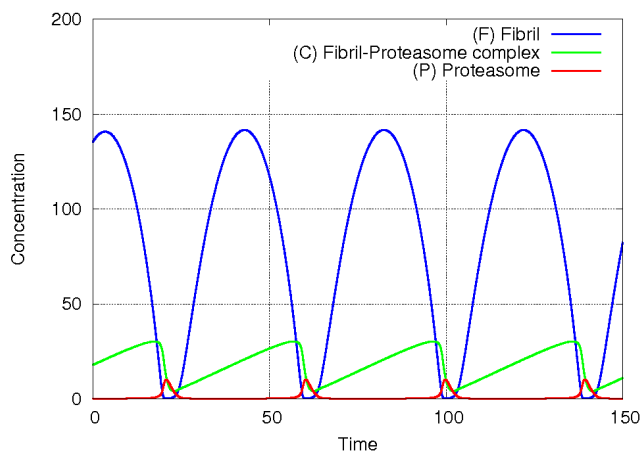


Sneppen2009 - Modeling proteasome dynamics in Parkinson's disease


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Curator's comment:

(added: 10 Sep 2014, 12:15:50, updated: 10 Sep 2014, 12:15:50)

Figure 3 of the reference publication has been reproduced here. Dynamics of proteasome (P), fibrils (F) and the complex (C) concentration are plotted during 150 arbitrary units.

The simulation was done using Copasi v4.12 (Build 81) and the plots were generated using Gnuplot. The Copasi file of the model with simulation settings can be downloaded from the below link.

Build: [15671cb](#) (<https://bitbucket.org/biomodels/jummp-biomodels/commits/all?search=15671cb>) | Wed, 14 Feb 2024 21:14:41 +0000

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