

## Supplementary Material

**Table S1. Summary of reconstruction tools for GEMs of non-model species**

<b>Tool</b>	<b>Programming Language</b>	<b>Gap-filling</b>	<b>Databases used for reactions</b>	<b>References</b>
<i>CarveMe</i>	Python	Yes	BIGG Models	(1)
<i>FAME</i>	Python	No	KEGG	(2)
<i>MetaDraft</i>	Python	No	BIGG Models	(3)
<i>Model SEED</i>	Web	Yes	In-house reaction database	(4)
<i>RAVEN2.0</i>	Matlab	Yes	KEGG, MetaCyc	(5)

## REFERENCES

- [1] Machado D, Andrejev S, Tramontano M, Patil KR. Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. *Nucleic acids research*, 2018;46(15):7542–7553.
- [2] Boele J, Olivier BG, Teusink B. FAME, the flux analysis and modeling environment. *BMC systems biology*, 2012;6(1):8.
- [3] Hanemaaijer M, Olivier BG, Röling WF, Bruggeman FJ, Teusink B. Model-based quantification of metabolic interactions from dynamic microbial-community data. *PloS one*, 2017;12(3).
- [4] Henry CS, DeJongh M, Best AA, Frybarger PM, Linsay B, Stevens RL. High-throughput generation, optimization and analysis of genome-scale metabolic models. *Nature biotechnology*, 2010;28(9):977.
- [5] Wang H, Marcišauskas S, Sánchez BJ, Domenzain I, Hermansson D, Agren R, Nielsen J, Kerkhoven EJ. RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on *Streptomyces coelicolor*. *PLoS computational biology*, 2018;14(10):e1006541.