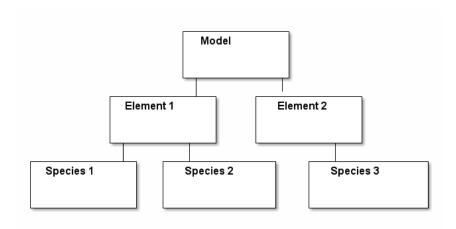
ESBMTK Quick Start Guide

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1 Overview

ESBMTK provides a couple of classes which are used to define a model. The classes are arranged in a hierarchical manner, starting with the model class. The model class (or object), set's global parameters like the model name, the time step etc. Next comes one or more element objects which define basic element properties. Each element can have one or more species. Note that these classes specify units, however at present, there is incomplete support for unit conversions. So it is up to the author to ensure proper unit conversions. It is therefore best, to use the same units throughout.

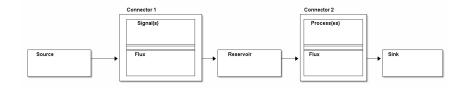


At present, these classes only specify the isotopic reference ratios, and plot labels.

Next comes the source and sink class, which simply specify the name and species, followed by reservoir object which specifies things like reservoir name, reservoir size, reservoir species etc. Each reservoir can only have one element. This is counter intuitive since we would think of the ocean as single reservoir with many elements. However, the model only attempts to track the transfer of mass between reservoirs, for a given element. For multi element models, you need to setup reservoirs and connections for each element.

Sources, sinks, and reservoirs are connected through fluxes, and fluxes are either forced by signals, or affected by processes. Most processes can be derived implicitly from the way we connect reservoirs (see below), however signal must be specified explicitly. It is thus best to define these first (see the worked example below).

The connection between a source and a sink (or two reservoirs) is handled by the connection class. This class will create the necessary fluxes, and where possible add processes. Fluxes and processes are also implemented as objects.

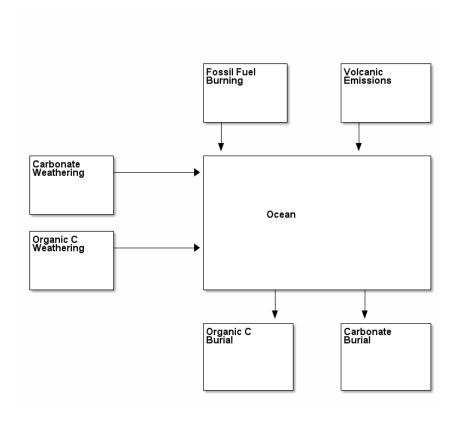


Each connector object can have more than one signal or process (or a mixture of signals and processes). Each reservoir can have more than one connector object.

1.1 A worked example

In the following example we will set up a simple carbon cycle model. The data forcing the anthropogenic carbon flux will be read from a csv file. Interaction with external data is handled through the external data object which allows to integrate external data into the model framework. It can then be used to generate a signal, or it can be associated with a reservoir so that the data is plotted with the reservoir data.

The model consists of four sources, two sinks, and one reservoir



1.2 Setting up the model

We need to load all required libraries and all classes we want to use. Interaction with the model classes is done through keyword/value pairs. Use help() to inquire about the supported keyword value pairs.

ESBMTK is unit aware. The units are used to map all input data to internal units. The type of internal units needs to specified when creating the model object. The time unit is derived from the timestep variable. I.e., if the timestep is given in seconds, all other time related input will be mapped to seconds. Similarly you have to define the base mass unit. Typically, this will be moles, but other units like grams etc can also be used. At present ESBMTK cannot convert between different types of mass units (e.g., kg to moles). The usual prefixes like kilo, mega, milli etc are recognized. Volume units like 1 or m**3 are recognized as well. ESBMTK also defines the sverdrup ("Sv")

Once the input units are mapped to base units specified by the model object, all data will be reported in the base units. The only exception is the object.plot() method which will transform the data back into the original unit. In other words, if your timestep is in years, but you specify your endtime in kyrs, the time axis will be plotted in kyrs. Similarly for all other data, with the exception of the isotope delta values.

```
from esbmtk import Model, Element, Species, Reservoir
   from esbmtk import Signal, Connect, Source, Sink, Flux
   from esbmtk import ExternalData
   # create model
5
   Model(
6
       name="C_Cycle",
                            # model name
7
        stop="200 yrs",
                            # end time of model
8
       timestep=" 1 yr",
                            # time unit
       mass unit = "mol",
                           # mass unit
10
       volume_unit = "1", # volume unit
11
   )
12
```

1.3 Declare elements and species

We register the elements(s) with the model by providing the model name. Note that this is not a string, but the model handle which is derived from the model name in the model definition above. We use the element handle in a similar way to register the species with an element.

```
# Element properties
   Element(
2
       name="C",
                                    # Element Name
3
       model=C_Cycle,
                                    # Model handle
4
       mass_unit="mmol",
                                    # base mass unit
       li_label="C^{12$S",
                                    # Name of light isotope
6
       hi_label="C^{13}$S",
                                    # Name of heavy isotope
7
        d_label="$\delta^{13}$C",
                                         # Name of isotope delta
8
                                    # Isotope scale. End of plot labels
        d_scale="VPDB",
       r=0.0112372, # VPDB C13/C12 ratio https://www-pub.iaea.org/MTCD/publications/PDF/te_825
10
   )
11
12
   # add species
13
   Species(name="CO2", element=C) # Name & element handle
```

```
15 Species(name="DIC", element=C)
16 Species(name="OM", element=C)
17 Species(name="CaCO3", element=C)
```

You can do this explicitly as in the example above, or use the builtin definition by providing the element keyword in the model definition. This keyword takes and element name, and causes the model to initialize an Element object and a variety of Species objects. At present ESBMT contains definitions for "Carbon" and "Sulfur" which will create the element objects C and S respectively. You can query which species are known to an element by calling the list_species method, e.g., C.list_species()

You can initialize more than one element by providing a list as argument (i.e., ["Sulfur", "Carbon"]). In other words, you can replace the above code block by adding =element = "Carbon" to the model parameters.

1.4 Using external data to initialize a signal

We can use an external csv file to create a signal. The first column contains the time coordinates, the second the flux rate, and the third the delta value of the flux. The first row must contain a header, and the header must contain a variable name followed by a unit:

Age [kyr]	Volcanic Flux [mol/s]	δ^{13} C [permille]
0	20	0
1	30	2

Note that the unit must be specified inside square brackets. All values will be mapped into the model units and interpolated to fit the model time resolution.

Signals can also by created by specifying a signal type. At present the class understands, square, and pyramidal signal forms, as well as repetition. Signal can be added to each other (i.e., you can specify a signal which effects the flux, and then add another signal which effects the isotope ratio).

```
Signal(name = "ACR", # Signal name

species = CO2, # Species

filename = "test-data.csv" # filename

)
```

Once a signal instance has been created, it can be passed to a connector object in order to associate it with a flux (see the first connection below as an example).

1.5 Sources, Sinks and Reservoirs

The fundamental model object is the reservoir. Reservoirs are connected to each other by one or more fluxes. Fluxes are created implicitly by connecting two reservoirs.

Connecting a reservoir with a Source or Sink also creates a flux, but unlike reservoirs, sources and sinks do not have any associated data. They are merely there to allow the creation of a flux.

```
Source(name="Fossil_Fuel_Burning", species=CO2)
   Source(name="Carbonate_Weathering", species=CO2)
   Source(name="Organic_Weathering", species=CO2)
   Source(name="Volcanic", species=CO2)
   Sink(name="Carbonate burial", species=CaCO3)
   Sink(name="OM burial", species=OM)
6
   Reservoir(
8
       name="Ocean",
                                     # Name of reservoir
       species=DIC,
                                     # Species handle
10
       delta=0,
                                     # initial delta
11
        concentration="2.62 mmol/l", # cocentration
12
       volume="1.332E18 m**3",
                                     # reservoir size (m^3)
13
   )
14
```

1.6 Connecting sources, reservoirs and sinks

Now that all model elements are specified, we can connect everything. The first statement below, connects the source Fossil_Fuel_Burning with the reservoir Ocean. This will create a flux with the name Fossil_Fuel_-Burning_to_Ocean. The rate and delta keywords indicate that this flux will be zero. However, we provide pl = [ACR] which is the carbon flux data which we imported via the signal object above. This data will be added to the Fossil_Fuel_Burning_to_Ocean flux (since the process is additive, the initial flux has to be zero!)

The type of flux depends on how we specify the connection. In the previous example we provided a signal, so the flux will change with time according to the signal data. If you look at the connection between Carbonate_-Weathering and Ocean below, we specify a given rate and delta value. So this flux will not change over time. If you look at the connection between Ocean and OM_burial the connection specifies a constant flux but with an alpha = -26.3. This indicates that this flux involves a fixed isotope offset relative to the upstream reservoir, i.e., the isotope ratio of this flux will change dynamically in response to the isotope ratio of the reservoir, but with a constant offset. See below for a full list of connection options.

Fluxes can be circular, care must however be taken in which sequence they are defined, since the solver computes each flux and reservoir in the order they are initialized (see the Examples directory for a more complete example).

```
# connect source to reservoir
   Connect(
2
3
        source=Fossil Fuel Burning, # source of flux
        sink=Ocean,
                                      # target of flux
4
        rate="0 mol/yr",
                                      # weathering flux in
5
                                      # set a default flux
        delta=0,
6
        pl=[ACR],
                                       # process list, here the anthropogenic carbon release
7
   )
8
9
   Connect(
10
        source=Carbonate_Weathering, # source of flux
11
                                        # target of flux
        sink=Ocean,
12
        rate="12.3E12 mol/yr",
                                       # weathering flux in
13
                                        # isotope ratio
14
        delta=0,
   )
15
16
   Connect(
17
        source=Organic_Weathering, # source of flux
18
                                     # target of flux
        sink=Ocean,
19
        rate="4.0E12 mol/yr",
                                     # flux rate
20
        delta=-20,
                                     # isotope ratio
21
   )
22
^{23}
   Connect(
24
        source=Volcanic,
                               # source of flux
25
        sink=Ocean,
                              # target of flux
26
        rate="6.0E12 mol/yr", # flux rate
27
```

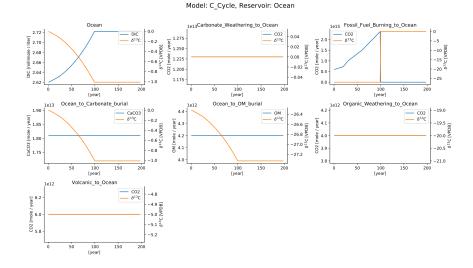
```
delta=-5,
                               # isotope ratio
28
   )
29
30
   Connect(
31
                                # source of flux
        source=Ocean,
32
                                # target of flux
33
        sink=OM_burial,
        rate="4.2E12 mol/yr", # burial rate
34
        alpha=-26.32,
                                # fractionation factor
35
   )
36
37
   Connect(
38
        source=Ocean,
                                # source of flux
39
        sink=Carbonate_burial, # target of flux
40
        rate="18.1E12 mol/yr", # burial rate
41
                                # set the istope fractionation
        alpha=0,
42
43
   )
```

1.7 Running the model

The model is executed via the run() method. The results can be displayed withe the plot_data() method which will generate an overview graph for each reservoir. Export of the results to a csv file is done via the save_data() method which will create csv file for each reservoir.

```
# Run the model
C_Cycle.run()

# plot the results
C_Cycle.plot_data()
# save the results
C_Cycle.save_data()
```



2 Controlling the flux type

The connect method has a variety of way to specify the flux:

- If both rate and delta are given, the flux is treated as a fixed flux with a given isotope ratio. This is usually the case for most source objects (they can still be affected by a signal, see above), but makes little sense for reservoirs and sinks.
- If both the rate and alpha are given, the flux rate is fixed (subject to any signals), but the isotopic ratio of the output flux depends on the isotopic ratio of the upstream reservoir plus and isotopic offset specified by alpha. This is typically the case for fluxes which include an isotopic fractionation (i.e., pyrite burial). This combination is not particularly useful for source objects.
- If the connection specifies only delta the flux is treated as a variable flux which is computed in such a way that the reservoir maintains steady state with respect to it's mass.
- If the connection specifies only rate the flux is treated as a fixed flux which is computed in such a way that the reservoir maintains steady state with respect to it's isotope ratio.
- Other connection types are possible, but currently untested.

- A flux can be scaled relative to another flux. To do so, provide the scale keyword, and a flux reference via the ref keyword
- A flux can be scaled relative to the mass or concentration of the upstream reservoir. This is achieved by providing a k_mass or a k_concentration keyword with an appropriate k-value. If one additionally provides the ref_value keyword, the mass/concentration is first normalized, then mapped to zero, and the difference is being scale by the k-value

$$F = (M/M0 - 1) * k$$
 where F is forced to be $>=0$

This allows to scale the rate dependence relative to an equilibrium value M0, i.e. when the reservoir approaches M0, the flux -> zero. The k-value then expresses how fast the system returns to the equilibrium value

• Fluxes can be scaled with a Michalis-Menten type scaling function

$$F = F * a * F0 x C/(b+C)$$

this type of scaling is invoked by providing the following keywords: a_-value, b_value, ref_value the latter being F0 in the above equation

• Last but not least, Reservoirs can be specified by either providing volume and concentration or volume and mass