Toycon visualization app documentation

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December 6, 2017

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# Input

## Model

As an SBML fbc V3L1 [file](http://sbml.org/Software/libSBML/docs/python-api/group__fbc.html)

## (potentially) Differential expression data

As a text file (Currently the data are randomly generated)

# Methods

* [GIMME](http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1000082)
* [FBA](https://www.nature.com/articles/nbt.1614)

# Software

## non default R packages

* [igraph: Network Analysis and Visualization](https://CRAN.R-project.org/package=igraph)
* [libSBML: application programming interface for the SBML format](http://sbml.org/Software/libSBML/Downloading_libSBML#R)
* [R support for SBML, using libsbml](https://www.bioconductor.org/packages/release/bioc/html/rsbml.html)
* [shiny: Web Application Framework for R](https://CRAN.R-project.org/package=shiny)
* [sna: Tools for Social Network Analysis](https://CRAN.R-project.org/package=sna)
* [intergraph: Coercion Routines for Network Data Objects](https://CRAN.R-project.org/package=intergraph)
* [GGally: Extension to 'ggplot2'](https://CRAN.R-project.org/package=GGally)
* [ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics](https://CRAN.R-project.org/package=ggplot2)
* [visNetwork: Network Visualization using 'vis.js' Library](https://CRAN.R-project.org/package=visNetwork)
* [xtable: Export Tables to LaTeX or HTML](https://CRAN.R-project.org/package=xtable)
* [dplyr: A Grammar of Data Manipulation](https://CRAN.R-project.org/package=dplyr)

## non default Python packages

* [framed: metabolic modeling for Python](https://pypi.python.org/pypi/framed)
* [COBRApy: constraints-based modeling of biological networks](https://pypi.python.org/pypi/cobra/0.9.1)

# Design

Diagram presenting the design of the application

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