1 Equilibrating two reservoirs

Two reservoirs which are connected via forward and backward fluxes will equilibrate their concentrations (and thus their isotope ratios). The equilibrium depends on the actual concentration plus any optional equilibrium constants.

We can model this situation by creating two explicit fluxes between two reservoirs, which mimics the actual nature of exchange fluxes. However, we can also express the flux balance between both fluxes, and only compute the difference. The latter approach is more succinct. ESBMTK implements this case with the `flux_balance` connection type, takes three parameters

- `left` is a list which can contain constants and/or reservoirs. The list must contain at least one valid element. All elements in this list will be multiplied with each other. E.g. if we have a list with one constant and one reservoir, the reservoir concentration will be multiplied with the constant. If we have two reservoirs, the respective reservoir concentrations will be multiplied with each other.
- `right` similar to `left` The final flux rate will be computed as the difference between `left` and `right`
- `k_value` a constant which will be multiplied with the difference between `left=and =right`

Here a simple example.

```
from esbmtk import Model, Reservoir, Signal
from esbmtk import Connect, Source, Sink

volume = "1 liter"

# create model
Model(
    name="equi4",  # model name
    stop="3 s",        # end time of model
    timestep="0.1 s",            # time step
    element=["Carbon"],  # initialize carbon species
    mass_unit="mol",
    volume_unit="l",
```

```
)

Reservoir(
    name="R1",    # Name of reservoir
    species=CO2,              # Species handle
    delta=10,                  # initial delta
    concentration=f"10 mol/l",       # concentration
    volume=volume,         # reservoir size (m^3)
)

Reservoir(
    name="R2",    # Name of reservoir
    species=CO2,              # Species handle
    delta=0,                  # initial delta
    concentration=f"11 mol/l",       # concentration
    volume=volume,         # reservoir size (m^3)
)

Connect(
    source=R1,   # target of flux
    sink=R2,    # source of flux
    rate="1 mol/s",            # flux rate
    ctype="flux_balance",
    k_value=1,
    left=[R1],
    right=[R2],
    #alpha=0,                 # isotope fractionation
    plot="no",
)


# Run the model
equi4.run()

# plot the results
equi4.plot_data()
```

```
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free software, and you are welcome to redistribute it under certain
conditions; See the LICENSE file for details.

Execution took 0.0010554550000003715 seconds
```

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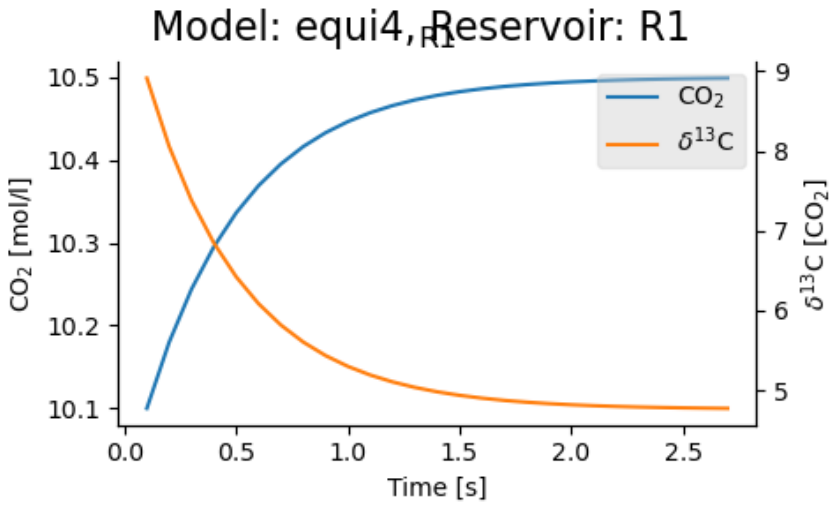

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