

Reference	Static/ Dynamic	GEM	# strains	Habitat	Omics data required	Validation	Micro- biome states	Temporal analysis	Pertur- bations	Software available	Study goal
<i>(This study)</i> MDP- biomeGEM	Dynamic	Yes	2-10	Human gut, soil	No	<i>In-silico</i> (MDP)	Yes, N>=2	Yes	Yes	Yes	Analyzing dynamics of GEM-simulated microbial communities under perturbations to suggest direct interventions for community engineering
García-Jiménez et al.,2018 MDPbiome	Dynamic	No	1000s	Human gut, chick gut, vaginal	Yes (OTU table, perturbations meta-data)	<i>In-silico</i> (MDP)	Yes, N>=2	Yes	Yes	Yes	Analyzing dynamics of microbiomes under perturbations to suggest interventions for community engineering
El-Semman et al., 2014	Static	Yes	2	Human gut	No	<i>In-silico</i>	No	No	No	No	Analyzing cross-feeding relations
Heinken and Thiele, 2015	Static	Yes	11 + host cell	Human gut	No	<i>In-silico</i>	No	No	No	No	Predicting host-microbe interactions using static simulations including simulated medium modifications
Diener et al.,2020 MI- COM	Static	Yes AGORA v1.03	100s	Human gut	Yes (abundances)	<i>In-silico</i>	No	No	No	Yes	Predicting growth rates and fluxes from abundances
Pryor et al.,2019	Static (uni- fied biomass reaction)	Yes AGORA v1.02	760	Human gut	Yes (16S rRNA sequencing and dietary uptake)	<i>In-vivo</i>	No	No	No	No	Use of GEMs to determine if metformin treatment increases agmatine production by gut microbiota
Garza et al.,2018 MAMBO	Static	Yes	Up to 1562	Human oral, skin, vaginal	Yes (relative abundances)	<i>In-vivo</i>	No	No	No	Yes	Predicting nutrients from metagenomics; optimizing correlation between real and predicted
Chan et al.,2017 SteadyCom	Static	Yes (merged)	9	Most-abundant genera in human gut	No	<i>In-silico</i>	No	No	No	Single case	Simulating microbial community, demanding the same growth rate per strain, affected by varying quantities of dietary fiber
Steinway et al., 2015	Static	Yes	<=12	Mouse	Yes (genus abundances)	<i>In-vivo</i> (2 strains)	Boolean states	Yes	Yes	Single case	Integrating GEMs (network expansion method) with quantitative longitudinal metagenomics data to identify bacteria that inhibit perturbations
Bauer and Thiele, 2018	Dynamic (BacArena, Static use)	Yes	{8-713} Avg=283 AGORA	Human gut	Yes (relative abundances are proportions in community model)	<i>In-silico</i>	Yes, N=2	No	No	Single case	Predicting SCFA levels; suggesting personalized diet to optimize SCFA as treatment for Crohn's disease
DiMucci et al., 2018	Dynamic (COMETS Static use)	Yes	2 (pairs among 100)	Human gut, soil	(optional: 16S rRNA sequencing)	<i>In-silico</i>	No	No	No	Singlecase	Prediction of pair-wise interactions in microbial networks with Machine Learning
Bauer et al.,2017 BacArena	Dynamic	Yes	2, 7	Human gut	No	<i>In-silico</i>	No	Yes	No	Yes	Analysis of interactions and spatial and temporal distributions of microbes in communities using individual agent-based metabolic modeling
Borer et al.,2019 diMeSH	Dynamic	Yes	1-2	Soil	No	No	No	Yes	Yes	Yes	To model metabolic networks, focused on soil, highlighting spatial properties.

<a href="#">Popp and Centler, 2019</a> microbialSim	Dynamic	Yes	1, 2 and 773 in AGORA	<i>Methanostrains</i> , human gut	No	<i>In-silico</i>	No	Yes	No	Yes	Dynamic simulation of microbial communities with dynamicFBA, with novel augmented forward Euler as the integrator
<a href="#">Costello and Garcia, 2018</a>	Dynamic	No	1	Indifferent	Yes (proteomics and metabolomics)	<i>In-silico</i>	No	Yes	No	Yes	Predicting metabolite concentration dynamics using Machine Learning in place of Michaelis Menten kinetics
<a href="#">Venturelli et al., 2018</a>	Dynamic	No	12	Human	Yes (biomass, 16S rRNA sequencing and metabolomics)	<i>In-silico (Lotka-Volterra)</i>	No	Yes	No	Single case	Predicting microbial community time-series; experimental data used to predict model parameters (growth rates, intra-/inter-species interaction coefficients)
<a href="#">Shaw et al. 2019</a>	Dynamic	No	100(0)s	Human oral and gut	Yes (16S rRNA sequencing)	<i>In-silico (Bayes)</i>	Yes, N=2	Yes	Yes	Single case	Bayes modeling of human gut and oral microbiome after antibiotic perturbations
<a href="#">Bucci et al., 2016</a> MDSINE	Dynamic	No	~15-25	Mouse gut	Yes (OTU table, qPCR)	<i>In-silico (Bayes)</i>	Yes, N=2	Yes	Yes	Yes	"Inferring dynamical systems models from microbiome time-series datasets, and predicting biologically relevant behaviors of the ecosystems"
<a href="#">Mallick et al., 2019</a> Melon-nPan	Static	No	1000s	Human gut and vaginal, reef coral, mouse gut	Yes (16S rRNA or metagenomics sequencing)	<i>In-vivo</i>	No	No	No	Yes	Predicting metabolites from amplicon or metagenomics sequences; identifying predictive taxonomic or functional features for each metabolite
<a href="#">Morton et al., 2019</a> mmvec	Static	No	100s	Cystic fibrosis lung and desert biological soil crust wetting	Yes (metagenomics, mass spectrometry for metabolites)	<i>In-silico (ANN)</i>	No	No	No	Yes	Predicting microbe-metabolite relationships with Deep Learning