| | Knockout mutants | | | | | Other algorithms | | | | | | | | | Input files | | Network tools | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | FBA | gene knockouts (FBA) | MOMA | ROOM | series of knockouts[a] | FVA | total flux minimisation[b] | robustness analysis | PhPP[c] | dynamic FBA | series of optimisations[d] | flux coupling | sampling | elementary modes/ extreme pathways | SBML | column based[e] | fluxomics data | integration of gene expression data | network visualisation | network reconstruction |
| sybil | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓[f] | ✓ | | ✓ | | ✓[g] | ✓ | | ✓[h] | | |
| abcdeFBA | ✓ | | | | | ✓ | | ✓ | | | | | | | | | | | | |
| BiGGR | ✓ | | | | | | | | | | | | | | | | | | | |
| COBRA Toolbox | ✓ | ✓ | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |
| COBRApy | ✓ | ✓ | ✓ | | ✓ | ✓ | | | | | ✓ | | | | ✓ | | | | | |
| fastFVA | | | | | | ✓ | | | | | ✓ | | | | | | | | | |
| CellNetAnalyzer | ✓ | ✓ | | | | ✓ | | | | | | | | ✓ | ✓ | | ✓ | | ✓ | ✓ |
| SBRT | ✓ | ✓ | | | | ✓ | | | | | ✓ | | | | ✓ | | | | | |
| OptFlux | ✓ | ✓ | ✓ | ✓ | | ✓ | | | | | | | | | ✓ | ✓ | | | | |
| FASIMU | ✓ | ✓ | ✓ | | | ✓ | ✓ | | | | | | | | ✓ | | | ✓ | ✓[i] | ✓ |
| F2C2 | | | | | | | | | | | | ✓ | | | | | | | | |

[a] In an automated fashion for a given set of genes, i. e., knocking out one gene per optimisation.
[b] Sum of absolute flux values.
[c] Phenotypic phase planes
[d] Optimised for speed by only applying changes rather than rebuilding the problem object.
[e] e. g., compatible to the output of the BiGG database.
[f] Add-on package sybilDynFBA required, available separately from CRAN.
[g] Add-on package sybilSBML required (Additional file 3).
[h] Add-on package sybilEFBA required, available separately from CRAN.
[i] Cytoscape required.