**COMMUNITY SIMULATOR: NEW FEATURES**

The community simulator package has been modified to add the following new features:

* Instead of a single metabolic matrix (D) common to all species, the user can now decide whether they want a different matrix for each species. To enable/disable this behavior, a new item has been added to the assumptions dictionary:

assumptions[‘metabolism’]

This item can take two possible values: ‘common’ (for the default behavior of the original version of the package, with one matrix D shared by all species), or ‘specific’ (for each species having its own metabolic matrix D). If the ‘specific’ option is chosen, the functions MakeParams() and MakeMatrices() will return D as a list of matrices. Downstream functions (such as Propagate(), RunExperiment(), etc.) have been modified to support this new format.

* If the ‘specific’ option is chosen, the user can decide whether metabolic matrices should be random (with values sampled from Dirichlet distributions modulated by input parameters like ‘fs’, ‘fw’ or ‘sparsity’ that can be passed to the assumptions dictionary) or instead be modulated by the uptake rates of each species and resource. This is done by passing the control parameter:

assumptions[‘rs’]

which can take values from 0 to 1 (included). If it is 0, metabolic matrices will be generated randomly following the same pipeline as in the original community simulator package. If it is greater than 0, an additional layer of regulation is included so that every species preferentially secretes byproducts that can be consumed by itself. In the limit case where the control parameter is 1, species will not secrete any byproduct that they cannot consume. However, when there are resources considered “waste resources” (the original community simulator package treats the last resource type as the default set of waste resources, but this can be controlled by passing the ‘waste\_type’ tag to the assumptions dictionary), those are not subject to this extra layer of regulation, i.e., the values of the metabolic matrix of species *i* corresponding to the waste resources are sampled independently of whether they can be consumed by *i*, regardless of the value of the control parameter ‘rs’. Note that if no resource types are specified, all resources are treated as waste resources and the value of the control parameter ‘rs’ has no effect. In all other cases, this regulation is introduced in a way that is consistent with the energy fluxes specified by the parameters ‘fs’ and ‘fw’ (controlling the energy flux towards resources of the same type as the consumed one or towards waste resources, respectively). It is also consistent with the parameter ‘sparsity’ controlling the sparsity of the D matrices. In some very specific scenarios, when a species cannot consume any resource of a given type but the choices of ‘fs’ and ‘fw’ indicate that there should be energy flux towards that resource type, fluxes are redistributed proportionally towards all other resource types to compensate for the missing flux.

The modified package is in: <github.com/jdiazc9/coalescence>