Integrating workflows and data across scales in KBase

Tool contributors	Molecule	Moloculo structuro	Equilibrator	Droportion
EMSL	Molecule		NWchem	Properties
IGL Banfield Chain		Reads	Assembly	Contigs
ENGIMA		Contigs	Binning	Genomes
	Sequence	Genomes	Gene calling	Genes
		Protein	Annotation	> Function
Mitchell, PDB	Protein	Protein structure	Docking	Predicted
JGI, Stuart		Annotated genome	Model reconstruction	FBA model
CLEMSI Janson Schoibo	Single cell	FBA model N Omics data	Inp	roved FBA mode
JGI, EMSL, Jansen, Scheibe	Multicellular	FBA model Multi- Omics data	-omics pathway prediction	Active pathway profile
lansen Scheibe	community	FBA models Comm Omics data	nunity steady state FBA	ophic interactions
Jansen, Scheibe	Microcosm	FBA models	Dynamic FBA Micro	cosm simulation
Kemner		Amplicon profile	TU correlation Species int	eraction network
Versteeg, Wrighton, ENIGMA, Jansen, Scheibe, IDEAS	Ecosystem	Species reactions System definition	Reaction transport modeling Ecos	ystem simulation
In development In beta	In produc	ction Of	ffice of Biological and wironmental Research Office of Science	OE Systems Biology Knowledgebase

Supporting Seamless Data Transfer Among DOE Facilities

1.) Discussing consolidated ID system to represent data samples across all DOE systems

- A biosample / experiment will have a common ID across all facilities
- Possibly developing common metadata system with shared types, attributes, ontologies
- still in design/conceptualization stages



2.) Adding interfaces to KBase to support search and import from external data sources (e.g. JGI)

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