Intro and references

Nanocompartments proteins and promoters

VP1

There is no Uniprot reference exactly for this protein, here is the similar wild type protein:

P49302 (VP1_POVMP)

Promoter used:

Gal1
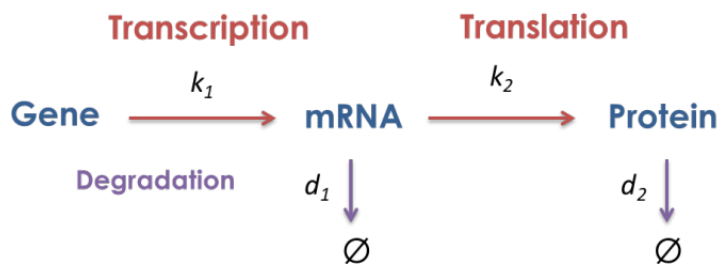
VP2C-GFP

P12908 (VP2_POVMC)

Promoter used:

Gal10

Model: constitutive gene expression

Define model constants

```
p.CN = 17; % initial number of plasmids
% TODO: how to +- calculate it from the lab protocol?
p.d1 = log(2)/3; % mRNA degradation rate
p.d2 = 0.02; % degradation rate
p.k2 = 8.23; % translation rate
p.k1 = 1.19; % transcription rate
```

Define simulation parameters

```
tfin = 60*5;
step = 0.1;
tspan = 0:step:tfin-step;
```
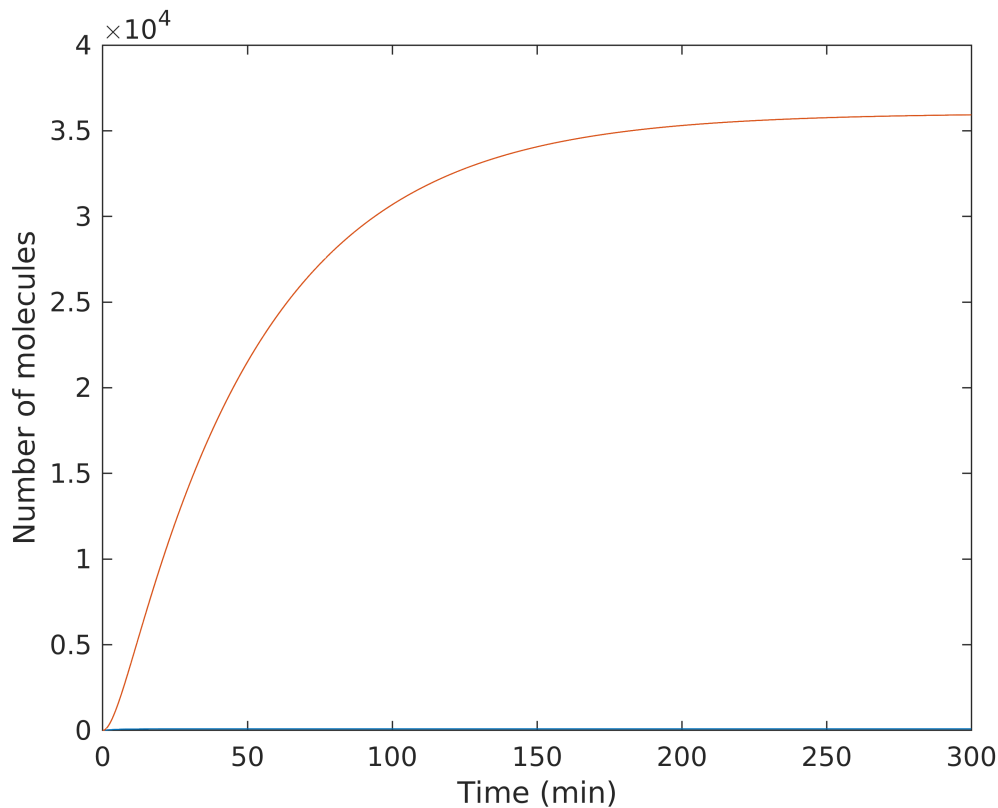
Run the simulation

```
opti = odeset('AbsTol', 1e-8, 'RelTol', 1e-6);

Init = [0 0];

[t0, x0] = ode23t(@(t, x) model_const(t, x, p), tspan, Init, opti);

plot(t0, x0);
xlabel('Time (min)');
ylabel('Number of molecules')
```


Discussion

Actually, all this modeling doesn't make any sence, because I couldn't find all the needed constants.

Here is my suggestion what we can do - "reverse engineer" it, using GFP(t) graph frome the article:

- Adjust the constants so that the peak is on 5 mins and derivative of the curve is the same
- Estimate the initial number of plasmids (read the lab protocol)
- Get the number of molecules, calculate the concentration

```
function [dxdt] = model_const(t, x, p)
    dxdt(1,1) = p.CN*p.k1-p.d1*x(1);
    dxdt(2,1) = p.k2*x(1)-p.d2*x(2);
```

```
end
```