

GenSSI

2.0

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## 1 GenSSI 2.0 General Documentation

### 1.1 Introduction

GenSSI is a MATLAB implementation of generating series for structural identifiability as described in

- Chiş, O.-T., Banga, J.R. and Balsa-Canto, E. (2011) Structural Identifiability of Systems Biology Models: A Critical Comparison of Methods, PLoS ONE, 6, e27755.
- Chiş, O., Banga, J.R. and Balsa-Canto, E. (2011) GenSSI: a software toolbox for structural identifiability analysis of biological models, Bioinformatics, 27, 2610-2611.

With GenSSI, the user can specify differential equation models in terms of symbolic variables in MATLAB and analyze the models to determine which parameters are globally or locally identifiable. In addition, there are some utilities for converting models to polynomial form, creating multi-experiment models, transforming models to rescale variables and remove redundancies, or convert to/from AMICI format.

### 1.2 Availability

The sources for GenSSI are accessible as

- Source [tarball](#)
- Source [zipball](#)
- Git repository on [github](#)

Once you've obtained your copy check out the [Installation](#)

#### 1.2.1 Obtaining GenSSI via the Git versioning system

In order to stay up to date with the latest GenSSI versions, simply pull it from our Git repository and recompile it when a new release is available. For more information about Git checkout their [website](#)

The Git repository can currently be found at <https://github.com/thomassligon/GenSSI> and a direct clone is possible via

```
git clone https://github.com/thomassligon/GenSSI.git GenSSI
```

### 1.2.2 License Conditions

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## 1.3 Installation

If GenSSI was downloaded as a zip, it needs to be unpacked in a convenient directory. If GenSSI was obtained via cloning of the git repository, no further unpacking is necessary.

Models are generally stored in

```
GenSSI/Examples
```

but GenSSI should be able to find them in any directory that is in the MATLAB path.

When a model is analyzed GenSSI stores the results in

```
GenSSI/Results
```

To use GenSSI, start MATLAB and add the GenSSI directory to the MATLAB path. To add all toolbox directories to the MATLAB path, execute the MATLAB script

```
genssiStartup.m
```

To store the installation for further MATLAB session, the path can be saved via

```
savepath
```

## 2 Model Definition & Simulation

In the following we will give a detailed overview how to specify models in GenSSI and how to call the code for analyzing the model. We use the Goodwin oscillator as an example.

### 2.1 Model Definition

This manual will guide the user to specify models in MATLAB. For example implementations, see the models in the example directory.

#### 2.1.1 Header

The model definition needs to be defined as a function which returns a struct with all symbolic definitions and options.

```
function [model] = Goodwin()
```

#### 2.1.2 Name

Give the model a name.

```
model.Name = 'Goodwin';
```

The name will be used to create a subdirectory in the Results directory where the results of analysis will be stored.

#### 2.1.3 Derivatives

Set the number of derivatives to be calculated.

```
model.Nder = 8;
```

#### 2.1.4 Variables

Create the respective symbolic variables. The name of the symbolic variable can be chosen arbitrarily.

```
syms x1 x2 x3
```

Create the state vector containing all states:

```
model.X = [x1 x2 x3];
```

Define the number of variables.

```
model.Neq = 3;
```

### 2.1.5 Parameters

Create the respective symbolic variables. The name of the symbolic variable can be chosen arbitrarily.

```
syms p1 p2 p3 p4 p5 p6 p7 p8
```

Create the parameters vector of parameters to be considered for identifiability.

```
model.Par = [p1 p2 p3 p4 p5 p6 p7 p8];
```

Specify the number of parameters to be considered for identifiability.

```
model.Npar = 8;
```

### 2.1.6 Equations

Define the vector field of the model.

```
A1 = -p4*x1+p1/(p2+x3^p3);  
A2 = p5*x1-p6*x2;  
A3 = p7*x2-p8*x3;  
model.F=[A1 A2 A3];
```

### 2.1.7 Controls

Define the controls.

```
g1=0;  
g2=0;  
g3=0;  
model.G=[g1 g2 g3];
```

Define the number of controls.

```
model.Noc = 0;
```

The matrix G has as many columns as there are state variables and as many rows as there are inputs.

### 2.1.8 Observables

Define the observables.

```
h1 = x1;  
h2 = x2;  
h3 = x3;  
model.H = [h1 h2 h3];
```

Define the number of observables.

```
model.Nobs = 1;
```

### 2.1.9 Initial Conditions

Define the initial conditions. The initial conditions can be fixed numerical values or a function of model parameters.

```
model.IC = [0.3 0.9 1.3];
```

## 2.2 Model Analysis

The structural identifiability of the model can be analyzed by calling the MATLAB function `genssiMain`. The first parameter of `genssiMain` is the name of the model, and the second parameter is the format. If the format is absent, the model is assumed to be a function, as described above. If it is equal to 'mat', the model is assumed to be a MATLAB file with name `Modelname.mat` (e.g. `Goodwin.mat`) and containing the model struct.

```
genssiMain('Goodwin')
```

The function `genssiMain` will call the model function or load the `.mat` file, which puts the model struct in memory. After that, it will call all other GenSSI functions required to analyze the model. The results will be put into a directory created using the name of the model and the next available run number, for example `GenSSI/Results/Goodwin/run3`.

The results include a results file, with the name `'model_information.txt'`, and all identifiability tableaus created during analysis, in MATLAB format, for example `'Figure1.fig'`.

It is not necessary to analyze the identifiability tableaus unless you are looking for deeper insight into the structure of the model and its identifiability characteristics. They are described in more detail in:

- Chis, O.-T., J. R. Banga, et al. (2011). "Structural Identifiability of Systems Biology Models: A Critical Comparison of Methods." *PLoS ONE* 6(11): e27755.
- Balsa-Canto, E., A. Alonso, et al. (2010). "An iterative identification procedure for dynamic modeling of biochemical networks." *BMC Syst Biol* 4(1): 11.

The identifiability tableaus are binary versions of the Jacobian matrix, and help in determining identifiability of parameters during the analysis process. Columns consisting solely of zeros indicate that the respective parameter cannot be identified. Rows consisting solely of zeros provide no information and are deleted. Rows consisting of a single one indicate identifiability, and rows consisting of two or more ones indicate that there are relations that might be solved to provide identifiability.

The results file `'model_information.txt'` contains the main output of the identifiability analysis of GenSSI. It begins by documenting the primary features of the model and ends by stating which parameters are locally or globally identifiable. The middle part, which can be skipped during a first reading, documents the steps taken during analysis and which relations were solved to determine identifiability of individual parameters. Here is an example of the final part of this file for the Goodwin model used as an example in this reference manual:

```
-----> THE MODEL IS STRUCTURALLY LOCALLY IDENTIFIABLE

The structurally globally identifiable parameters are:

None

The structurally locally identifiable parameters are:

[      p1      p2      p4      p5      p6      p7      p8      ]

Report results elapsed time: 0.04445
Total elapsed time: 3.4703
```

## 2.3 Conversion Utilities

The GenSSI package also includes some functions for converting models from one format to another.

### 2.3.1 Convert to Polynomial Format

```
genssiToPolynomial(modelNameIn, modelNameOut)
```

`genssiToPolynomial` converts a model, expressed in terms of rational expressions, to pure polynomial format. This increases the number of state variables, but can sometimes significantly reduce the computational overhead for analyzing the model.

`modelNameIn`: name of model to be converted (string).

`modelNameOut`: name of model to be created (string).

### 2.3.2 Create Multi-Experiment Model

```
genssiMultiExperiment(modelNameIn, fileFormat, mExDef, modelNameOut)
```

`genssiMultiExperiment` converts a GenSSI model to a new GenSSI model based on a multi-experiment definition.

`modelNameIn`: the name of the input model (a string).

`fileFormat`: either 'function' (default), if the model is a MATLAB function, or 'mat', if the model is a .mat file.

`mExDef`: the name of a multi-experiment definition file (string).

`modelNameOut`: the name of the output model (a string).

GenSSI 2.0 supports structural identifiability analysis for systems with multiple experimental conditions. As the information content of an individual experiment is often limited, in most applications, multiple experiments are performed. These experiments usually differ in the experimental conditions, meaning that different initial conditions, perturbations or control inputs are used. This increases the amount of information and thereby the identifiability of the parameters.

To perform structural identifiability analysis for problems with multiple experimental conditions, GenSSI provides the MATLAB function `genssiMultiExperiment`, which generates a (multi-experiment) GenSSI model for a single experimental condition and a description of the changes in the experimental conditions.

To illustrate the functionality, we considered a model for mRNA transfection, accounting for translation and degradation. The model definition is:

```
function model = M1_1_U2()
    model.Name='M1_1_U1';
    syms m G d b kTL m0
    model.Nder=4;
    model.X=[m G];
    model.Neq=2;
    A1=-d*m;
    A2=0;
    model.F=[A1 A2];
    model.G=[0, kTL*m; ...
             0, -b*G];
    model.Noc=2;
    h1=G;
    model.H=[h1];
    model.Nobs=1;
    model.IC=[m0 0];
    model.P=[d b kTL m0];
    model.Par=[d b kTL m0];
    model.Npar=4;
end
```



The variables (model.X) are m (the level of mRNA) and G (the level of GFP, green fluorescent protein), of which only G is observed (model.H). The differential equations (model.F) define degradation of mRNA ( $-d \cdot m$ ), degradation of GFP ( $-b \cdot G$ ) and translation of mRNA to GFP ( $kTL \cdot m$ ). Note that translation and GFP degradation have been defined as controls (model.G).

Based on this model, we define a total of four experimental conditions, in the experiment definition function. The experiments are defined by modifying the controls and the initial conditions. The experiments are:

- 1) original configuration
- 2) change in transfection (m0) via IC: The initial concentration of mRNA is changed.
- 3) change in translation via control u1 = ulnh: The rate of translation is changed, for example by treating the cell with CHX (the antiseptic chlorhexidine).
- 4) change in GFP degradation via control u2 = uDeg: The rate of GFP degradation is changed, for example by using destabilized GFP (d2eGFP) instead of normal GFP (eGFP).

The experiment definition is:

```
function multiExp = M1_1_eDef4()
    multiExp.Name='M1_1_eDef4';
    syms d b kTL m0Exp1
    multiExp.Nexp=4;
    multiExp.U = [1,1;...
                  1,1;...
                  .5,1;...
                  1,.75];
    multiExp.IC = [m0Exp1,0,...
                  0.5*m0Exp1,0,...
                  m0Exp1,0,...
                  m0Exp1,0];
    multiExp.P=[d,b,kTL,m0Exp1];
    multiExp.Par=[d,b,kTL,m0Exp1];
end
```

The number of experiments is coded in multiExp.Nexp=4.

The variable multiExp.U defines the changes in the controls and the variable multiExp.IC defines the changes in the initial conditions. Both of these variables contain one row for each experiment and one column for each state variable. In the first experiment (original configuration), the controls are 1 and the initial mRNA concentration is m0Exp1. In the second experiment (change in transfection), the initial concentration of mRNA is changed. In the third experiment (change in translation), the rate of translation is changed by changing the value of the first control. In the fourth experiment (change in GFP degradation), the rate of GFP degradation is changed by changing the value of the second control.

The original model is converted to the multi-experiment model by means of this line of code:

```
genssiMultiExperiment('M1_1_U2','function','M1_1_eDef4','M1_1_ME4');
```

The result of the conversion is the following (multi-experiment) model:

```
function model = M1_1_ME4()
    syms mExp1 GExp1 mExp2 GExp2 mExp3 GExp3 mExp4 GExp4
    syms d b kTL m0Exp1
    model.Name = 'M1_1_ME4';
    model.Nder = 4;
    model.X = [mExp1,GExp1,mExp2,GExp2,mExp3,GExp3,mExp4,GExp4];
    model.Neq = 8;
    model.G = [0,0,0,0,0,0,0,0];
    model.Noc = 0;
    model.P = [d,b,kTL,m0Exp1];
    model.Par = [d,b,kTL,m0Exp1];
    model.Npar = 4;
    model.IC = [m0Exp1,0,m0Exp1/2,0,m0Exp1,0,m0Exp1,0];
    model.H = [GExp1,GExp2,GExp3,GExp4];
    model.Nobs = 4;
    model.F = [-d*mExp1,...
               kTL*mExp1 - GExp1*b,...
               -d*mExp2,...
               kTL*mExp2 - GExp2*b,...
               -d*mExp3,...
               (kTL*mExp3)/2 - GExp3*b,...
               -d*mExp4,...
               kTL*mExp4 - (3*GExp4*b)/4];
end
```

Based on the original 2 state variables and 4 experiments, we now have  $2 \cdot 4 = 8$  state variables (model.X).

## 2.3.3 Transform Model

```
genssiTransformation(modelNameIn, fileFormat, transDef, modelNameOut)
```

genssiTransformation converts a GenSSI model to a new GenSSI model based on a transformation definition.

modelNameIn: the name of the input model (a string).

fileFormat: either 'function' (default), if the model is a MATLAB function, or 'mat', if the model is a .mat file.

transDef: the name of a transformation definition file (string).

modelNameOut: the name of the output model (a string).

When we analyze equations for the purpose of determining identifiability, it is sometimes useful to make two changes. The first change is removing redundant equations, which can reduce the number of state variables and the number of parameters. The second change is rescaling the variables, which can reduce the number of parameters. Both of these changes are supported by genssiTransformation.

We begin with a model for mRNA, including translation and degradation. In contrast with the simpler model used for the multi-experiment conversion (above), this model involves mRNA degradation via the action of an enzyme. The model definition is:

```
function model = M2_1_Y1()
    model.Name='M2_1_Y1';
    syms m G E1 mE d1 d2 d3 b kTL m0 E0
    model.Nder=8;
    model.Neq=4;
    model.Npar=7;
    model.Noc=0;
    model.Nobs=1;
    model.X=[m G E1 mE];
    A1=-d1*m-d2*m*E1;
    A2=+kTL*m-b*G;
    A3=+d3*mE-d2*m*E1;
    A4=-d3*mE+d2*m*E1;
    model.F=[A1 A2 A3 A4];
    g1=0;g2=0;g3=0;g4=0;
    model.G=[g1 g2 g3 g4];
    h1=G;
    model.H=[h1];
    model.IC=[m0 0 E0 0];
    model.P=[d1 d2 d3 b kTL m0 E0];
    model.Par=[d1 d2 d3 b kTL m0 E0];
end
```

The state variables in this model (model.X) are mRNA (m), GFP (G), enzyme (E1), and the mRNA-enzyme complex (mE). We have used E1 as the name of the enzyme instead of E since there are cases where MATLAB will treat the symbolic variable E as e or exp(1). The differential equations show mRNA (m) decreasing due to degradation ( $-d1*m$ ) and decreasing due to complexation ( $-d2*m*E1$ ). GFP (G) increases due to translation ( $kTL*m$ ) and decreases due to complexation ( $-d2*m*E1$ ). The enzyme (E1) decreases due to complexation ( $-d2*m*E1$ ) and increases due to decomplexation ( $d3*mE$ ). The change in the complex (mE) is exactly the opposite of the change in the enzyme. As a result of this, we know that  $E1-E1(0)=-(mE-mE(0))$  or, since  $mE(0)=0$ ,  $E1-E0+mE=0$ . In addition, we know that the concentration of GFP always depends on the product of  $mRNA(0)*kTL$ , so we will be able to reduce the number of parameters by rescaling (dividing by  $m0$ ).

With these observations, we can create our transformation definition:

```

function transDef = M2_1_tDef()
    transDef.Name='M2_1_tDef';
    syms m G E1 mE m0 E0
    syms mdm0 Eldm0
    syms d1 d2 d3 b kTL
    syms d2tm0 kTLtm0 E0dm0
    transDef.Transformation = [m/m0;G;E1/m0];
    transDef.Constraint = [E1-E0+mE];
    transDef.P = [d1,d2tm0,d3,b,kTLtm0,E0dm0];
    transDef.Par = [d1,d2tm0,d3,b,kTLtm0,E0dm0];
    syms mnew Gnew E1new
    transDef.stateSubs = [mdm0,mnew;...
                        G,Gnew;...
                        Eldm0,E1new];
    transDef.parSubs = [d2*m0,d2tm0;...
                      kTL*m0,kTLtm0;...
                      E0/m0,E0dm0];
end

```

The transformation is defined by two variables. The first, `transDef.Transformation`, defines the rescaling. It contains one entry for each element of the final state vector. Since we are converting a model with 4 state variables to 3, this contains 3 elements. The second part of the definition is the constraint, `transDef.Constraint`. This will be equated to zero during the transformation, so it is  $E1 - E0 + mE = 0$ , or, equivalently,  $E1 - E1(0) = -(mE - mE(0))$ . The variable `transDef.Constraint` can contain multiple constraints, separated by a semicolon. Finally, there are two optional definitions of substitutions. They contain a variable number of rows, each of which is a substitution, or change of names. During the transformation process, new variables are created for the state vector and the parameters, and the names are changed via the rules `"*"->"t"` (for "times") and `"/"->"d"` (for "divided by"). These names can be considered as suggestions for the new names, and the user can override them with the `stateSubs` and `parSubs` definitions. For example, `mdm0` is replaced by `mnew` in the state vector, and `d2*m0` is replaced by `d2tm0` in the parameters. It is considered good practice to leave these 2 definitions out the first time the transformation is run, and then add them in later in order to gain more control over the naming.

This transformation is started by running the following line of code:

```
genssiTransformation('M2_1_Y1','function','M2_1_tDef','M2_2_test');
```

The result of the transformation is the following new model:

```

function model = M2_2_test()
    syms mnew Gnew E1new
    syms d1 d2tm0 d3 b kTLtm0 E0dm0
    model.Name = 'M2_2_test';
    model.Nder = 8;
    model.X = [mnew,Gnew,E1new];
    model.Neq = 3;
    model.G = [0,0,0,0];
    model.Noc = 0;
    model.P = [d1,d2tm0,d3,b,kTLtm0,E0dm0];
    model.Par = [d1,d2tm0,d3,b,kTLtm0,E0dm0];
    model.Npar = 6;
    model.IC = [1,0,E0dm0];
    model.H = [Gnew];
    model.Nobs = 1;
    model.F = [- d1*mnew - E1new*d2tm0*mnew,...
              kTLtm0*mnew - Gnew*b,...
              (E0*d3)/m0 - E1new*d2tm0*mnew - E1new*d3];
end

```

In this transformed model, the new state variables are `mnew`, `Gnew`, and `E1new`, based on the definition `transDef.stateSubs`.

### 2.3.4 Export to AMICI Format

```
genssiToAmici(modelNameIn, modelNameOut)
```

genssiToAMICI converts a GenSSI model to AMICI format. The AMICI package uses Sundials CVODES and IDAS to efficiently solve ODEs from within MATLAB. It is available at <https://github.com/AMICI-developer/AMICI>.

modelNameIn: name of the GenSSI model (string).

modelNameOut: name of the AMICI model (string).

This is an important feature, since AMICI supports SBML import, thereby effectively providing GenSSI with an SBML import.

Note: There are limitations to this conversion. The GenSSI model contains a list of parameters to be considered for analysis, but AMICI needs a "sym" statement containing a list of all parameters used by the model. It may be necessary to manually edit the AMICI model after conversion. In order to avoid this, the GenSSI model can contain a variable model.P, containing all parameters (model.Par only contains the parameters to be considered for identifiability).

### 2.3.5 Import from AMICI Format (and SBML Models)

```
genssiFromAmici(modelNameIn, modelNameOut)
```

genssiFromAMICI converts an AMICI model to GenSSI format.

modelNameIn: name of the AMICI model (string).

modelNameOut: name of the GenSSI model (string).

Note: There are limitations to this conversion. The AMICI model contains a list of all parameters used by the model, but GenSSI needs a list of parameters to be considered for analysis. In addition, the GenSSI model created by the conversion contains default values for parameters such as the number of derivatives. It may be necessary to manually edit the GenSSI model after conversion.

### 2.3.6 Convert from Model Structure to Model Source Format

```
genssiStructToSource(model)
```

```
amiciStructToSource(model)
```

genssiStructToSource reads the GenSSI model struct and converts it to source format (MATLAB function definition), and amiciStructToSource does the same for AMICI models. In general, the source format is more convenient for smaller models, since it is easier to modify, but the struct format, typically saved in a MATLAB file (e.g. Goodwin.mat) is more convenient for large models, since it does not require editing of long lines of code.

model: model definition (struct).

## 3 Code Organization

In the following we will briefly outline how the GenSSI code is organized. For a more detailed description we refer the reader to the documentation of the individual functions.

### 3.1 Directory Structure

The main, or root, directory, which we refer to as GenSSI, contains most of the GenSSI functions. In addition, the following subdirectories are used:

- GenSSI/Auxiliary contains some auxiliary functions, such as `genssiRemoveZeroRows`.
- GenSSI/Examples contains a collection of model definitions.
- GenSSI/Results contains the results of analysis.
- GenSSI/Docu contains tools for creating the GenSSI documentation, as well as input and output of that process.
- GenSSI/Docu/config contains configuration files for the documentation tools.
- GenSSI/Docu/input contains input for document creation, including `.dox` files.
- GenSSI/Docu/output contains

### 3.2 Document Creation

New versions of the documentation are created with the help of:

- `MatlabDocMaker.m` (in GenSSI/Docu)
- `mtoc++` (needs to be installed and available via the path variable)
- Doxygen (needs to be installed and available via the path variable)
- LaTeX (needs to be installed and available via the path variable)
- Graphviz (needs to be installed and available via the path variable)
- Ghostscript (needs to be installed and available via the path variable)

The documentation configuration is changed by editing the files in the GenSSI/Docu/config directory and by running

```
MatlabDocMaker.setup
```

A new version of the documentation is created by calling

```
MatlabDocMaker.create('latex',true)
```

This results in an html version of the guide (`index.html` and many other files in GenSSI/Docu/output), and a pdf version (`refman.pdf` in GenSSI/Docu/output/latex).

## 4 File Documentation

### 4.1 `amiciStructToSource.m` File Reference

`amiciStructToSource` converts a model definition (`struct`) to a source format (MATLAB function file) and saves the results in the examples directory.

## Functions

- `noret::substitute amiciStructToSource` (`matlabtypesubstitute model`)  
*amiciStructToSource converts a model definition (struct) to a source format (MATLAB function file) and saves the results in the examples directory.*

### 4.1.1 Function Documentation

#### 4.1.1.1 `noret::substitute amiciStructToSource ( matlabtypesubstitute model )`

## Parameters

<i>model</i>	model definition (struct)
--------------	---------------------------

## Return values

<i>model</i>	void
--------------	------

Definition at line 17 of file amiciStructToSource.m.

Here is the caller graph for this function:



## 4.2 genssiComputeLieDerivatives.m File Reference

`genssiComputeLieDerivatives` computes Lie derivatives of the output functions (`model.H`), the state vectors (`model.X`), and the initial conditions (`model.IC`) with respect to the equations (`model.F`) and controls (`model.G`)

## Functions

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiComputeLieDerivatives` (`matlabtypesubstitute model`, `matlabtypesubstitute options`)  
*genssiComputeLieDerivatives computes Lie derivatives of the output functions (`model.H`), the state vectors (`model.X`), and the initial conditions (`model.IC`) with respect to the equations (`model.F`) and controls (`model.G`)*
- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > mtoc\_subst\_genssiComputeLieDerivatives\_m\_tsbus\_cotm\_jacRank` (`matlabtypesubstitute LDer`, `matlabtypesubstitute rankVector`, `matlabtypesubstitute order`, `matlabtypesubstitute model`, `matlabtypesubstitute options`)  
*jacRank computes jacobian and rank, producing output text*

### 4.2.1 Function Documentation

- #### 4.2.1.1 `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiComputeLieDerivatives ( matlabtypesubstitute model, matlabtypesubstitute options )`

## Parameters

<i>model</i>	model definition (struct)
<i>options</i>	processing options (struct)

## Return values

<i>options</i>	processing options (struct)
<i>VectorLieDerivatives</i>	a vector of all Lie derivatives

Definition at line 17 of file genssiComputeLieDerivatives.m.

Here is the call graph for this function:



Here is the caller graph for this function:



4.2.1.2 mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > >  
 mtoc\_subst\_genssiComputeLieDerivatives\_m\_tsbust\_cotm\_jacRank ( matlabtypesubstitute *LDer*, matlabtypesubstitute  
*rankVector*, matlabtypesubstitute *order*, matlabtypesubstitute *model*, matlabtypesubstitute *options* )

## Parameters

<i>LDer</i>	model definition (struct)
<i>rankVector</i>	vector of ranks (for results)
<i>order</i>	for output text, computing derivatives of order
<i>model</i>	model definition
<i>options</i>	processing options (struct)

## Return values

<i>rankFull</i>	boolean, true if rank is full
<i>rankVector</i>	vector of ranks (for results)

Definition at line 106 of file genssiComputeLieDerivatives.m.



### 4.3 genssiComputeReducedTableau.m File Reference

genssiComputeReducedTableau computes reduced tableaus of the jacobian by eliminating rows and columns where solutions to relationships can found or excluded.

#### Functions

- mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiComputeReducedTableau](#) (matlabtypesubstitute model, matlabtypesubstitute results, matlabtypesubstitute VectorLieDerivatives, matlabtypesubstitute JacParam, matlabtypesubstitute options)

*genssiComputeReducedTableau computes reduced tableaus of the jacobian by eliminating rows and columns where solutions to relationships can found or excluded.*

#### 4.3.1 Function Documentation

4.3.1.1 mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiComputeReducedTableau](#) ( matlabtypesubstitute *model*, matlabtypesubstitute *results*, matlabtypesubstitute *VectorLieDerivatives*, matlabtypesubstitute *JacParam*, matlabtypesubstitute *options* )

#### Parameters

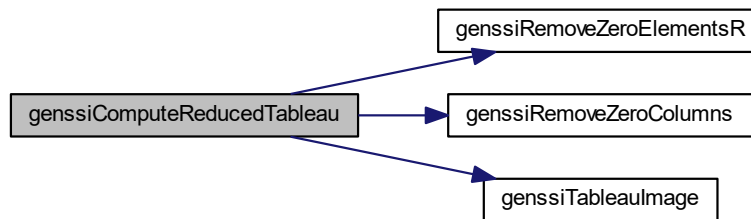
<i>model</i>	model definition (struct)
<i>results</i>	results of compute tableau (symbolic matrix)
<i>VectorLieDerivatives</i>	vector of Lie derivatives (symbolic array)
<i>JacParam</i>	jacobian with respect to parameters (symbolic matrix)
<i>options</i>	options (struct)

#### Return values

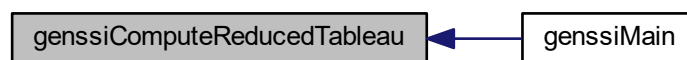
<i>options</i>	options (struct)
<i>results</i>	results of compute tableau (symbolic matrix)
<i>RJacParam01</i>	reduced tableau (binary matrix)
<i>ECC</i>	equations (symbolic matrix)
<i>rParam</i>	reduced list of parameters (symbolic array)

Definition at line 17 of file genssiComputeReducedTableau.m.

Here is the call graph for this function:



Here is the caller graph for this function:



## 4.4 genssiComputeTableau.m File Reference

`genssiComputeTableau` computes the tableau based on the jacobian of the Lie derivatives.

### Functions

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiComputeTableau (matlabtypesubstitute model, matlabtypesubstitute VectorLieDerivatives, matlabtypesubstitute options)`

*genssiComputeTableau computes the tableau based on the jacobian of the Lie derivatives.*

### 4.4.1 Function Documentation

- #### 4.4.1.1 `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiComputeTableau ( matlabtypesubstitute model, matlabtypesubstitute VectorLieDerivatives, matlabtypesubstitute options )`

### Parameters

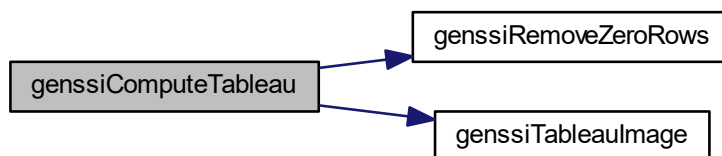
<i>model</i>	model definition (struct)
<i>VectorLieDerivatives</i>	vector of Lie derivatives (symbolic array)
<i>options</i>	options (struct)

## Return values

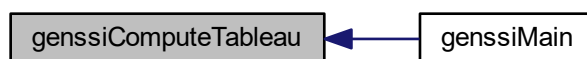
<i>options</i>	options (struct)
<i>results</i>	results of calculations (struct)
<i>JacParam</i>	jacobian of the Lie derivatives with respect to the parameters (symbolic matrix)

Definition at line 17 of file genssiComputeTableau.m.

Here is the call graph for this function:



Here is the caller graph for this function:



## 4.5 genssiFromAmici.m File Reference

GenSsiFromAmici converts an AMICI model to a GenSSI model and puts the results into the examples directory.

### Functions

- `mlhsInnerSubst< matlabtypesubstitute > genssiFromAmici (matlabtypesubstitute modelNameIn, matlabtypesubstitute modelNameOut)`

*GenSsiFromAmici converts an AMICI model to a GenSSI model and puts the results into the examples directory.*

#### 4.5.1 Function Documentation

- ##### 4.5.1.1 `mlhsInnerSubst< matlabtypesubstitute > genssiFromAmici ( matlabtypesubstitute modelNameIn, matlabtypesubstitute modelNameOut )`

## Parameters

<i>modelNameIn</i>	name of the AMICI model (string)
<i>modelNameOut</i>	name of the GenSSI model (string)

## Return values

<i>modelNameOut</i>	void
---------------------	------

Definition at line 17 of file `genssiFromAmici.m`.

Here is the call graph for this function:

4.6 `genssiMain.m` File Reference

`genssiMain` is the main function of GenSSI. It reads a model and calls all other functions necessary for analyzing the model.

## Functions

- `mlhsInnerSubst` < `matlabtypesubstitute` > [genssiMain](#) (`matlabtypesubstitute` `varargin`)  
*genssiMain* is the main function of GenSSI. It reads a model and calls all other functions necessary for analyzing the model.

## 4.6.1 Function Documentation

4.6.1.1 `mlhsInnerSubst` < `matlabtypesubstitute` > `genssiMain` ( `matlabtypesubstitute` *varargin* )

## Parameters

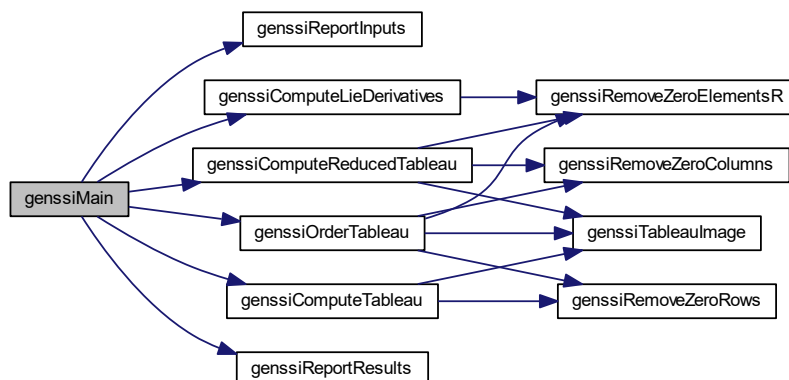
<i>varargin</i>	generic input arguments  1 genssiMain ( modelName, fileFormat, model, mat )  <i>Required Parameters for varargin:</i> <ul style="list-style-type: none"><li>• modelName the name of the model to be analyzed (a string)</li><li>• fileFormat the format of the model file</li><li>• model (default) if the model is a function file (e.g. Goodwin.m)</li><li>• mat if the model is a MATLAB file (e.g. Goodwin.mat)</li></ul>
-----------------	-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

## Return values

<i>varargout</i>	generic output arguments
<i>options</i>	struct containing options

Definition at line 17 of file genssiMain.m.

Here is the call graph for this function:



## 4.7 genssiMultiExperiment.m File Reference

genssiMultiExperiment converts a GenSSI model to a new GenSSI model based on a multi-experiment definition.

## Functions

- mlhsInnerSubst< matlabtypesubstitute > [genssiMultiExperiment](#) (matlabtypesubstitute varargin)  
*genssiMultiExperiment converts a GenSSI model to a new GenSSI model based on a multi-experiment definition.*

### 4.7.1 Function Documentation

#### 4.7.1.1 mlhsInnerSubst< matlabtypesubstitute > genssiMultiExperiment ( matlabtypesubstitute varargin )

## Parameters

<i>varargin</i>	<p>generic input arguments</p> <pre>1 genssiMultiExperiment ( modelNameIn, fileFormat, mExDef, modelNameOut )</pre> <p><i>Required Parameters for varargin:</i></p> <ul style="list-style-type: none"> <li>• modelNameIn the name of the input model (a string)</li> <li>• fileFormat either <code>function</code> (default), if the model is a MATLAB function, or <code>mat</code>, if the model is a <code>.mat</code> file</li> <li>• mExDef the name of a multi-experiment definition file (string)</li> <li>• modelNameOut the name of the output model (a string)</li> </ul>
-----------------	-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

## Return values

<i>varargout</i>	generic output arguments
------------------	--------------------------

Definition at line 17 of file genssiMultiExperiment.m.

Here is the call graph for this function:



## 4.8 genssiOrderTableau.m File Reference

`genssiOrderTableau` orders tableaus, searches for new opportunities to eliminate rows or columns by solving equations, and creates new (reduced) tableaus.

## Functions

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiOrderTableau` (matlabtypesubstitute model, matlabtypesubstitute results, matlabtypesubstitute RJacParam01, matlabtypesubstitute ECC, matlabtypesubstitute rParam, matlabtypesubstitute options)

*genssiOrderTableau orders tableaus, searches for new opportunities to eliminate rows or columns by solving equations, and creates new (reduced) tableaus.*

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > mtoc\_subst\_genssiOrderTableau\_m` (matlabtypesubstitute Param, matlabtypesubstitute Param\_local, matlabtypesubstitute global\_ident\_par, matlabtypesubstitute Mat\_index, matlabtypesubstitute RJacparam\_new, matlabtypesubstitute RJacParam01\_nonzero\_rows, matlabtypesubstitute sum\_RJacParam01\_nonzero\_rows\_t, matlabtypesubstitute ECC, matlabtypesubstitute ECC\_new, matlabtypesubstitute options)

*displayRelevantParameters displays relevant parameters*

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >> mtoc\_subst\_genssiOrderTableau\_m\_tsbust\_cotm\_displayReducedTableau (matlabtypesubstitute ECC_remaining, matlabtypesubstitute Param_local, matlabtypesubstitute Param_display, matlabtypesubstitute global_ident_par, matlabtypesubstitute display_tableau_RJacparam_new, matlabtypesubstitute number_fig, matlabtypesubstitute options)`

*displayReducedTableau displays reduced tableaus*

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >> mtoc\_subst\_genssiOrderTableau\_m\_tsbust\_cotm\_displayRemainingParameters (matlabtypesubstitute ECC_remaining, matlabtypesubstitute Param_local, matlabtypesubstitute Param_remaining, matlabtypesubstitute global_ident_par, matlabtypesubstitute display_tableau_RJacparam_new, matlabtypesubstitute row_index_1, matlabtypesubstitute tableau_for_second_reduced_tableau, matlabtypesubstitute parameters_for_second_reduced_tableau, matlabtypesubstitute number_fig, matlabtypesubstitute options)`

*displayReducedTableau displays the remaining parameters*

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >> mtoc\_subst\_genssiOrderTableau\_m\_tsbust\_cotm\_solveRemPar (matlabtypesubstitute ECC, matlabtypesubstitute Param, matlabtypesubstitute Param_local, matlabtypesubstitute global_ident_par)`

*solveRemPar solves the remaining parameters*

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >> mtoc\_subst\_genssiOrderTableau\_m\_tsbust\_cotm\_getIndexOfDuplicateParams (matlabtypesubstitute ECC, matlabtypesubstitute RJacParam01_nonzero_rows)`

*getIndexOfDuplicateParams gets index of duplicate parameters*

#### 4.8.1 Function Documentation

- 4.8.1.1 `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >> genssiOrderTableau ( matlabtypesubstitute model, matlabtypesubstitute results, matlabtypesubstitute RJacParam01, matlabtypesubstitute ECC, matlabtypesubstitute rParam, matlabtypesubstitute options )`

##### Parameters

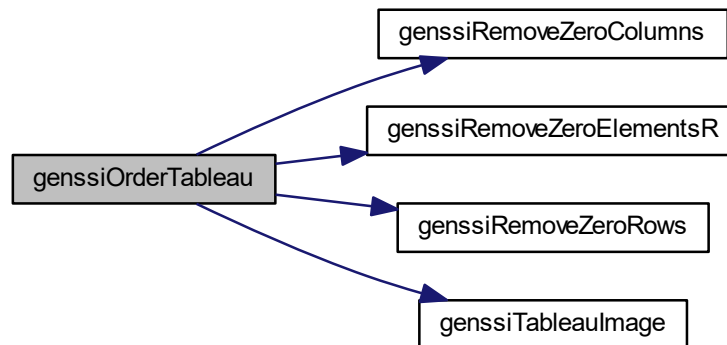
<i>model</i>	model definition (struct)
<i>results</i>	results of previous steps (struct)
<i>RJacParam01</i>	reduced tableau, i.e. binary form of jacobian of the Lie derivatives with respect to the parameters (binary matrix)
<i>ECC</i>	equations (symbolic array)
<i>rParam</i>	reduced list of parameters (symbolic array)
<i>options</i>	options (struct)

##### Return values

<i>options</i>	options (struct)
<i>results</i>	results of previous steps (struct)

Definition at line 17 of file `genssiOrderTableau.m`.

Here is the call graph for this function:



Here is the caller graph for this function:



## 4.9 `genssiRemoveZeroColumns.m` File Reference

`genssiRemoveZeroColumns` removes zero columns from a matrix

### Functions

- `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiRemoveZeroColumns (matlabtypesubstitute matrixIn)`  
*genssiRemoveZeroColumns removes zero columns from a matrix*

### 4.9.1 Function Documentation

4.9.1.1 `mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiRemoveZeroColumns ( matlabtypesubstitute matrixIn )`

### Parameters

<i>matrixIn</i>	input (matrix)
-----------------	----------------

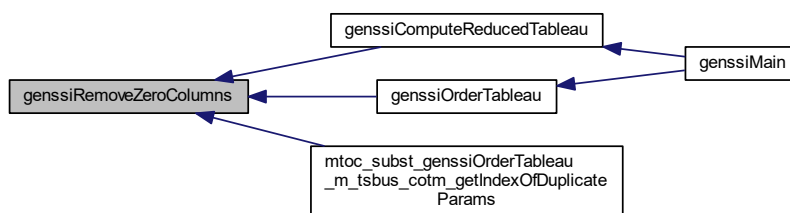


## Return values

<i>matrixOut</i>	output (matrix)
<i>keepBoolean</i>	boolean vector of indices kept (array)
<i>keepIndex</i>	vector of indices kept (array)

Definition at line 17 of file genssiRemoveZeroColumns.m.

Here is the caller graph for this function:



#### 4.10 genssiRemoveZeroElementsC.m File Reference

genssiRemoveZeroElements removes zero columns from a row vecor

## Functions

- mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiRemoveZeroElementsC](#) (matlabtypesubstitute vectorIn)  
*genssiRemoveZeroElements removes zero columns from a row vecor*

##### 4.10.1 Function Documentation

- ##### 4.10.1.1 mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > genssiRemoveZeroElementsC ( matlabtypesubstitute vectorIn )

## Parameters

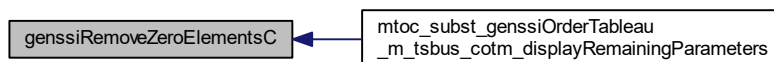
<i>vectorIn</i>	input (array)
-----------------	---------------

## Return values

<i>vectorOut</i>	output (array)
<i>keepBoolean</i>	boolean vector of indices kept (array)
<i>keepIndex</i>	vector of indices kept (array)

Definition at line 17 of file genssiRemoveZeroElementsC.m.

Here is the caller graph for this function:



## 4.11 genssiRemoveZeroElementsR.m File Reference

genssiRemoveZeroElements removes zero columns from a row vecor

### Functions

- mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiRemoveZeroElementsR](#) (matlabtypesubstitute vectorIn)  
*genssiRemoveZeroElements removes zero columns from a row vecor*

### 4.11.1 Function Documentation

4.11.1.1 mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiRemoveZeroElementsR](#) ( matlabtypesubstitute *vectorIn* )

### Parameters

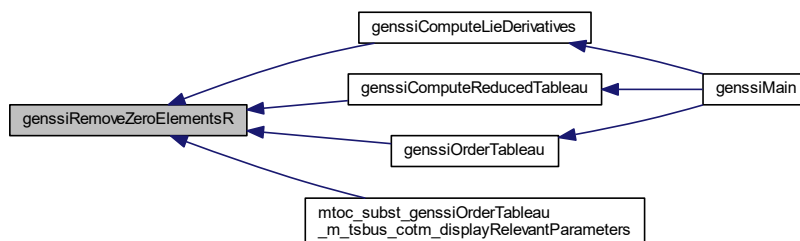
<i>vectorIn</i>	input (array)
-----------------	---------------

### Return values

<i>vectorOut</i>	output (array)
<i>keepBoolean</i>	boolean vector of indices kept (array)
<i>keepIndex</i>	vector of indices kept (array)

Definition at line 17 of file genssiRemoveZeroElementsR.m.

Here is the caller graph for this function:



## 4.12 genssiRemoveZeroRows.m File Reference

genssiRemoveZeroRows removes zero rows from a matrix

### Functions

- mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiRemoveZeroRows](#) (matlabtypesubstitute matrixIn)  
*genssiRemoveZeroRows removes zero rows from a matrix*

### 4.12.1 Function Documentation

4.12.1.1 mlhsSubst< mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute >,mlhsInnerSubst< matlabtypesubstitute > > [genssiRemoveZeroRows](#) ( matlabtypesubstitute *matrixIn* )

### Parameters

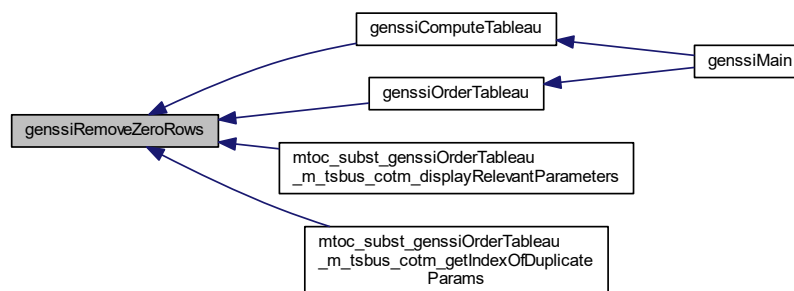
<i>matrixIn</i>	input (matrix)
-----------------	----------------

### Return values

<i>matrixOut</i>	output (matrix)
<i>keepBoolean</i>	boolean vector of indices kept (array)
<i>keepIndex</i>	vector of indices kept (array)

Definition at line 17 of file genssiRemoveZeroRows.m.

Here is the caller graph for this function:



## 4.13 genssiReportInputs.m File Reference

genssiReportInputs reports inputs, i.e. model definition.

### Functions

- mlhsInnerSubst< matlabtypesubstitute > [genssiReportInputs](#) (matlabtypesubstitute model, matlabtypesubstitute options)  
*genssiReportInputs reports inputs, i.e. model definition.*

### 4.13.1 Function Documentation

#### 4.13.1.1 mlhsInnerSubst< matlabtypesubstitute > genssiReportInputs ( matlabtypesubstitute *model*, matlabtypesubstitute *options* )

#### Parameters

<i>model</i>	model definition (struct)
<i>options</i>	options (struct)

#### Return values

<i>options</i>	options (struct)
----------------	------------------

Definition at line 17 of file genssiReportInputs.m.

Here is the caller graph for this function:



#### 4.14 genssiReportResults.m File Reference

genssiReportResults reports the results of the analysis.

##### Functions

- mlhsInnerSubst< matlabtypesubstitute > [genssiReportResults](#) (matlabtypesubstitute model, matlabtypesubstitute results, matlabtypesubstitute options)  
*genssiReportResults reports the results of the analysis.*

##### 4.14.1 Function Documentation

4.14.1.1 mlhsInnerSubst< matlabtypesubstitute > genssiReportResults ( matlabtypesubstitute *model*, matlabtypesubstitute *results*, matlabtypesubstitute *options* )

##### Parameters

<i>model</i>	model definition (struct)
<i>results</i>	results of previous steps (struct)
<i>options</i>	options (struct)

##### Return values

<i>options</i>	options (struct)
----------------	------------------

Definition at line 17 of file genssiReportResults.m.

Here is the caller graph for this function:



## 4.15 `genssiStartup.m` File Reference

`genssiStartup` adds all paths required for GenSSI. It should be called at the beginning of a session.

### Functions

- `noret::substitute genssiStartup ()`  
*`genssiStartup` adds all paths required for GenSSI. It should be called at the beginning of a session.*

## 4.16 `genssiStructToSource.m` File Reference

`genSsiStructToSource` converts a model definition (struct) to a source format (Matlab function file) and saves the results in the examples directory.

### Functions

- `noret::substitute genssiStructToSource (matlabtypesubstitute model)`  
*`genSsiStructToSource` converts a model definition (struct) to a source format (Matlab function file) and saves the results in the examples directory.*

### 4.16.1 Function Documentation

#### 4.16.1.1 `noret::substitute genssiStructToSource ( matlabtypesubstitute model )`

#### Parameters

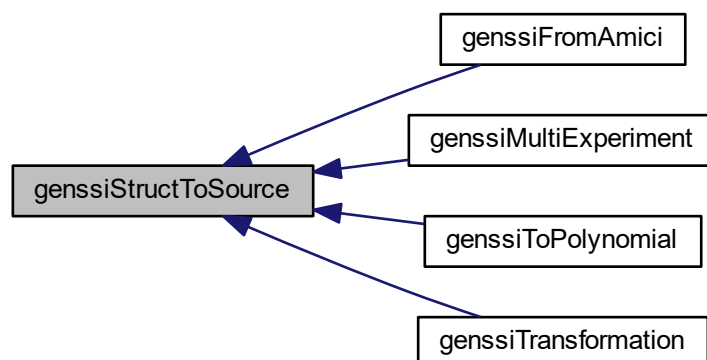
<i>model</i>	model definition (struct)
--------------	---------------------------

#### Return values

<i>model</i>	void
--------------	------

Definition at line 17 of file `genssiStructToSource.m`.

Here is the caller graph for this function:



## 4.17 genssiTableauImage.m File Reference

genssiTableauImage displays an identifiability tableau

### Functions

- noret::substitute [genssiTableauImage](#) (matlabtypesubstitute *figNum*, matlabtypesubstitute *tabMat*, matlabtypesubstitute *paramDisplay*, matlabtypesubstitute *options*)  
*genssiTableauImage displays an identifiability tableau*

### 4.17.1 Function Documentation

4.17.1.1 noret::substitute genssiTableauImage ( matlabtypesubstitute *figNum*, matlabtypesubstitute *tabMat*, matlabtypesubstitute *paramDisplay*, matlabtypesubstitute *options* )

### Parameters

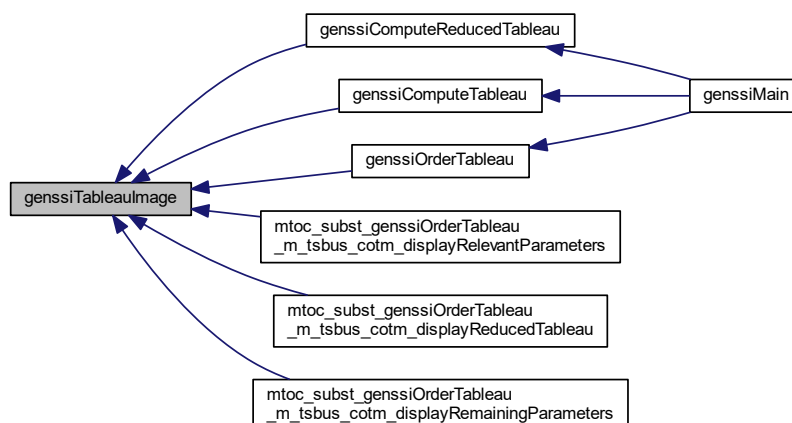
<i>figNum</i>	figure number
<i>tabMat</i>	matrix containing tableau
<i>paramDisplay</i>	parameter vector
<i>options</i>	options

### Return values

<i>options</i>	void
----------------	------

Definition at line 17 of file genssiTableauImage.m.

Here is the caller graph for this function:



## 4.18 genssiToAmici.m File Reference

GenSsiToAmici converts a GenSSI model to AMICI model format and saves the results in the examples directory.

### Functions

- `mlhsInnerSubst< matlabtypesubstitute > genssiToAmici (matlabtypesubstitute modelNameIn, matlabtypesubstitute modelNameOut)`

*GenSsiToAmici converts a GenSSI model to AMICI model format and saves the results in the examples directory.*

### 4.18.1 Function Documentation

#### 4.18.1.1 `mlhsInnerSubst< matlabtypesubstitute > genssiToAmici ( matlabtypesubstitute modelNameIn, matlabtypesubstitute modelNameOut )`

##### Parameters

<i>modelNameIn</i>	name of the GenSSI model (string)
<i>modelNameOut</i>	name of the AMICI model (string)

##### Return values

<i>modelNameOut</i>	void
---------------------	------

Definition at line 17 of file genssiToAmici.m.



Here is the call graph for this function:



## 4.19 genssiToPolynomial.m File Reference

`genssiToPolynomial` converts a GenSSI model to polynomial form. It reads the input model, converts to polynomial form, and creates an output model as a MATLAB function `modelNameOut.m` and as a MATLAB file `modelNameOut.mat`, both in the Examples folder.

### Functions

- `mlhsInnerSubst< matlabtypesubstitute > genssiToPolynomial` (`matlabtypesubstitute modelNameIn`, `matlabtypesubstitute modelNameOut`)

*genssiToPolynomial converts a GenSSI model to polynomial form. It reads the input model, converts to polynomial form, and creates an output model as a MATLAB function `modelNameOut.m` and as a MATLAB file `modelNameOut.mat`, both in the Examples folder.*

### 4.19.1 Function Documentation

#### 4.19.1.1 `mlhsInnerSubst< matlabtypesubstitute > genssiToPolynomial ( matlabtypesubstitute modelNameIn, matlabtypesubstitute modelNameOut )`

##### Parameters

<code>modelNameIn</code>	the name of the input model (a string)
<code>modelNameOut</code>	the name of the output model (a string)

##### Return values

<code>modelNameOut</code>	void
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Definition at line 17 of file `genssiToPolynomial.m`.

Here is the call graph for this function:



## 4.20 `genssiTransformation.m` File Reference

`genssiTransformation` converts a GenSSI model to a new GenSSI model based on a transformation definition.

### Functions

- `mlhsInnerSubst< matlabtypesubstitute > genssiTransformation (matlabtypesubstitute varargin)`  
*genssiTransformation converts a GenSSI model to a new GenSSI model based on a transformation definition.*

### 4.20.1 Function Documentation

#### 4.20.1.1 `mlhsInnerSubst< matlabtypesubstitute > genssiTransformation ( matlabtypesubstitute varargin )`

### Parameters

<i>varargin</i>	<p>generic input arguments</p> <pre>1 genssiTransformation ( modelNameIn, fileFormat, transDef, modelNameOut )</pre> <p><i>Required Parameters for varargin:</i></p> <ul style="list-style-type: none"> <li>• <code>modelNameIn</code> the name of the input model (a string)</li> <li>• <code>fileFormat</code> either <code>function</code> (default), if the model is a MATLAB function, or <code>mat</code>, if the model is a <code>.mat</code> file</li> <li>• <code>transDef</code> the name of a transformation definition file (string)</li> <li>• <code>modelNameOut</code> the name of the output model (a string)</li> </ul>
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### Return values

<i>varargout</i>	generic output arguments
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Definition at line 17 of file `genssiTransformation.m`.

Here is the call graph for this function:



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