- *MOCCASIN: "Model ODE Converter for Creating Awesome SBML INteroperability"*

- Translates a common form of MATLAB ODE model into SBML by inferring reaction network

  - Uses algorithm developed by Fages et al. (http://doi.org/f2vbzg)

- Does **not** require MATLAB

  - Parser & translator written in Python; uses libSBML + BIOCHAM web service

- Offers both graphical and command-line interfaces

- Currently limited to relatively basic MATLAB models of a certain form

- Near-future goals:

  - Interpret and support more MATLAB constructs

  - Implement Fages et al. inference algorithm in MOCCASIN itself

- Developed by Mike Hucka (Caltech), Sarah Keating (EBI) and Harold Gómez (Boston University). NIH funding via Mount Sinai School of Medicine (NY) thanks to Stuart Sealfon.

Welcome to MOCCASIN

File selection

Choose a file for conversion: /Users/mhucka/moccasin/moccasin-demo/antagonist.m Browse

File conversion

Variable encoding: (•) SBML Species ( ) SBML Parameters Convert

Output format: (•) SBML (reactions) ( ) SBML (equations) ( ) XPPAUT

MATLAB File

```
function y=resi(t,x)


% viral antagonism parameters, 1st (myf) for IFNb induction, 2nd (myfs)

%  for CPFS binding

y=zeros(4,1);

b1=0.4;

b4=0.2;
```

Converted File

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level3/version1/core" level="3" version="1">
  <model id="sauro1" name="sauro1 translated by MOCCASIN" substanceUnits="substance" timeUnits="second"
volumeUnits="volume" areaUnits="area" lengthUnits="metre" extentUnits="substance">
    <listOfUnitDefinitions>
      <unitDefinition id="volume">
        <listOfUnits>
          <unit kind="litre" exponent="1" scale="0" multiplier="1"/>
        </listOfUnits>
      </unitDefinition>
      <unitDefinition id="substance">
        <listOfUnits>
          <unit kind="mole" exponent="1" scale="0" multiplier="1"/>
```

Output file after conversion

Done! SBML format - reactions Version: (local)

Simple interface

MATLAB file

SBML output