Enumerator Architectural Documentation

Application lifecycle

The enumerator application is bootstrapped from the main function defined in enumerator.py. This function:

- Parses command line arguments using the Python argparse module
- Invokes an input parser from the input module to parse the passed input file. Input parsers generate Enumerator objects.
- Sets various parameters on the Enumerator object that is created, such as
 the maximum complex size and the maximum number of reactions to be
 enumerated.
- Instructs the Enumerator object to run the reaction enumeration.
- Invokes an output generator to serialize the output from the enumerator to a file.

Key data structures

The utils module defines several classes that are used to represent the state of the enumeration:

- Domain objects represent single domains (continuous regions of nucleotides that hybridize as a unit).
- Strand objects represent strands—ordered collections of Domains.
- Complex objects represent complexes of strands—comprised of an ordered list of Strands and a secondary structure specifying how strands are hybridized together.
- RestingState objects represent collections of Complexes that form a resting state—that is, a complex with no outgoing fast reactions.

Additionally, the reactions module defines the ReactionPathway class: *ReactionPathway objects represent a reaction between some number of substrate Complexes and some number of product Complexes.

Reaction functions

The reactions module defines a number of "reaction functions"; these functions correspond to different types of reactions—for instance, unimolecular binding (bind11), bimolecular binding (bind21), 3-way branch migration (branch_3way), etc. Reaction functions all accept some number of Complexes as arguments, and return a list of ReactionPathway objects. The number of arguments accepted

by a reaction function (which is therefore also the number of substrates for the reaction) is its *arity*.

Reaction functions are grouped by their arity and their "speed" in two dictionaries within the enumerator module: fast_reactions and slow_reactions. Each is a dictionary where the keys are arities (e.g. 1 for unimolecular, 2 for bimolecular, etc.), and the values are lists of reaction functions. Currently, all unimolecular reaction functions are fast, and the bind21 reaction is slow. The fast/slow distinction is used by the enumerator to group complexes into "resting state complexes" and "transient complexes"—resting state complexes exist in strongly-connected neighborhoods with no out-going fast reactions ("resting states"), while transient complexes are those complexes in neighborhoods with one or more outgoing fast reactions.

Reaction enumeration

The main reaction enumeration is performed by the Enumerator class. The Enumerator class is initialized with a set of Domains and Strands, as well as a set of initial Complexes. The enumerate method is called to begin the following procedure, which exhaustively enumerates the network of possible reactions starting from those initial Complexes:

- First, fast reactions are considered between the initial complexes: For each complex in initial_complexes, the process_neighborhood method is called and passed that Complex.
 - This method generates the "neighborhood" of complexes reachable by fast reactions from the passed reaction, and classifies the resulting complexes as either transient or resting state. This is a depth-first search, which proceeds as follows:
 - * The starting complex is placed in a list _F by itself.
 - * While that list is not empty:
 - · an element is taken from the list and get_fast_reactions is passed that complex. get_fast_reactions executes each of the reaction functions in fast_reactions on the passed complex.
 - · Resulting ReactionPathway objects are added to the list N-reactions.
 - Product Complexes from these reactions are added to the list
 F and the list
 N.
 - * The segment_neighborhood function is passed the list _N, which contains all complexes that have been enumerated through fast reactions. segment_neighborhood breaks the complexes in _N into strongly-connected components using Tarjans' algorithm. The resulting transient_state_complexes,

resting_state_complexes, and resting_states are collected into the appropriate lists and stored in the Enumerator object.

- Slow reactions are then considered between all complexes classified as resting states. For each complex classified as a resting state:
 - get_slow_reactions is called and passed the Complex. get_slow_reactions works similarly to get_fast_reactions: it executes each of the reactions in slow_reactions. However, while fast_reactions can only be unimolecular, reaction functions in slow_reactions may be bimolecular; therefore, get_slow_reactions must iterate through all complexes classified as resting states and attempt slow reactions between those complexes and the passed complex.
 - Resulting ReactionPathways and product Complexes are collected.
 For each of the product Complexes, process_neighborhood is invoked.
 process_neighborhood enumerates fast reactions and segments strongly-connected components, as described above.

Input and output

The input module defines a number of *input parsers*, which are functions that accept input filenames and return Enumerator objects. The output module defines a number of *output generators*, which are functions that accept Enumerator objects and output filenames, and serialize the Enumerator objects to the output file as text.

Input parsers are collected in the text_input_functions and load_input_functions dictionaries of the input module. text_input_functions generate new Enumerator objects which can then be used to enumerate reactions; load_input_functions generate Enumerator objects which have been serialized from a previous run of the enumerator.

Output parsers are collected in the text_output_functions and graph_output_functions dictionaries of the output module. text_output_functions contains text-based output generators, while graph_output_functions generate graphical output.