Table 1. Main characteristics of a panel of gap-filling methods

Name	**Input data**	**Technological platform**	**Application models**
GapFill [1]	Target metabolites	GAMS platform	*Escherichia coli* strains, *Gordonia alkanivorans* [2] *Salmonella Typhimurium LT2* [3] *Clostridium beijerinckii NCIMB 8052* [4]
FastGapFill [5]	Target metabolites	Matlab & Cplex	*E. coli* [5] *Synechocystis sp.* [5]
Meneco	Target metabolites	Python	*Ectocarpus siliculosus* [6] *Candidatus* Phaeomarinobacter ectocarpi [7]
Christian *et al.* [8]	Target metabolites Likelihood of reactions	No available distribution	*E. coli* [8] *Ostreococcus* [9] *Chlamydomonas reinhardtii* [8]
Benedict *et al.* [10]	Target metabolites Likelihood of reactions	KBase framework	21 bacterial species [10]
Mintz-Oron *et al.* [11]	Target metabolites Proteomic data	No available distribution	*Arabidopsis thaliana* [11]
Mirage [12]	Target metabolites Taxonomic weights Co-expression transcriptomic weights	Matlab	*Cyanobacteria* [12]
Growmatch [13]	Targeted metabolites Growth/no growth data	Matlab	*Methanosarcina acetivorans* [14] *Saccharomyces cerevisiae* [15]
OMNI [16]	Flux data	Matlab & GAMS	*E. coli* [16]

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