# Independent Section

iNlan20 Expand All Readme 2020-11-25 10:41

## Consistency

| | |
|---|---|
| Stoichiometric Consistency | 100.0% |
| Mass Balance | 100.0% |
| Charge Balance | 100.0% |
| Metabolite Connectivity | 100.0% |
| Unbounded Flux In Default Medium | 87.7% |
| Sub Total | 98% |

## Annotation - Metabolites

| | |
|---|---|
| Presence of Metabolite Annotation | 100.0% |
| Metabolite Annotations Per Database | Info |
| pubchem.compound | 0.0% |
| kegg.compound | 84.6% |
| seed.compound | 87.7% |
| inchikey | 77.7% |
| inchi | 0.6% |
| chebi | 85.4% |
| hmdb | 0.0% |
| reactome | 54.2% |
| metanetx.chemical | 96.1% |
| bigg.metabolite | 97.8% |
| biocyc | 83.9% |
| Metabolite Annotation Conformity Per Database | Info |
| pubchem.compound | 0.0% |
| kegg.compound | 99.6% |
| seed.compound | 100.0% |
| inchikey | 100.0% |
| inchi | 0.0% |
| chebi | 100.0% |
| hmdb | 0.0% |
| reactome | 100.0% |

| | |
|---|---|
| metanetx.chemical | 100.0% |
| bigg.metabolite | 100.0% |
| biocyc | 100.0% |
| Uniform Metabolite Identifier Namespace | 100.0% |
| Sub Total | 83% |

## Annotation - Reactions

| | |
|---|---|
| Presence of Reaction Annotation | 100.0% |
| Reaction Annotations Per Database | Info |
| rhea | 51.9% |
| kegg.reaction | 52.4% |
| seed.reaction | 72.2% |
| metanetx.reaction | 90.4% |
| bigg.reaction | 94.6% |
| reactome | 20.4% |
| ec-code | 73.3% |
| brenda | 0.0% |
| biocyc | 53.6% |
| Reaction Annotation Conformity Per Database | Info |
| rhea | 99.6% |
| kegg.reaction | 99.8% |
| seed.reaction | 100.0% |
| metanetx.reaction | 100.0% |
| bigg.reaction | 100.0% |
| reactome | 100.0% |
| ec-code | 97.4% |
| brenda | 0.0% |
| biocyc | 100.0% |
| Uniform Reaction Identifier Namespace | 100.0% |
| Sub Total | 86% |

## Annotation - Genes

| | |
|---|---|
| Presence of Gene Annotation | 100.0% |
| Gene Annotations Per Database | Info |
| refseq | 0.0% |

| | |
|---|---|
| uniprot | 0.0% |
| ecogene | 0.0% |
| kegg.genes | 0.0% |
| ncbigi | 0.0% |
| ncbigene | 0.0% |
| ncbiprotein | 0.0% |
| ccds | 0.0% |
| hprd | 0.0% |
| asap | 0.0% |
| Gene Annotation Conformity Per Database | Info |
| refseq | 0.0% |
| uniprot | 0.0% |
| ecogene | 0.0% |
| kegg.genes | 0.0% |
| ncbigi | 0.0% |
| ncbigene | 0.0% |
| ncbiprotein | 0.0% |
| ccds | 0.0% |
| hprd | 0.0% |
| asap | 0.0% |
| Sub Total | 33% |

## Annotation - SBO Terms

| | |
|---|---|
| Metabolite General SBO Presence | 100.0% |
| Metabolite SBO:0000247 Presence | 100.0% |
| Reaction General SBO Presence | 100.0% |
| Metabolic Reaction SBO:0000176 Presence | 100.0% |
| Transport Reaction SBO:0000185 Presence | 100.0% |
| Exchange Reaction SBO:0000627 Presence | 100.0% |
| Demand Reaction SBO:0000628 Presence | 100.0% |
| Sink Reactions SBO:0000632 Presence | 100.0% |
| Gene General SBO Presence | 100.0% |
| Gene SBO:0000243 Presence | 100.0% |
| Biomass Reactions SBO:0000629 Presence | 100.0% |

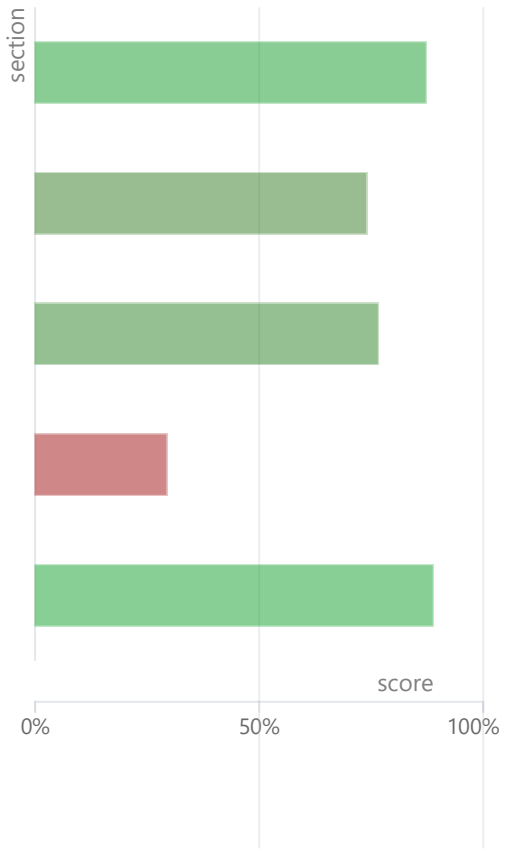
| Sub Total | 100% |
| --- | --- |

| Total Score | 93% |
| --- | --- |

Total Score

93%

Score per Category




## Specific Section

Covers general statistics and specific aspects of a metabolic network that are not universally applicable. See readme for more details.

## SBML

| | |
| --- | --- |
| SBML Level and Version | SBML Level 3 Version 1 |
| FBC enabled | true |

## Basic Information

| | |
|---|---|
| Model Identifier | iNlan20 |
| Total Metabolites | 816 |
| Total Reactions | 1,023 |
| Total Genes | 1,018 |
| Total Compartments | 3 |
| Metabolic Coverage | 1.00 |
| Uncoserved Metabolites | 0 |
| Minimal Inconsistent Net Stoichiometries | 0 |

## Metabolite Information

| | |
|---|---|
| Unique Metabolites | 701 |
| Duplicate Metabolites in Identical Compartments | 0 |
| Metabolites without Charge | 0 |
| Metabolites without Formula | 0 |
| Medium Components | 17 |

## Reaction Information

| | |
|---|---|
| Purely Metabolic Reactions | 791 |
| Purely Metabolic Reactions with Constraints | 19 |
| Transport Reactions | 128 |
| Transport Reactions with Constraints | 15 |
| Reactions With Partially Identical Annotations | 0.07 |
| Duplicate Reactions | 0.00 |
| Reactions With Identical Genes | 0.43 |

## Gene-Protein-Reaction (GPR) Associations

| | |
|---|---|
| Reactions without GPR | 216 |
| Fraction of Transport Reactions without GPR | 0.83 |
| Enzyme Complexes | 0 |

## Biomass

| | |
|---|---|
| Biomass Reactions Identified | 1 |
| Biomass Consistency | 1.00 |
| Biomass Production In Default Medium | 0.04 |
| Unrealistic Growth Rate In Default Medium | false |

| | |
|---|---|
| Biomass Production In Complete Medium | 38.01 |
| Blocked Biomass Precursors In Default Medium | 0 |
| Blocked Biomass Precursors In Complete Medium | 0 |
| Ratio of Direct Metabolites in Biomass Reaction | 0.00 |
| Number of Missing Essential Biomass Precursors | 6 |

## Energy Metabolism

| | |
|---|---|
| Non-Growth Associated Maintenance Reaction | 1 |
| Growth-associated Maintenance in Biomass Reaction | true |
| Number of Reversible Oxygen-Containing Reactions | 0 |
| Erroneous Energy-generating Cycles | Info |
| MNXM3 | Skipped |
| MNXM63 | Skipped |
| MNXM51 | Skipped |
| MNXM121 | Skipped |
| MNXM423 | Skipped |
| MNXM6 | Skipped |
| MNXM10 | Skipped |
| MNXM38 | Skipped |
| MNXM208 | Skipped |
| MNXM191 | Skipped |
| MNXM223 | Skipped |
| MNXM7517 | Skipped |
| MNXM12233 | Skipped |
| MNXM558 | Skipped |
| MNXM21 | Skipped |
| MNXM89557 | Skipped |

## Network Topology

| | |
|---|---|
| Universally Blocked Reactions | 304 |
| Orphan Metabolites | 63 |
| Dead-end Metabolites | 60 |
| Stoichiometrically Balanced Cycles | 60 |
| Metabolite Production In Complete Medium | 236 |
| Metabolite Consumption In Complete Medium | 334 |

## Matrix Conditioning

| | |
|---|---|
| Ratio Min/Max Non-Zero Coefficients | 0.00 |
| Independent Conservation Relations | 59 |
| Rank | 757 |
| Degrees Of Freedom | 266 |

## Experimental Data Comparison

| | |
|---|---|
| Growth Prediction | Skipped |
| Gene Essentiality Prediction | Skipped |

## Misc. Tests

## Environment

| | |
|---|---|
| Python Version | 3.8.3 |
| Platform | Windows |
| Memote Version | 0.12.0 |