eco0"

Macro expansion for executable current name.

### 6.21.3 Enumeration Type Documentation

#### 6.21.3.1 enum valid\_options

Valid options available upon execution of the code.

Enumeration of valid options for executing the ecosystem code. More options become available as the code updates. Some options that appear here may not be viewable in the "help" screen of the executable. Those options are hidden, but are still valid entries.

#### Enumerator

**TEST**

**EXECUTE**

**EXIT**

**CONTINUE**

**HELP**

**dogfish**

**eel**

**egret**

**finch**

**lark**

**macaw**

**mola**

*monkfish*  
*sandbox*  
*scopsowl*  
*shark*  
*skua*  
*gsta\_opt*  
*magpie*  
*scops\_opt*  
*skua\_opt*  
*trajectory*

#### 6.21.4 Function Documentation

##### 6.21.4.1 void aui\_help ( )

Function to display help for Advanced User Interface.

The Advanced User Interface help screen is accessed by including run option -h or -help when executing the program from command line.

##### 6.21.4.2 void bui\_help ( )

Function to display help for Basic User Interface.

The Basic User Interface help screen is accessed by running the executable, then typing "help" at any point during the console prompts. Exception to this occurs when the console prompts you to provide input files for your chosen routine. In this circumstance, the executable always assumes that what the user types in will be an input file.

##### 6.21.4.3 bool exit ( const std::string & input )

Function returns true if user requests exit.

This function will check the input string for "exit" or "quit" and terminate the executable. Only checked if using the Basic User Interface.

###### Parameters

<i>input</i>	input string user gives to the console
--------------	--

##### 6.21.4.4 bool help ( const std::string & input )

Function returns true if the user requests help.

This function will check the input string for "help", "-h", or "-help" and will tell the executable to display the help menu. The help menu that gets displayed depends on how the executable was run to begin with.

###### Parameters

<i>input</i>	input string user gives to the console
--------------	--

##### 6.21.4.5 bool version ( const std::string & input )

Function returns true if user requests to know the executable version.

This function will check the input string for "version", "-v", or "-version" and will tell the executable to display version information about the executable.

## Parameters

<i>input</i>	input string user gives to the console
--------------	--

6.21.4.6 bool test ( const std::string & *input* )

Function returns true if user requests to run a test.

This function will check the input string for "-t" or "&ndash;test" and determine whether or not the user requests to run an ecosystem test function.

## Parameters

<i>input</i>	input string user gives to the console
--------------	--

6.21.4.7 bool exec ( const std::string & *input* )

Function returns true if the user requests to run a simulation/executable.

This function will check the input string for "-e" or "&ndash;execute" and determine whether or not the user requests to run an ecosystem executable function.

## Parameters

<i>input</i>	input string the user gives to the console
--------------	--

6.21.4.8 bool path ( const std::string & *input* )

Function returns true if the user indicates that input files share a common path.

This function will check the input string for "-p" or "&ndash;path" and determine whether or not the user will give a common path to all input files needed for the specified simulation. Only used in Advanced User Interface.

## Parameters

<i>input</i>	input string the user gives to the console
--------------	--

6.21.4.9 bool input ( const std::string & *input* )

Function returns true if the user indicates that the next arguments are input files.

This function will check the input string for "-i" or "&ndash;input" and determine whether or not the user's next arguments are input files for a specific simulation. Only used in Advanced User Interface.

## Parameters

<i>input</i>	input string the user gives to the console
--------------	--

6.21.4.10 bool valid\_test\_string ( const std::string & *input*, UI\_DATA \* *ui\_dat* )

Function returns true if the user gave a valid test option.

This function will check the input string given by the user and determine whether that string denotes a valid test. Then, it will mark the option variable in *ui\_dat* with the appropriate option from the *valid\_options* enum.

## Parameters

<i>input</i>	input string the user gives to the console
<i>ui_dat</i>	pointer to the data structure for the ui object

**6.21.4.11 bool valid\_exec\_string ( const std::string & input, UI\_DATA \* ui\_dat )**

Function returns true if the user gave a valid execution option.

This function will check the input string given by the user and determine whether that string denotes a valid execution option. Then, it will mark the option variable in ui\_dat with the appropriate option from the valid\_options enum.

**Parameters**

<i>input</i>	input string the user gives to the console
<i>ui_dat</i>	pointer to the data structure for the ui object

**6.21.4.12 int number\_files ( UI\_DATA \* ui\_dat )**

Function returns the number of expected input files for the user's run option.

This function will check the option variable in the ui\_dat structure to determine the number of input files that is expected to be given. Running different executable functions in ecosystem may require various number of input files.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.13 bool valid\_addon\_options ( UI\_DATA \* ui\_dat )**

Function returns true if the user has choosen a valid additional runtime option.

This function will check all additional input options in the user\_input variable of ui\_dat to determine if the user requests any additional options during runtime. Valid additional options are -p or -path and -i or -input.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.14 void display\_help ( UI\_DATA \* ui\_dat )**

Function to call the appropriate help menu based on type of interface.

This function looks at the ui\_dat structure and the user's OS files to determine what help menu to display and how to display it. There are two different types of help menus that can be displayed: (i) Advanced Help and (ii) Basic Help. Additionally, this function checks the OS file system for the existence of installed help files. If it finds those files, then it instructs the command terminal to read the contents of those files with the "less" command. Otherwise, it will just print the appropriate help menu to the console window.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.15 void display\_version ( UI\_DATA \* ui\_dat )**

Function to display ecosystem version information to the console.

This function will check the ui\_dat structure to see which type of interface the user is using, then print out the version information for the executable being run.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.16** int invalid\_input ( int *count*, int *max* )

Function returns a CONTINUE or EXIT when invalid input is given.

This function looks at the current count and the max iterations and determines whether or not to force the executable to terminate. If the user provides too many incorrect options during the Basic User Interface, then the executable will force quit.

**Parameters**

<i>count</i>	number of times the user has provided a bad option
<i>max</i>	maximum allowable bad options before force quit

**6.21.4.17** bool valid\_input\_main ( UI\_DATA \* *ui\_dat* )

Function returns true if user gave valid input in Basic UI.

This function is only called if the user is running the Basic UI. It checks the given console argument stored in user\_input of ui\_dat for a valid option. If no valid option is given, then this function returns false.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.18** bool valid\_input\_tests ( UI\_DATA \* *ui\_dat* )

Function returns true if user gave a valid test function to run.

This function checks the user\_input argument of ui\_dat for a valid test option. If no valid test was given, then this function returns false.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.19** bool valid\_input\_execute ( UI\_DATA \* *ui\_dat* )

Function returns true if user gave a valid executable function to run.

This function checks the user\_input argument of ui\_dat for a valid executable option. If no valid executable was given, then this function returns false.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.20** int test\_loop ( UI\_DATA \* *ui\_dat* )

Function that loops the Basic UI until a valid test option was selected.

This function loops the Basic UI menu for running a test until a valid test is selected by the user. If a valid test is not selected, and the maximum number of loops has been reached, then this function will cause the program to force quit.

**Parameters**

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

**6.21.4.21** int exec\_loop ( UI\_DATA \* *ui\_dat* )

Function that loops the Basic UI until a valid executable option was selected.



This function loops the Basic UI menu for running an executable until a valid executable is selected by the user. If a valid executable is not selected, and the maximum number of loops has been reached, then this function will cause the program to force quit.

## Parameters

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

## 6.21.4.22 int run\_test ( UI\_DATA \* ui\_dat )

Function will call the user requested test function.

This function checks the option variable of the ui\_dat structure and runs the corresponding test function.

## Parameters

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

## 6.21.4.23 int run\_exec ( UI\_DATA \* ui\_dat )

Function will call the user requested executable function.

This function checks the option variable of the ui\_dat structure and runs the corresponding executable function.

## Parameters

<i>ui_dat</i>	pointer to the data structure for the ui object
---------------	---

## 6.21.4.24 int run\_executable ( int argc, const char \* argv[] )

Function called by the main and runs both user interfaces for the program.

This function is called in the main.cpp file and passes the console arguments given at run time.

## Parameters

<i>argc</i>	number of arguments provided by the user at the time of execution
<i>argv</i>	list of C-strings that was provided by the user at the time of execution

## 6.22 yaml\_wrapper.h File Reference

C++ Wrapper for the C-YAML Library.

```
#include "yaml.h"
#include "error.h"
#include <map>
#include <string>
#include <iostream>
#include <utility>
#include <stdexcept>
```

## Classes

- class [ValueTypePair](#)  
*Value-Type Pair object to recognize data type of a string that was read.*
- class [KeyValueMap](#)  
*Key-Value-Type Map object creating a map of the KeyValuePair objects.*

- class `SubHeader`  
*Object for the Lowest level of `Header` for the `yaml_wrapper`.*
- class `Header`  
*Object for headers in a yaml document (inherits from `SubHeader`)*
- class `Document`  
*Object for the various documents in the yaml file.*
- class `YamlWrapper`  
*Object for the entire yaml file holding all documents, header, sub-headers, keys, and values.*
- class `yaml_cpp_class`  
*Primary object used when reading and digitally storing yaml files.*

#### Typedefs

- typedef enum `data_type data_type`  
*Enum for valid data types in `ValueTypePair`.*
- typedef enum `header_state header_state`  
*Enum for state of the headers in the `yaml_wrapper`.*

#### Enumerations

- enum `data_type` {  
    `STRING`, `BOOLEAN`, `DOUBLE`, `INT`,  
    `UNKNOWN` }
- enum `header_state` { `ANCHOR`, `ALIAS`, `NONE` }

#### Functions

- `std::string allLower` (const `std::string` &`input`)  
*Function to return an all lower case string based on the passed argument.*
- `bool isEven` (int `n`)  
*Function to return true if the given argument is an even number.*
- int `YAML_WRAPPER_TESTS` ()  
*Function to run tests on all the objects that `yaml_cpp_class`.*
- int `YAML_CPP_TEST` (const char \*`file`)  
*Function to run a test read for the `yaml_cpp_class` on a given file.*

##### 6.22.1 Detailed Description

C++ Wrapper for the C-YAML Library. `yaml_wrapper.cpp`

This file holds objects, structures, and functions associated with using the C-YAML library. A C++ wrapper has been created for the Kirill Simonov (2006) LibYAML library to more easily store and query information in yaml style input files. The wrapper uses the C-YAML parser to identify the file structure and store the read in information from that document into an object using C++ maps. Those maps are hold information in a series of Key-Value pairs as well as lists of Key-Value pairs. This allows the user to create well organized input files to change the behavior of simulations.

The `yaml_wrapper` is restricted to the same limitations in the C-YAML source code in terms of how the documents are allowed to be structured for TOKEN based parsing. C-YAML only recognizes specific tokens and will only allow a certain level of Sub-Header mapping. Therefore, this wrapper has the same limitations. Below is an example of acceptable formatting for a C-YAML document.

```
#Test input file for YAML and SHARK
```

```
TestDoc1: &hat
```

---

- scenario:  
  numvar: 25  
  act\_fun: DAVIES  
  steadystate: FALSE  
  t\_out: 1  
  pH: 0

- testblock:  
  another: block  
  
    – subblock:  
      sub: block  
    ...

TestDoc2: \*hat

---

- masterspecies:  
  "Cl - (aq)": 0  
  "Na + (aq)": 1  
  "H2O (l)": 2  
  3: NaCl (aq)  
  ...

TestDoc3:

---

apple: red  
pear: green

- array: #Block  
  banana: yellow  
  #List 1 in array  
  
    – list1: &a #also a block  
      a: 1 #key : value  
      b: 2  
      c: 3  
      #List 2 in array  
  
    – list2: \*a  
      a: 4  
      b: 5  
      c: 6  
    ...

TestDoc4:

---

- anchor: &anchor  
stuff: to do
- alias: \*anchor  
add: to stuff
- list:
  - anchored: &list\_anchor  
info: blah  
atta: boy
  - aliased: \*list\_anchor  
info: bruh  
atta: ber  
...

#WARNING: MAKE SURE FILE DOES NOT CONTAIN TABS!!!

TestDoc5:

—

- grab: \*anchor  
add2: more adds
  - listcopy: \*a
- block: {1: 2, 3: 4}  
still: in block  
...

#### Note

You can view the actual yaml example file in the `input_files/SHARK/test_input.yml` sub-directory of the project folder.

#### Author

Austin Ladshaw

#### Date

07/29/2015

#### Copyright

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**6.22.2 Typedef Documentation****6.22.2.1 typedef enum data\_type data\_type**

Enum for valid data types in [ValueTypePair](#).

**6.22.2.2 typedef enum header\_state header\_state**

Enum for state of the headers in the yaml\_wrapper.

**6.22.3 Enumeration Type Documentation****6.22.3.1 enum data\_type**

Enumerator

**STRING**  
**BOOLEAN**  
**DOUBLE**  
**INT**  
**UNKNOWN**

**6.22.3.2 enum header\_state**

Enumerator

**ANCHOR**  
**ALIAS**  
**NONE**

**6.22.4 Function Documentation**

#### 6.22.4.1 std::string allLower ( const std::string & *input* )

Function to return an all lower case string based on the passed argument.

This function will copy the input paramter and convert that copy to all lower case. The copy is then returned and can be checked against valid or allowed strings.

##### Parameters

<i>input</i>	string to copy and convert to lower case
--------------	--

#### 6.22.4.2 bool isEven ( int *n* )

Function to return true if the given argument is an even number.

#### 6.22.4.3 int YAML\_WRAPPER\_TESTS ( )

Function to run tests on all the objects that [yaml\\_cpp\\_class](#).

This test function is currently NOT callable from the UI.

#### 6.22.4.4 int YAML\_CPP\_TEST ( const char \* *file* )

Function to run a test read for the [yaml\\_cpp\\_class](#) on a given file.

This test/executable function is currently NOT callable from the UI.

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