

SYSTEMS CANCER CHRONOTHERAPEUTICS : IN VITRO MOLECULAR CHRONOPHARMACOLOGY OF THE ANTICANCER DRUG IRINOTECAN

Annabelle Ballesta^{1,2} and collaborators

1 Mount Sinai school of medicine, department of pharmacology & systems therapeutics, New York, USA

2 Inserm team U776: Biological Rhythms and Cancer, Hôpital Paul Brousse, Villejuif, France

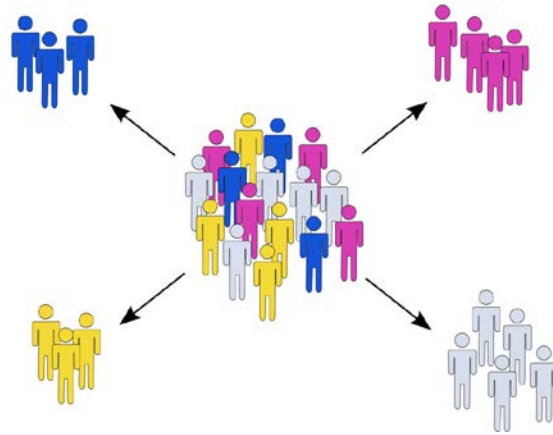
18 May, 2014 Stuttgart

OUTLINE

1. In vitro molecular chronopharmacology of irinotecan
2. Personalizing irinotecan circadian delivery: a tutorial in Scilab.

Molecular-based personalization of cancer chronotherapeutics

- Recent clinical evidence of the **need for personalized** chronomodulated administration scheme.



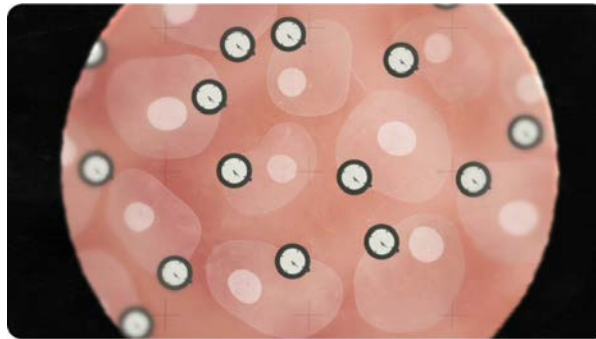
- Require molecular **understanding of drug chronoPK-PD** (pharmacokinetics-pharmacodynamics) towards identification of potential **clinical biomarkers**.
- **In vitro combined biological and mathematical** study of irinotecan (CPT11) molecular chronoPK-PD

In vitro circadian studies

- Rationale of in vitro studies: every nucleated cell endowed with a molecular circadian clock.



- In the absence of synchronizer, clocks do not display the same period or phase.
- Seric shocks (ie. exposing cells to a large amount of nutrients during 2 hours) synchronize the circadian clock of the cells which oscillate in synchrony:



- Choice of **Caco-2 human colorectal cancer cells for irinotecan study**: well-established in vitro model for human intestine + express clock genes



Irinotecan (CPT11)

- Clinically-approved for the treatment of colorectal cancer since 1994.
- Part of the **camptothecin** family. Active principle comes from the chinese tree *Camptotheca acuminata decne.*





CPT11 Pharmacokinetics (PK)

CPT11



CES

SN38



UGT1A1

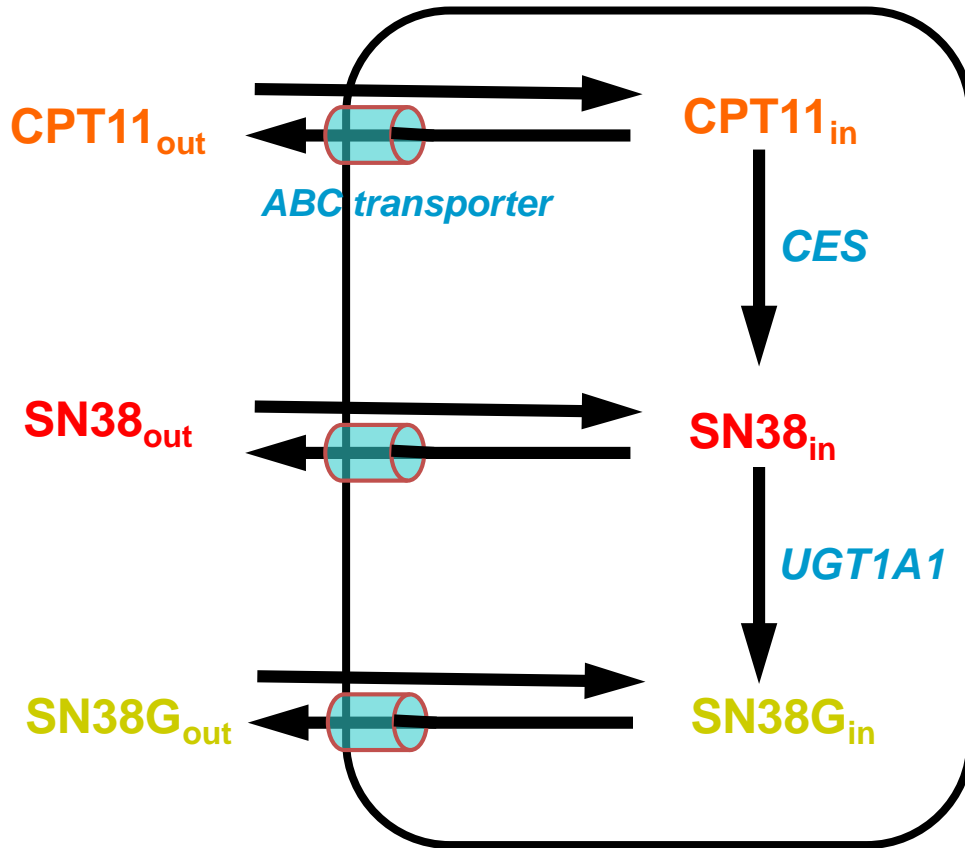
SN38G

➤ **CPT11** is bioactivated into **SN38** by carboxylesterases (**CES**). **SN38** is 100 to 1000 fold more cytotoxic than **CPT11**.

➤ **SN38** is transformed into **SN38G** mainly under the enzymatic activity of **UGT1A1**. **SN38G** is completely inactive.



CPT11 Pharmacokinetics (PK)



- CPT11, SN38 and SN38G are pumped outside of the cells by ABC transporters (ABC= ATP-Binding Cassette)

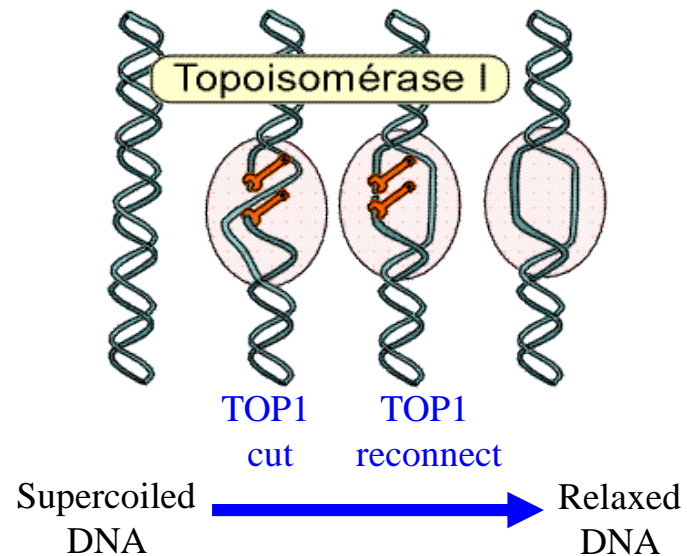
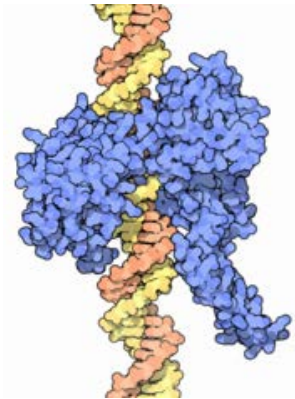


CPT11 Pharmacodynamics (PD)

- CPT11 is an inhibitor of topoisomerase 1 (TOP1).
- What is TOP1? An enzyme present in all nucleated cells whose function is to relax supercoiled DNA.

TOP1

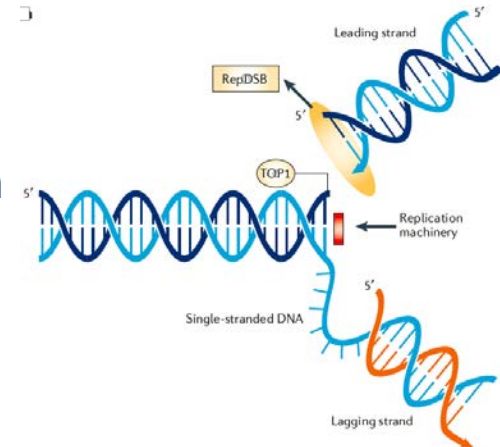
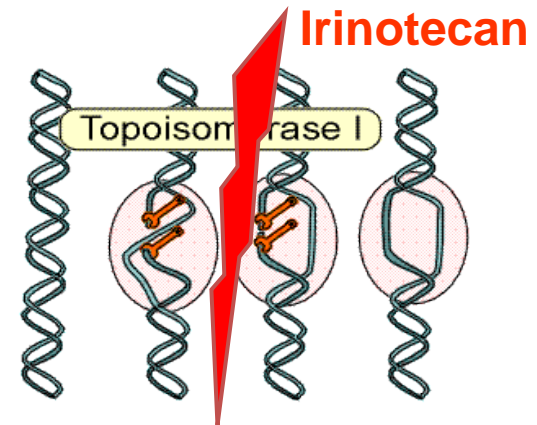
DNA





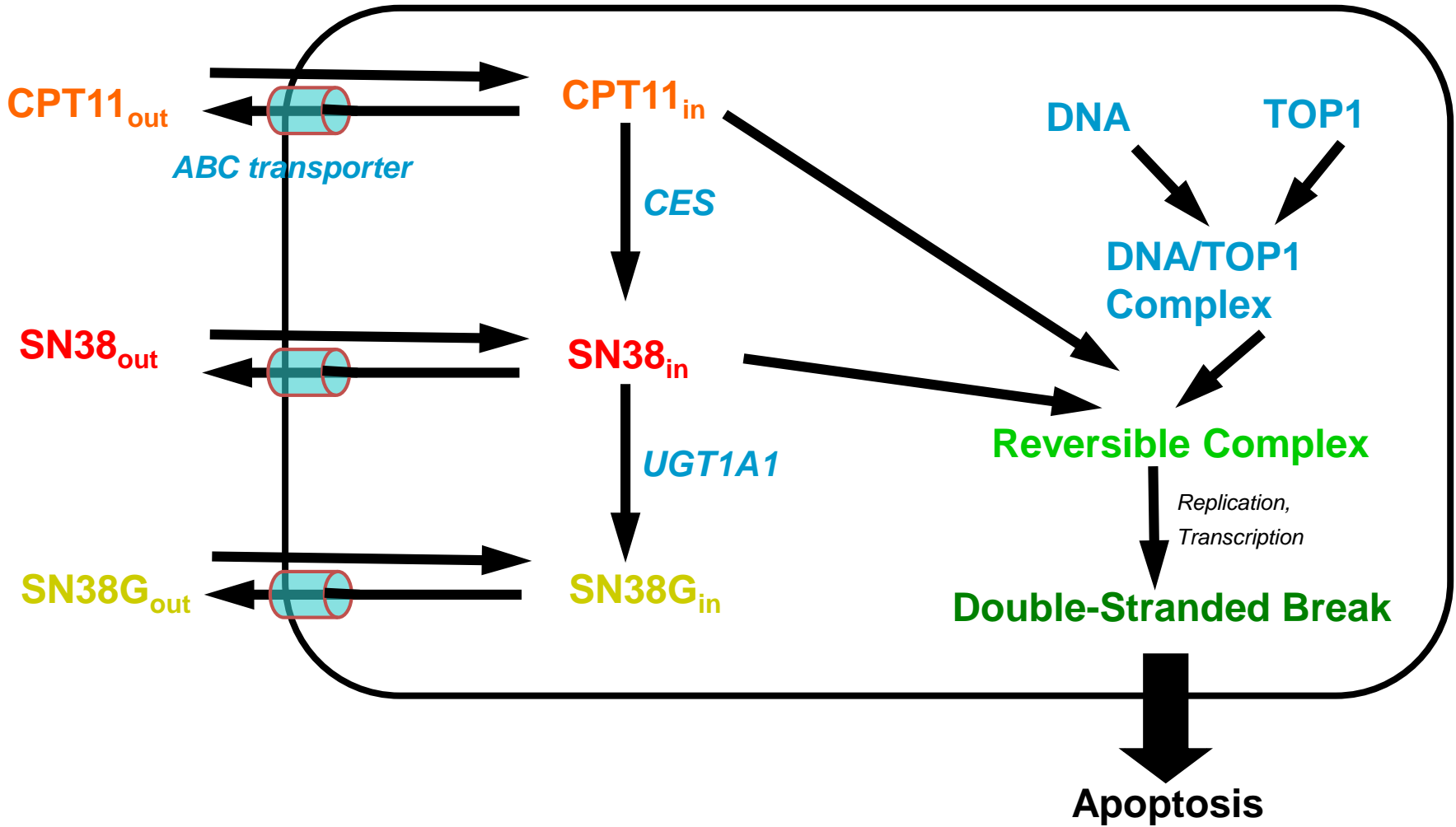
CPT11 Pharmacodynamics (PD)

- Irinotecan prevents **TOP1** from reconnecting the broken **DNA strand**, creating reversible TOP1/DNA/Irinotecan complexes.
- **Collisions** between those complexes and replication forks or transcription mechanisms create **DNA double-stranded breaks**, which can be lethal for the cell.



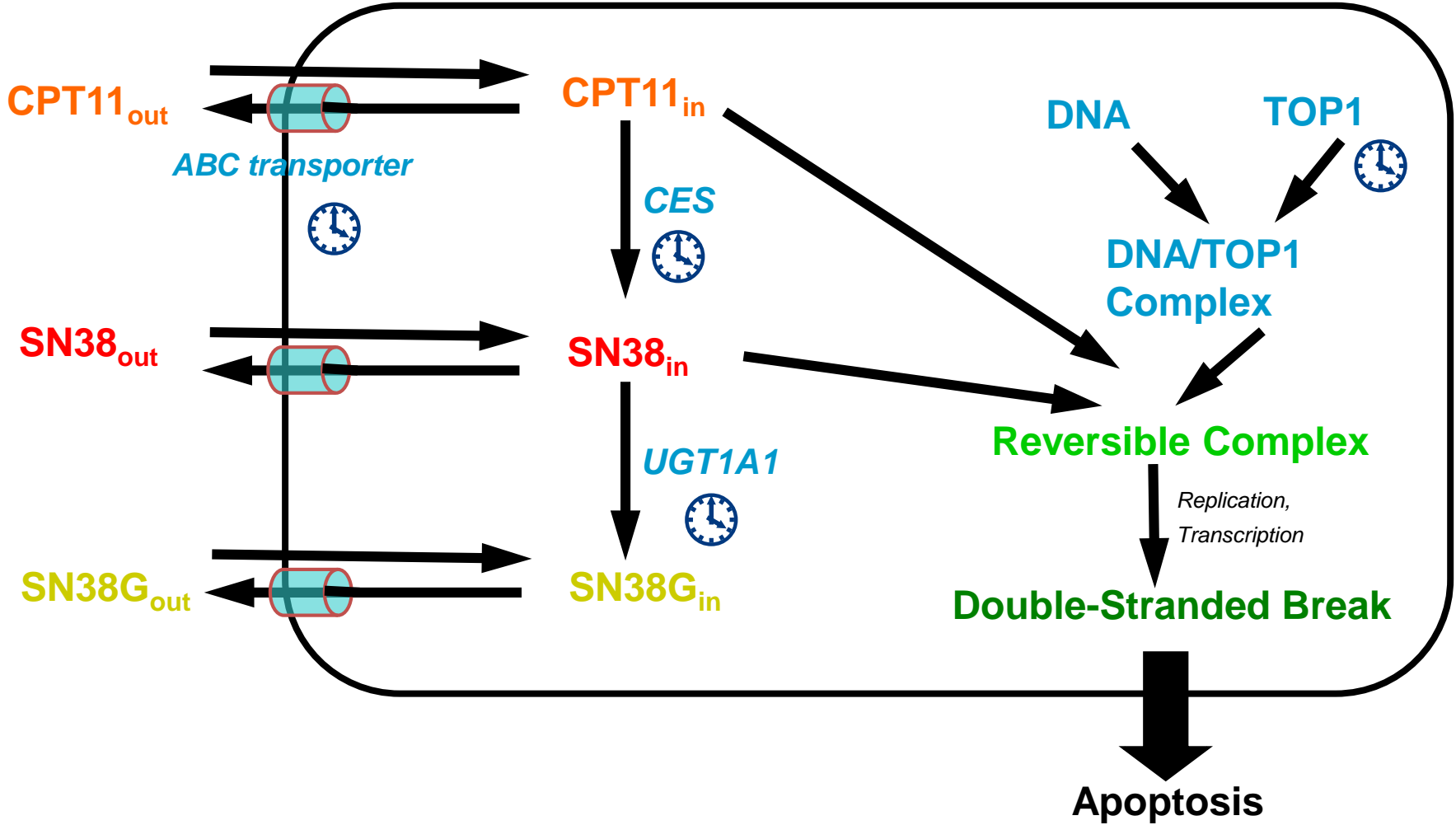


CPT11 molecular PK-PD



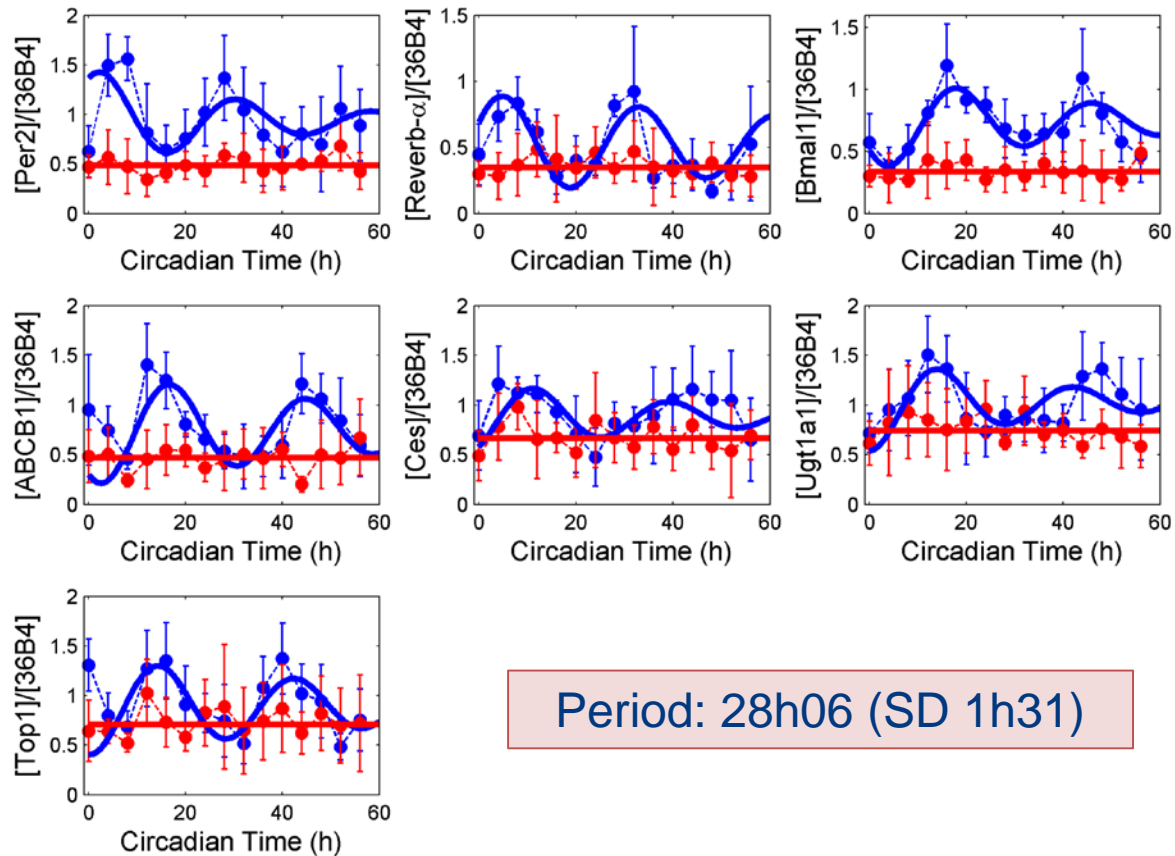


CPT11 molecular PK-PD



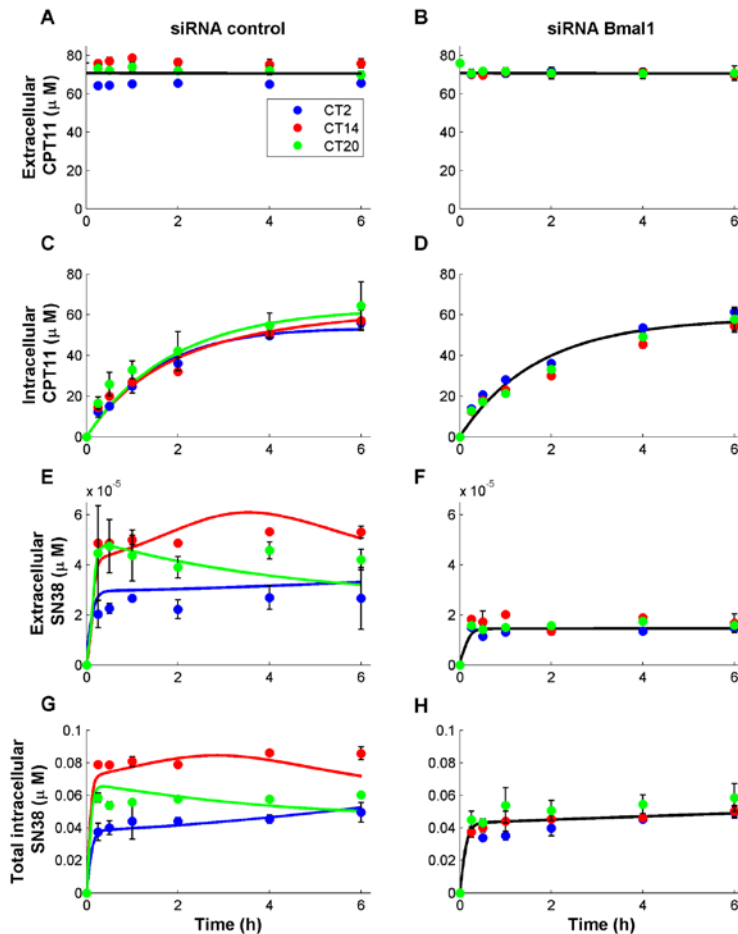
IRINOTECAN MOLECULAR CHRONOPHARMACOLOGY IN CACO-2 CELLS

mRNA circadian rhythms



- Circadian variations of mRNA expression of 3 clock genes and 4 drug metabolism genes in synchronized Caco-2 cells.
- ...disrupted in clock-deficient cells (siRNA Bmal1).

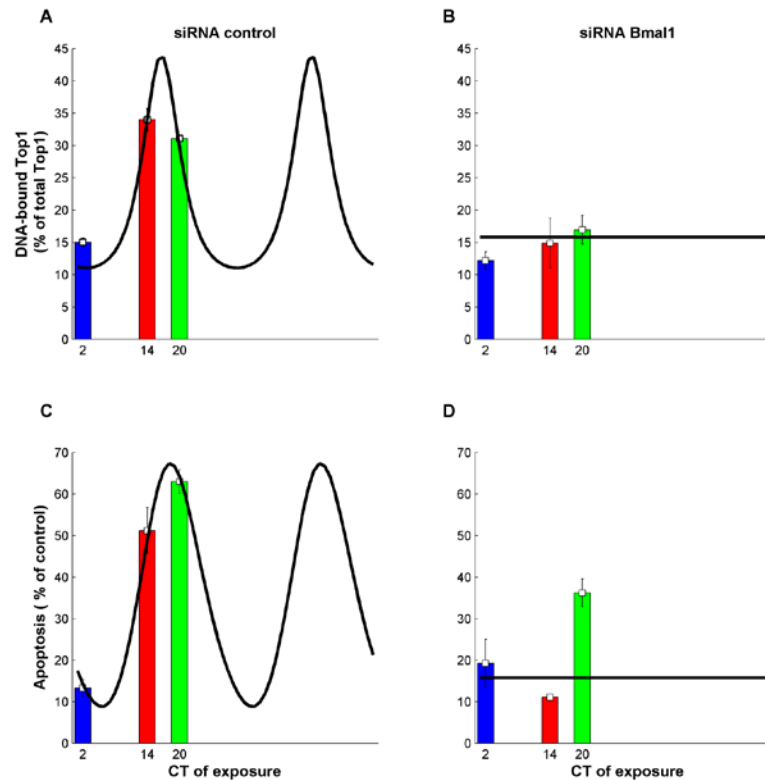
CPT11 PK in Caco-2 cells



Cells exposed to CPT11 (76 μM) during 6h.

- Large and statistically significant circadian variations of SN38in and out in the presence of functional clock.
- ...which are disrupted in clock-deficient cells

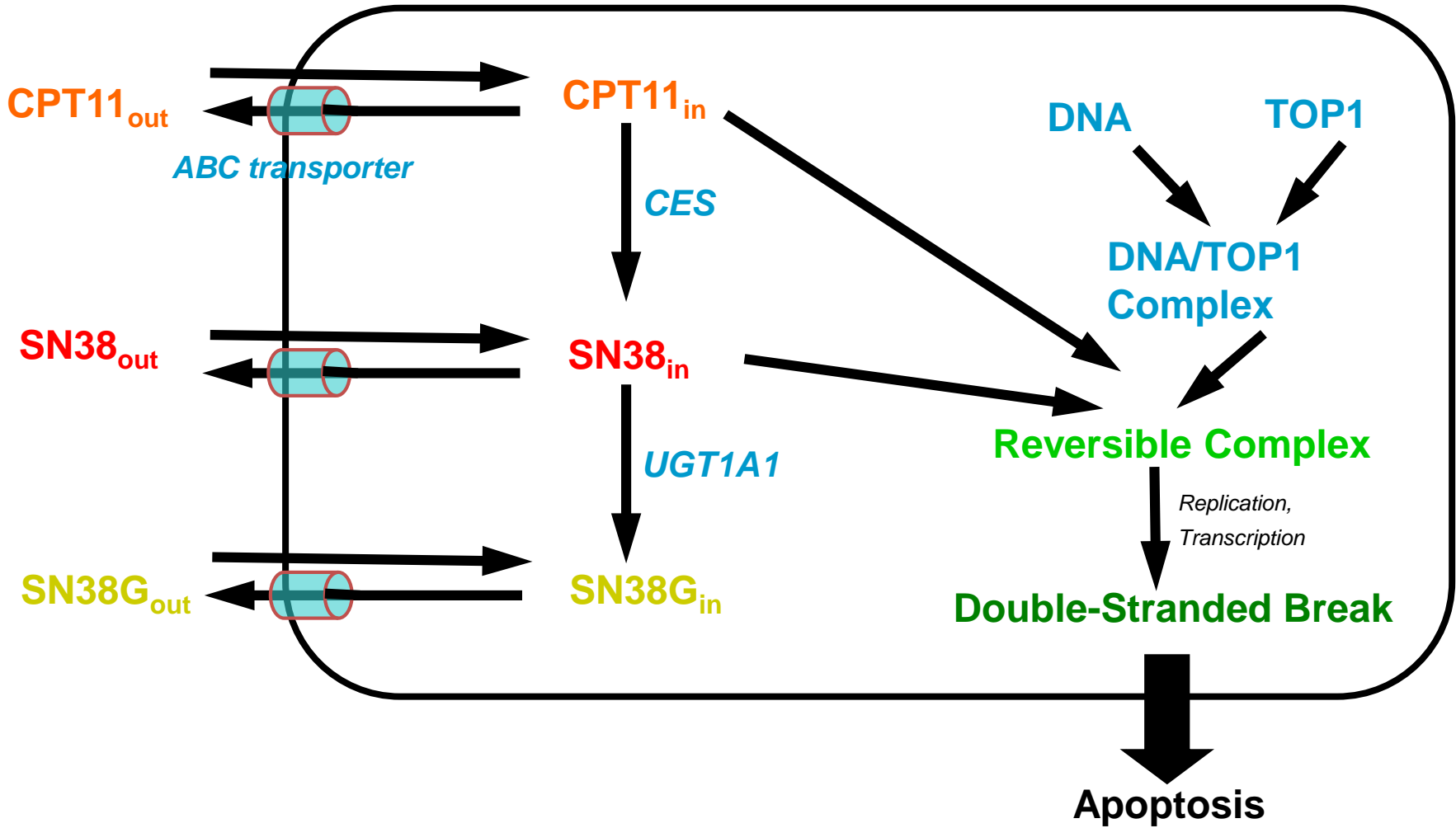
Circadian rhythms of CPT11 PD



- Circadian variations of % of DNA-bound TOP1 (PD marker) and apoptosis in the presence of irinotecan
- ...disrupted in clock-deficient cells.

MODEL OF IRINOTECAN MOLECULAR CHRONO PK-PD

CPT11 molecular PK-PD



Ordinary differential equations

$$\begin{aligned} \frac{d[CPT_{out}]}{dt} \frac{V_{out}}{V_{in}} &= -k_{upCPT}[CPT_{out}] + \frac{V_{effCPT}[ABC_CPT][CPT_{in}]}{K_{effCPT} + [CPT_{in}]} \\ \frac{d[CPT_{in}]}{dt} &= k_{upCPT}[CPT_{out}] - \frac{V_{effCPT}[ABC_CPT][CPT_{in}]}{K_{effCPT} + [CPT_{in}]} - \frac{V_{ces}[CES][CPT11_{in}]}{K_{ces} + [CPT11_{in}]} \\ \frac{d[SN_{out}]}{dt} \frac{V_{out}}{V_{in}} &= -k_{upSN}[SN_{out}] + \frac{V_{effSN}[ABC_SN][SN_{in}]}{K_{effSN} + [SN_{in}]} \\ \frac{d[SN_{in}]}{dt} &= k_{upSN}[SN_{out}] - \frac{V_{effSN}[ABC_SN][SN_{in}]}{K_{effSN} + [SN_{in}]} + \frac{V_{ces}[CES][CPT_{in}]}{K_{ces} + [CPT_{in}]} \\ &\quad - \frac{V_{ugt}[UGT][SN_{in}]}{K_{ugt} + [SN_{in}]} - k_{f2}[DNA_{TOP1}][SN38_{in}] + k_{r2}[Compl] \\ \frac{d[TOP1]}{dt} &= k_{ftop} - k_{dtop}[TOP1] - k_{f1}[TOP1][DNA_{free}] + k_{r1}[DNA/TOP1] + k_{r2}[Compl] \\ \frac{d[DNA/TOP1]}{dt} &= k_{f1}[TOP1][DNA_{free}] - k_{f2}[DNA/TOP1][SN_{in}] - k_{r1}[DNA/TOP1] \\ \frac{d[Compl]}{dt} &= k_{f2}[DNA/TOP1][SN_{in}] - k_{r2}[Compl] - k_{Irr}[Compl] \\ \frac{d[Icompl]}{dt} &= k_{Irr}[Compl] \end{aligned}$$

Mathematical model for protein circadian rhythm

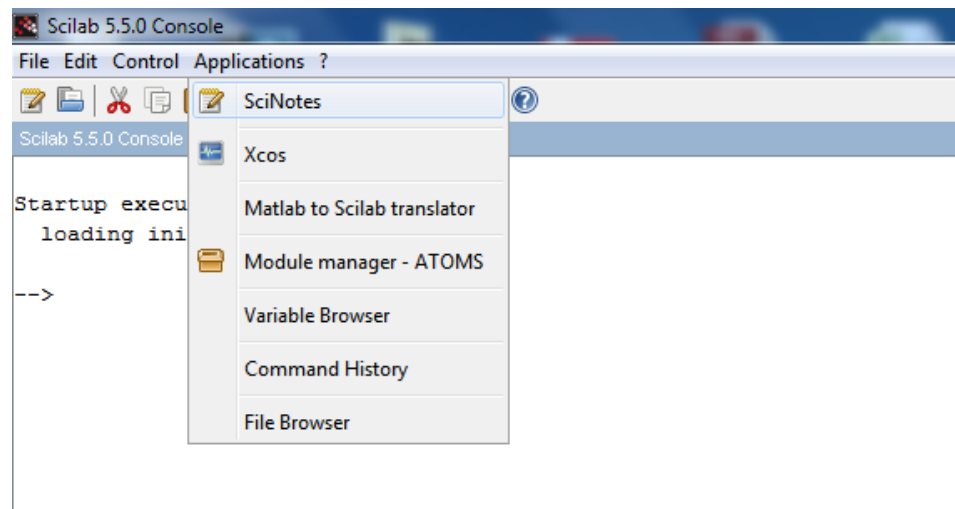
- Equation for protein concentrations:

$$[Protein] = M + A \cos\left(\frac{2\pi}{T}(t - \phi)\right).$$

- Parameter estimation utilizing Caco-2 cell datasets, through least square method and Monte carlo simulations (Matlab)

Scilab Tutorial

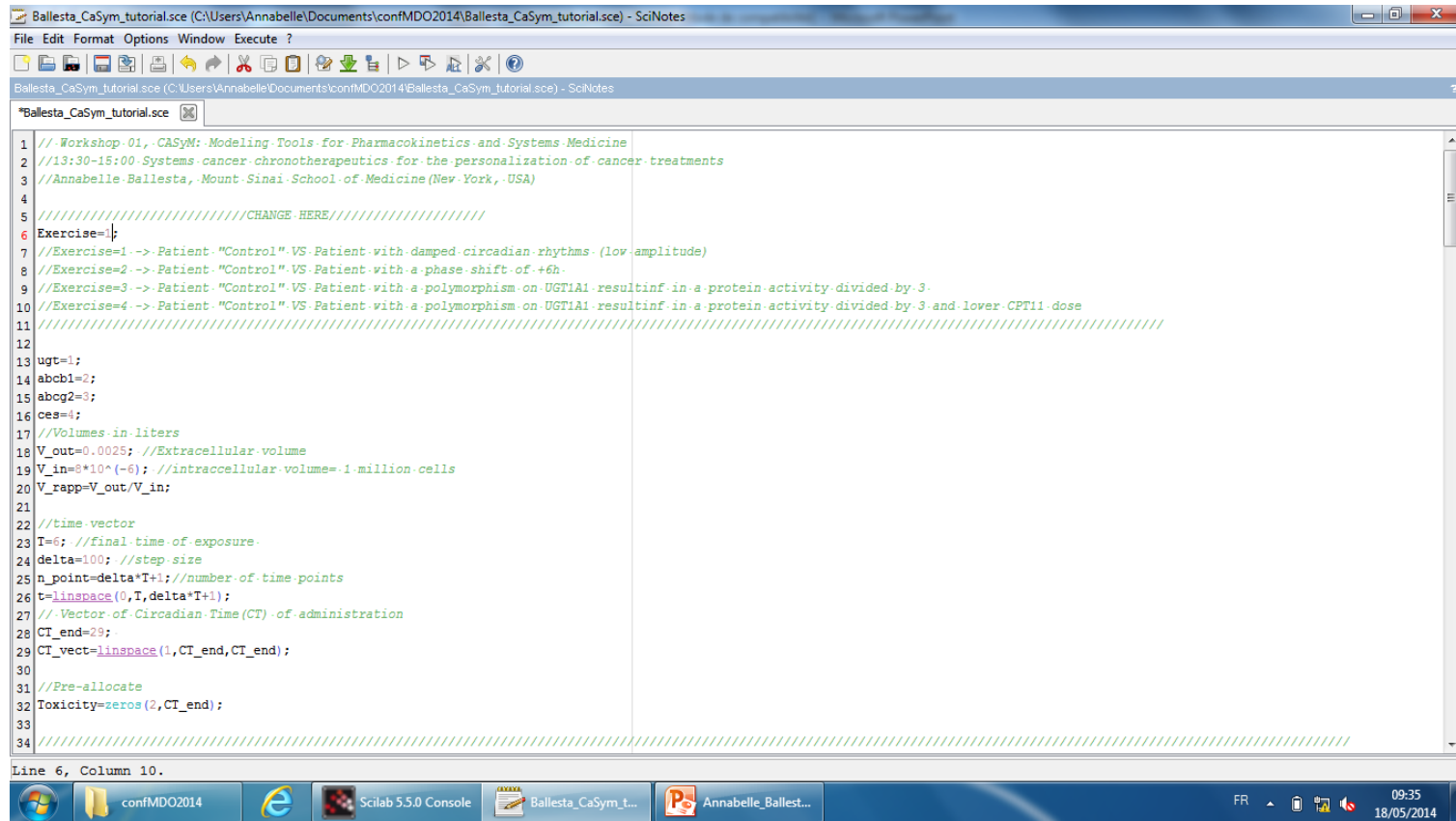
- Download file from: <http://dl.free.fr/mVDfpR5va>
- Open Scilab (Start -> Scilab)
- Open Scinotes : Applications->Scinotes



- Open file in Scinotes

Scilab Tutorial

Desktop should look like this:



```
Ballesta_CaSym_tutorial.sce (C:\Users\Annabelle\Documents\confMDO2014\Ballesta_CaSym_tutorial.sce) - SciNotes
File Edit Format Options Window Execute ?
Ballesta_CaSym_tutorial.sce (C:\Users\Annabelle\Documents\confMDO2014\Ballesta_CaSym_tutorial.sce) - SciNotes
*Ballesta_CaSym_tutorial.sce
1 // Workshop 01, CASym: Modeling Tools for Pharmacokinetics and Systems Medicine
2 //13:30-15:00: Systems cancer chronotherapeutics for the personalization of cancer treatments
3 //Annabelle Ballesta, Mount Sinai School of Medicine (New York, USA)
4
5 ///////////////////////////////////////////////////////////////////CHANGE HERE/////////////////////////////////////////////////////////////////
6 Exercise=1;
7 //Exercise=1 -> Patient "Control" VS Patient with damped circadian rhythms (low amplitude)
8 //Exercise=2 -> Patient "Control" VS Patient with a phase shift of +6h.
9 //Exercise=3 -> Patient "Control" VS Patient with a polymorphism on UGT1A1 resultinf in a protein activity divided by 3.
10 //Exercise=4 -> Patient "Control" VS Patient with a polymorphism on UGT1A1 resultinf in a protein activity divided by 3 and lower CPT11 dose
11 ///////////////////////////////////////////////////////////////////
12
13 ugt=1;
14 abcb1=2;
15 abcg2=3;
16 ces=4;
17 //Volumes in liters
18 V_out=0.0025; //Extracellular volume
19 V_in=8*10^(-6); //intracellular volume= 1 million cells
20 V_repp=V_out/V_in;
21
22 //time vector
23 T=6; //final time of exposure.
24 delta=100; //step size
25 n_point=delta*T+1; //number of time points
26 t=linspace(0,T,delta*T+1);
27 // Vector of Circadian Time (CT) of administration
28 CT_end=29;
29 CT_vect=linspace(1,CT_end,CT_end);
30
31 //Pre-allocate
32 Toxicity=zeros(2,CT_end);
33
34 ///////////////////////////////////////////////////////////////////
```

Line 6, Column 10.

Taskbar: Windows Start, confMDO2014, Scilab 5.5.0 Console, Ballesta_CaSym_t..., Annabelle_Ballesta...

System tray: FR, 09:35, 18/05/2014

Scilab Tutorial

Aim: Demonstrate the need of personalization through modeling.

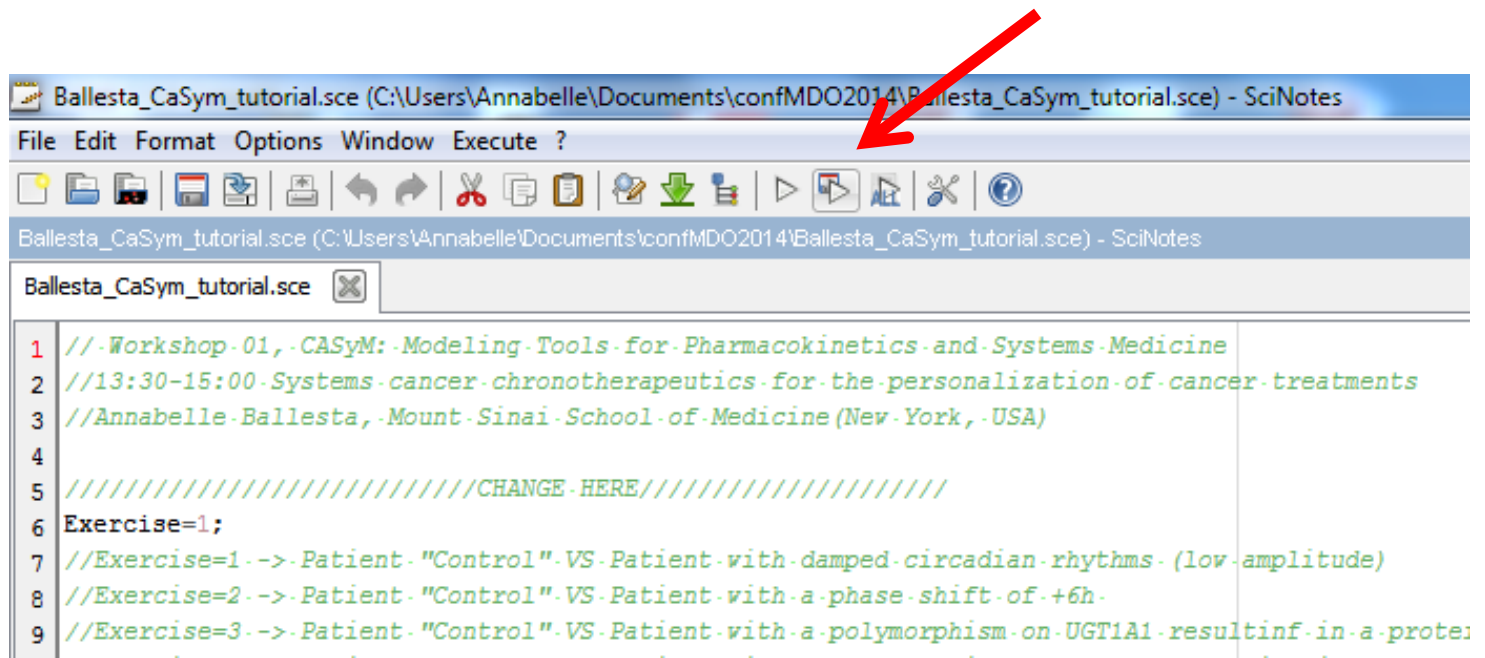
Definitions:

- Irinotecan chronotoxicity = sum of reversible+irreversible complexes.
- Exposure to CPT11 (100 μ M) during 6h.
- Patient control= parameters estimated from Caco-2 cells experiments

Scilab Tutorial

Exercise 1: Compare CPT11 chronotoxicity for Patient Control
VS Patient with damped circadian rhythms = all amplitudes
divided by 2 compared to control

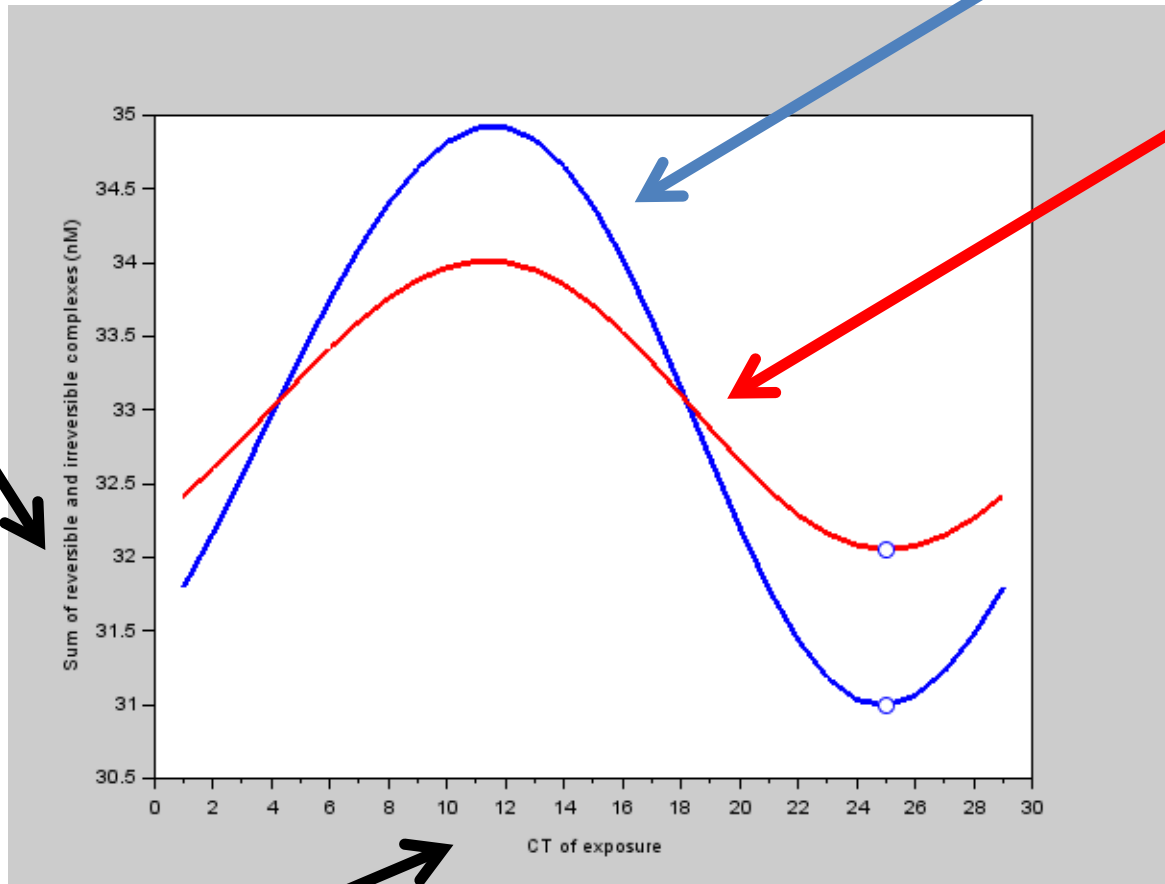
- **Run the file**: press F5 or Click the button:



```
Ballesta_CaSym_tutorial.sce (C:\Users\Annabelle\Documents\confMDO2014\Ballesta_CaSym_tutorial.sce) - SciNotes
File Edit Format Options Window Execute ?
Ballesta_CaSym_tutorial.sce (C:\Users\Annabelle\Documents\confMDO2014\Ballesta_CaSym_tutorial.sce) - SciNotes
Ballesta_CaSym_tutorial.sce
1 // -Workshop-01, -CASyM: -Modeling-Tools-for-Pharmacokinetics-and-Systems-Medicine
2 //13:30-15:00-Systems-cancer-chronotherapeutics-for-the-personalization-of-cancer-treatments
3 //Annabelle-Ballesta, -Mount-Sinai-School-of-Medicine(New-York, -USA)
4
5 //////////////////////////////////CHANGE-HERE////////////////////////////////////
6 Exercise=1;
7 //Exercise=1 -> Patient-"Control"-VS-Patient-with-damped-circadian-rhythms-(low-amplitude)
8 //Exercise=2 -> Patient-"Control"-VS-Patient-with-a-phase-shift-of-+6h.
9 //Exercise=3 -> Patient-"Control"-VS-Patient-with-a-polymorphism-on-UGT1A1-resultinf.in.a-prote:
```

Scilab Tutorial: Exercise 1

Graphical window open:



Patient control

Patient with lower amplitude

Toxicity

Circadian Time of beginning of exposure

Scilab Tutorial: exercise 1

In the Scilab console:

```
Scilab 5.5.0 Console
File Edit Control Applications ?
Scilab 5.5.0 Console

Startup execution:
  loading initial environment

-->exec('C:\Users\Annabelle\Documents\confMDO2014\Ballesta_CaSym_tutorial.sce', -1)

Toxicity Mean (nM)
  32.962115
  33.022366

Toxicity amplitude (nM)
  1.963252
  0.9775148

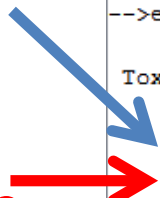
Minimum Toxicity (nM)
  30.994817
  32.053948

CT of Minimum Toxicity (h)
  25.
  25.

-->|
```

Patient control

Patient with lower amplitude



Scilab Tutorial: exercise 1

In the Scilab console:

```
Scilab 5.5.0 Console
File Edit Control Applications ?
Scilab 5.5.0 Console

Startup execution:
  loading initial environment

-->exec('C:\Users\Annabelle\Documents\confMDO2014\Ballesta_CaSym_tutorial.sce', -1)

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1.963252
0.9775148

Minimum Toxicity (nM)
30.994817
32.053948

CT of Minimum Toxicity (h)
25.
25.

-->|
```

Patient control

Patient with lower amplitude



Toxicity amplitude divided by 2

Scilab Tutorial: Exercise 2

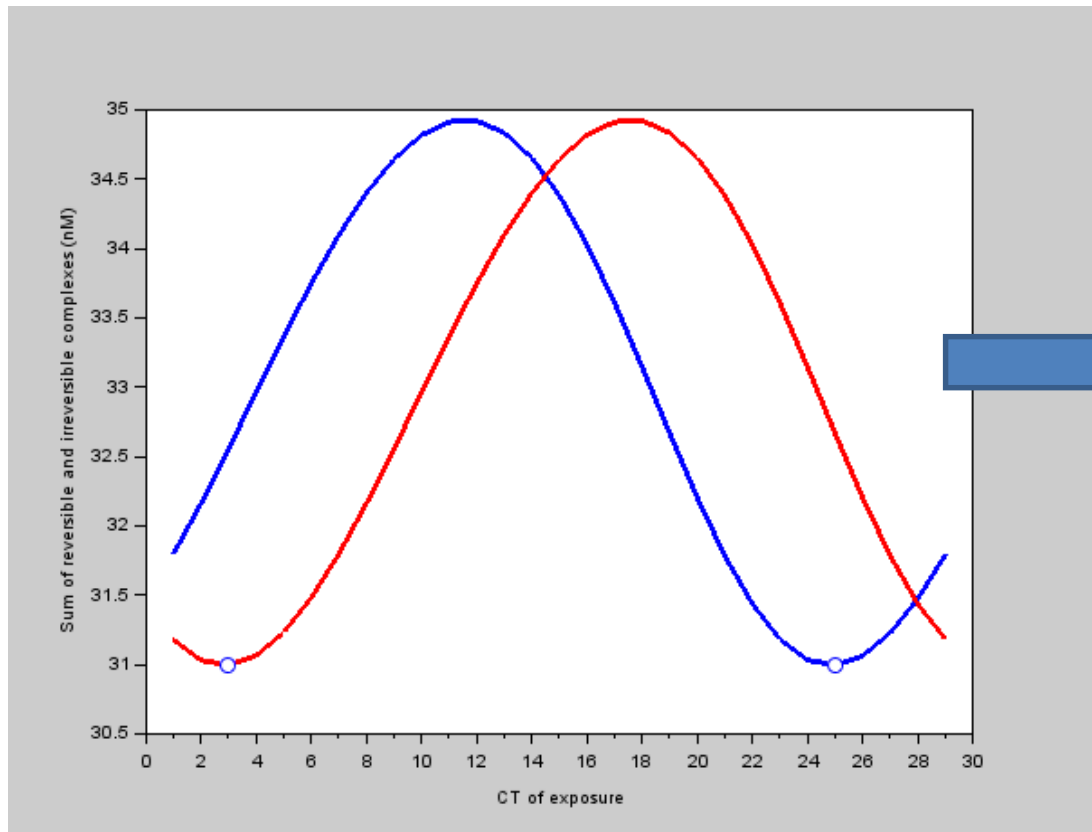
Exercise 2: Patient Control VS Patient with phase shift =all phases shifted of +6h compared to control.

➤ In Scinotes: change variable Exercise to 2

Scilab Tutorial: Exercise 2

Exercise 2: Patient Control VS Patient with phase shift =all phases shifted of +6h compared to control.

➤ In Scinotes: change variable Exercise to 2



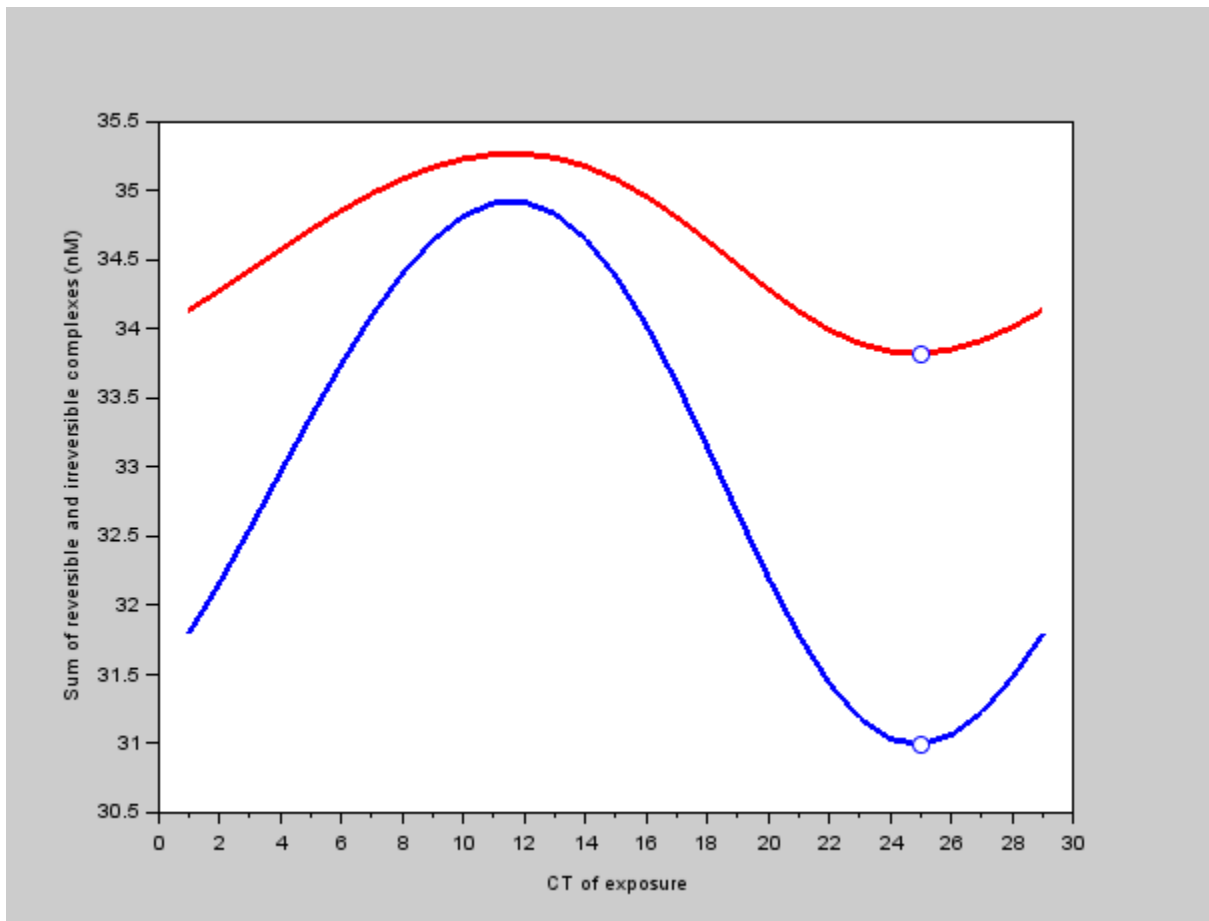
**Toxicity shifted by +6h
(modulo the 28.1h period)**

Scilab Tutorial

Exercise 3: Patient Control VS Patient with UGT1A1 polymorphism leading to a division by 3 of the protein activity.

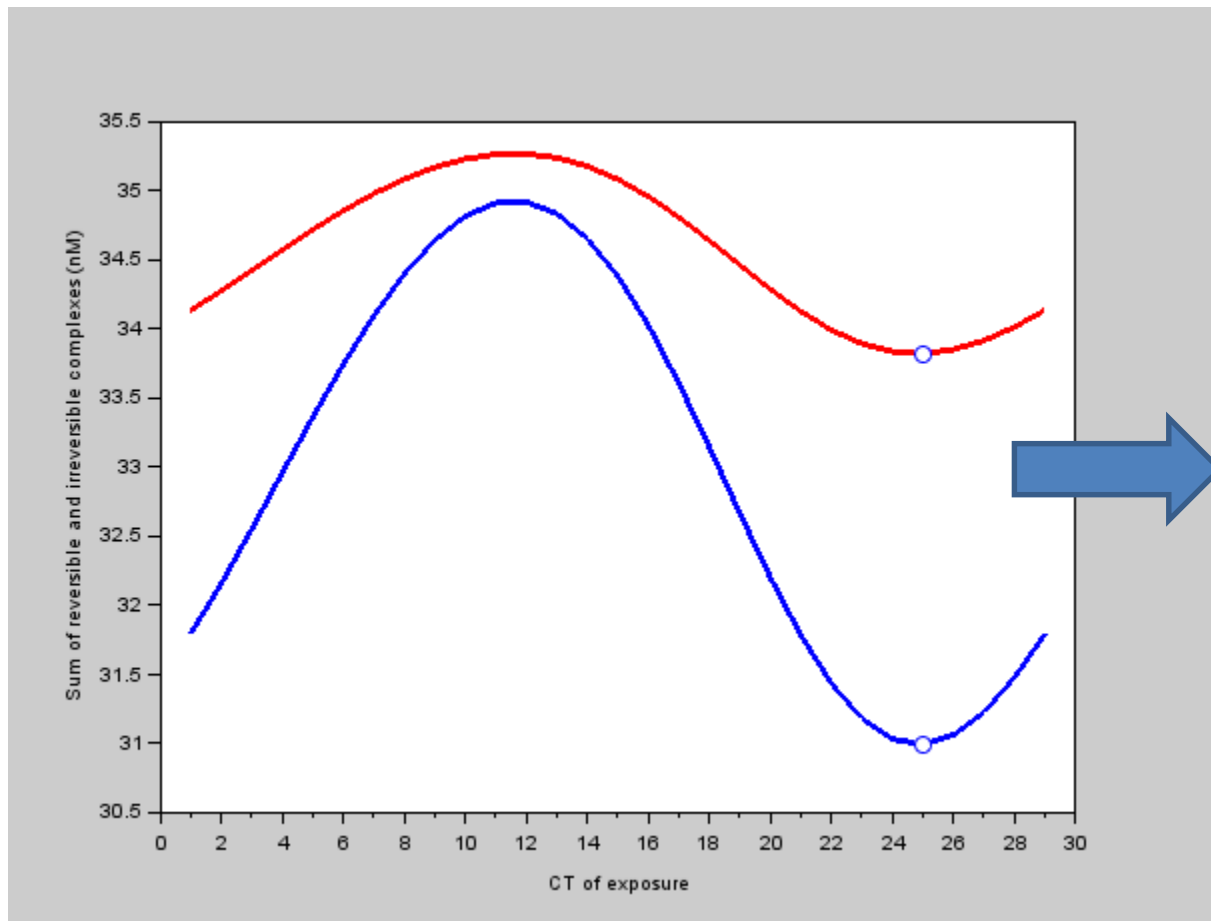
Scilab Tutorial

Exercise 3: Patient Control VS Patient with UGT1A1 polymorphism leading to a division by 3 of the protein activity.



Scilab Tutorial

Exercise 3: Patient Control VS Patient with UGT1A1 polymorphism leading to a division by 3 of the protein activity.



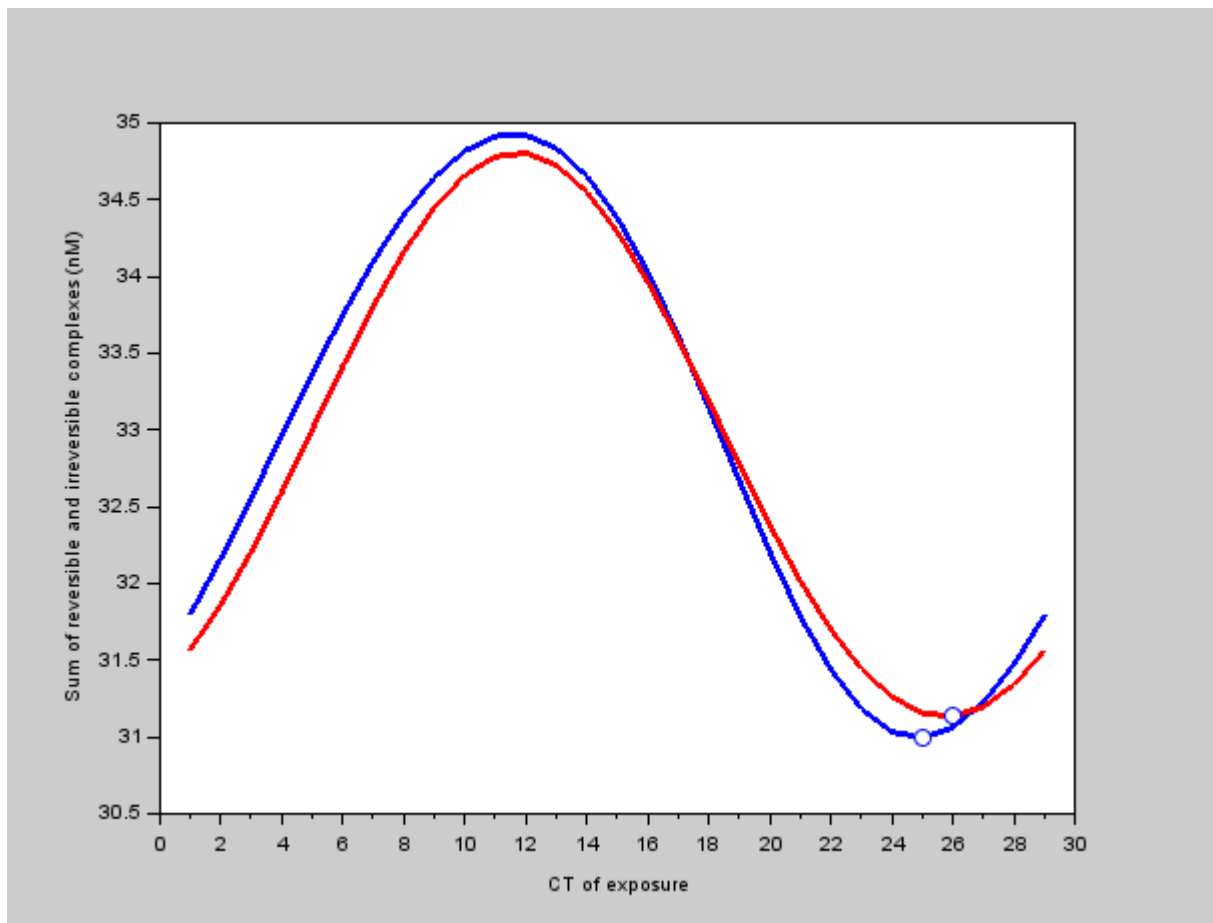
**Increased mean toxicity,
decreased amplitude**

Scilab Tutorial

Exercise 4: Patient with UGT1A1 polymorphism leading to a division by 3 of the protein activity AND lower CPT11 dose (1.4 μ M)

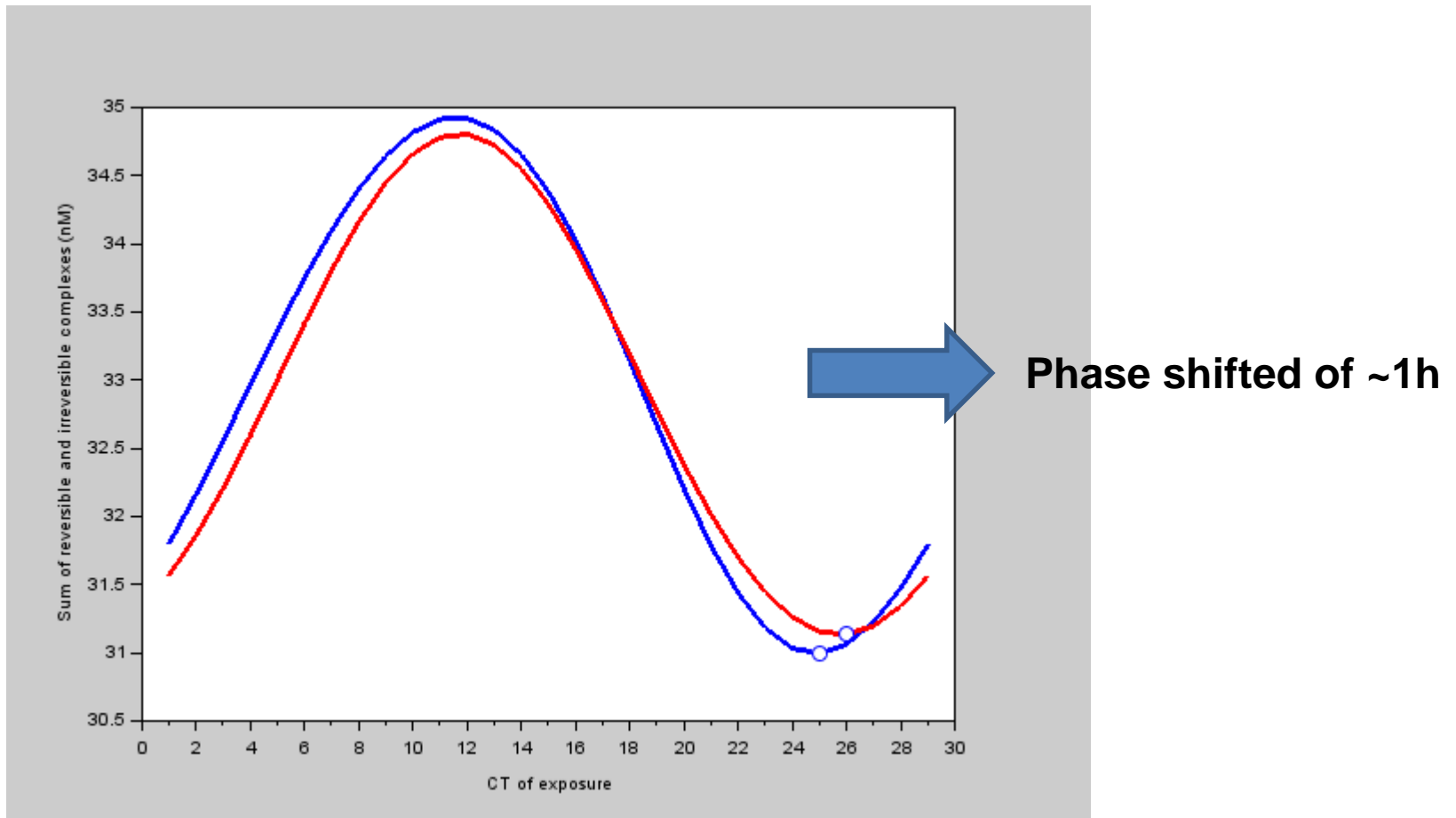
Scilab Tutorial

Exercise 4: Patient with UGT1A1 polymorphism leading to a division by 3 of the protein activity AND lower CPT11 dose (1.4 μ M)



Scilab Tutorial

Exercise 4: Patient with UGT1A1 polymorphism leading to a division by 3 of the protein activity AND lower CPT11 dose (1.4 μ M)





Conclusions of the in vitro study

- **Experimentally-demonstrated circadian organization** in synchronized Caco-2 cell culture
- **A mechanistic mathematical model for CPT11 chronoPK-PD.**
- In vitro systems medicine study demonstrates different chronotoxicity patterns for different circadian and kinetic profiles:
 - **Need for personalized chronotherapeutics**