Running EC

Current version of EC supports only command-line mode. In order to investigate a model using EC you should:

1) Prepare a model specification file, using EC script language;
2) Run EC being specified the prepared file (for instance, modFile.txt) as an input: `ec.exe modFile.txt`
3) Wait until EC stopped and analyze output files.

Note: In order to avoid filename conflicts and prevent data losses, as well as for convenience we recommend you to make calculations and store all files related to your model in the unique directory.

EC output files

During calculations EC generates several data files that may be analyzed:

1) `popSize.txt` –populations sizes dynamics file, each particular population is located in its own row;
2) `events.txt` – file of events (such as mutations, HGT etc) history;
3) `dump.substr.txt` – file for substrates concentrations dynamics (in environment);
4) `spectra.pop###.txt` – file for population### genetic diversity dynamics. Each gene is presented with its own genetic spectrum (genetic spectrum is displayed as a list of pairs *allele-value : allele-frequency*).
5) `log.txt` – EC log-file.