# Appendix: Syntax of RCaN constraints

Constraints are at the heart of the Chance and Necessity modelling. They relate fluxes and biomass in the trophic network. The basis is a mass balance equation: the variation of biomass of a trophic compartment is the result of input fluxes (e.g. feeding, imports, migration) minus output fluxes (e.g. predation, fishing, losses due to somatic maintenance). As somatic maintenance is proportional to biomass, this constraint is a linear one. The parameters: assimilation efficiency, trophic maintenance are given for all compartments in the RCaN-file. All linear constraints on fluxes and biomass can be expressed as constraints on trophic fluxes only. See (Planque and Mullon, 2020) for precise formulation.

## A.1    Implicit and explicit constraints

There are two types of constraints.

1. Standard or implicit constraints. These are part of any RCaN model by default. They are defined by the value of the parameters in the Components sheet of the RCaN-file. These constraints express that (a) biomass must be positive and above the refuge biomass (beta), (b) fluxes between two compartments are always positive, (c) the sum of fluxes into a compartment, from time t to t+1, cannot exceed *B*(*t*) ∗ *σ*, where *B*(*t*) is the biomass at time t and *σ* is the satiation parameter, (d) the biomass of a compartment at time t+1 cannot be greater than *B*(*t*)*exp*(*ρ*) or lower than *B*(*t*)*exp*(−*ρ*), where *ρ* is the inertia coefficient.
2. Explicit constraints. These are specific to individual RCaN models. They express specific knowledge about how different biomass, fluxes and observations are related, i.e. constrained by each other. These explicit constraints are formulated in the constraints sheet of the RCaN-file, and must be written according to specific syntax rules. In this section we provide details and examples of this syntax.

## A.2    Symbolic expression of explicit constraints

Constraints are symbolic expressions, i.e. equalities or inequalities. They relate elements of the model (trophospecies or fluxes) on the left side of the expression to observations or other elements of the model on the right side of the expression. To interpret these expressions in a numerical framework, RCaN uses the R interface to the library Symengine, a fast symbolic manipulation library in C++, (Ma et al., 2020).

## A.3    Explicit constraints, principles and examples

The rules to write constraints explicitly are as follows.

1. Constraints are written in the form of inequalities or equalities.

The left side of the (in)equality must contain a reference to one or several model components or fluxes.

2. The right side of the (in)equality can contain fixed values, components, fluxes, and observational time-series.

In the following constraints: *spA* and *spB* are the names (in the RCaN file) of two components, *fluxA*\_*B* is the name of the flux between the two components, *obsA* is the name of an observational time-series of species *spA*. Some examples of standard constraints:

1. *spA <*= 100

the biomass of species A must be lower or equal to 100.

1. *spA* + *spB <*= 100

the combined biomasses of species A and B must be lower or equal to 100.

1. *fluxA*\_*B <*= 50

the flux from species A to species B must be lower or equal to 50.

1. *spA* = *obsA* the biomass of species A must equate the observational time series of species A
2. *spA <*= *spB*: the biomass of species A must be lower or equal to the biomass of speciesB

## A.4    Explicit constraints using timeless absolute bounds

This type of constraint is useful when there are no data series available to inform on the temporal variations in certain biomass or fluxes but there is some knowledge about the maximum or minimum values that a compartment or a flux may take. For example, if the total biomass of species A (*spA*) is expected to lie between 100 and 1000 tonnes for the whole time series, one can write the two following constraints:

*spA >*= 100

*spA <*= 1000

## A.5    Explicit constraints from imprecise biomass observations

Constraints using biomass time series, absolute estimates When times-series of absolute biomass estimates are available (e.g. from stock assessments) these can be used to constraint the corresponding modelled biomass. Consider a compartment inside the model (*spA*); a series of observed biomass named *obsA*.

1. If we assume the observation to precisely reflect the true biomass, we can write the model constraint:

*spA* = *obsA*

If we assume that the observed biomass is uncertain by 10% we can write the 2 model constraints:

*spA >*= *obsA/*1*.*1

*spA <*= *obsA* ∗ 1*.*1

3. If we assume that the observed biomass only represent a fraction of the population and the the true biomass lies somewhere between what is estimated and twice this amount, we can write:

*spA >*= *obsA*

*spA <*= *obsA* ∗ 2

## A.6    Explicit constraints on Fisheries catches

The specific case of fisheries catches can be handled in the following way. Consider a species *A* (*spA*) ; a fishery on species *A* (compartment outside the model) with name *FA*. Catches are a flux from the species to the fishery (non-trophic flux): *spA*\_*FA*. *CatchA* is a time-series of reported catches of species *A* by the fishery. All are expressed in the same units (e.g. tonnes).

1. If we assume that the reported catches reflect the true catches exactly, we can write the model constraint:

*spA*\_*FA* = *CatchA*

1. If we assume that the reported catches are uncertain by 10% we can write the model constraints:

*spA*\_*FA >*= *CatchA/*1*.*1

*spA*\_*FA <*= *CatchA* ∗ 1*.*1

1. If we assume that the catches are under-reported and that the true catches are somewhere between what is reported and twice this amount, we can write:

*spA*\_*FA >*= *CatchA*

*spA*\_*FA <*= *CatchA* ∗ 2

## A.7    Explicit constraints from relative estimates

When times-series of relative biomass estimates are available (e.g. from surveys) these can be used to constraint the corresponding modelled biomass. Consider compartment *A* (*spA*), and a time-series of observations of relative biomass with name *surveyA*.

1. If we assume the observation to precisely reflect the relative variations in biomass over time, we can write the model constraint: *spA/mean*(*spA*[*f* : *l*]) = *obsA/mean*(*obsA*[*f* : *l*])

where *f* and *l* are the first and the last indices of the time period of reference.

If we assume that the observed relative changes in biomass are uncertain by 10% we can write the 2 model constraints:

(*spA/mean*(*spA*[*f* : *l*])) *>*= (*obsA/mean*(*obsA*[*f* : *l*]))*/*1*.*1

(*spA/mean*(*spA*[*f* : *l*])) *<*= (*obsA/mean*(*obsA*[*f* : *l*])) ∗ 1*.*1

## A.8    Explicit structural constraints

In addition to constraining compartments/fluxes based on data or absolute bounds, it is also possible to express structural constraints within the model that are independent of observational time-series or absolute bounds. For example, if species C (*spC*) can feed on species A and B (*spA* and *spB*), but we know that species A is always more abundant in the diet of species C, we can write.

*spA*\_*spC >*= *spB*\_*spC*,

which expresses that the flux from *spA* to *spC* is always greater than the flux from *spB* to *spC*.

## A.9    Applying constraints over limited time periods

A time period is associated with each constraint. By default this is the period from the first year of available observation to the last. However, constraints can be applied to restricted time periods or specific years (or even a single year) when necessary. The selected years are indicated in the third column of the constraint table in the RCaN-constructor / RCaN-file.