

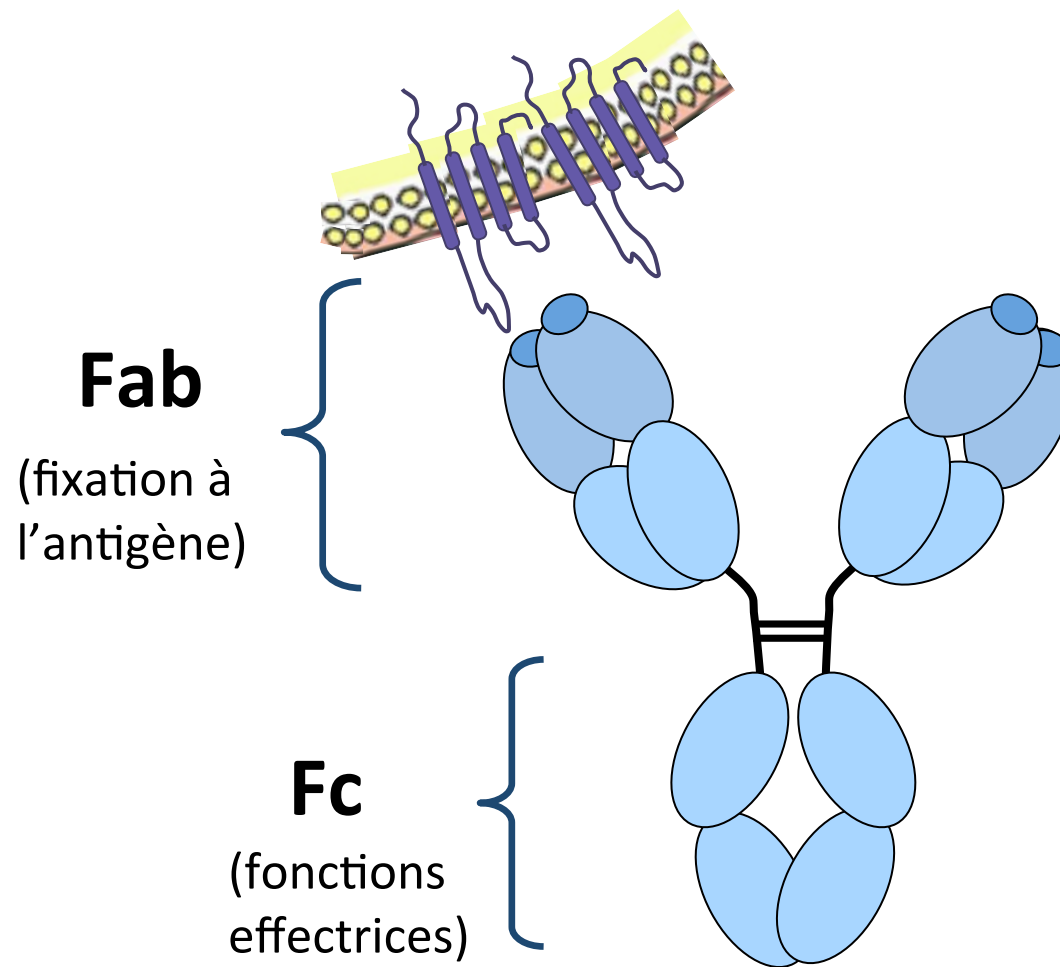
Influence de la masse antigénique sur la PK des anticorps thérapeutiques – modèles TMDD

¹Azzopardi N, ²Madec S, ²Perrolaz V, ¹Ternant D

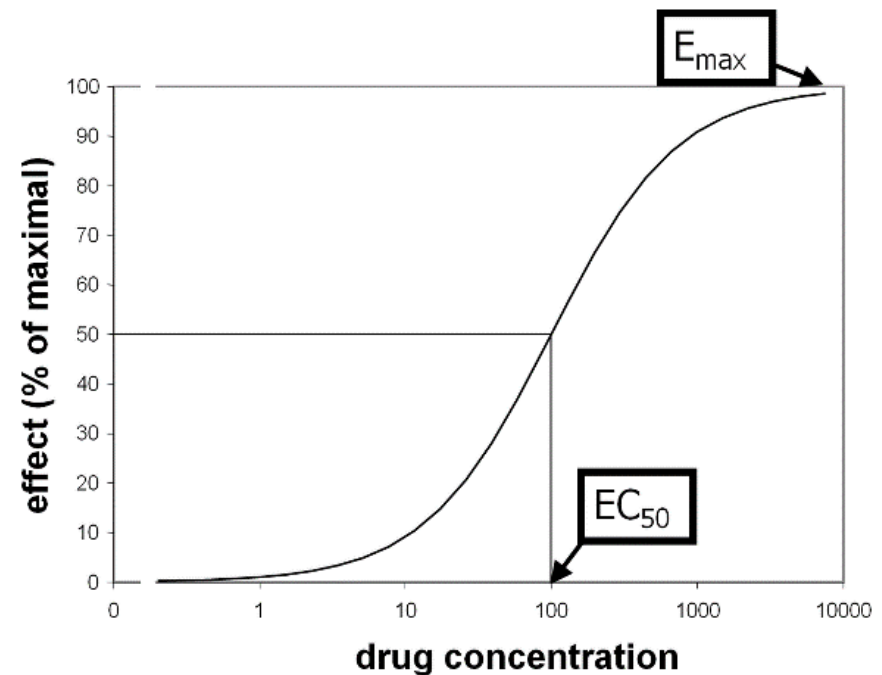
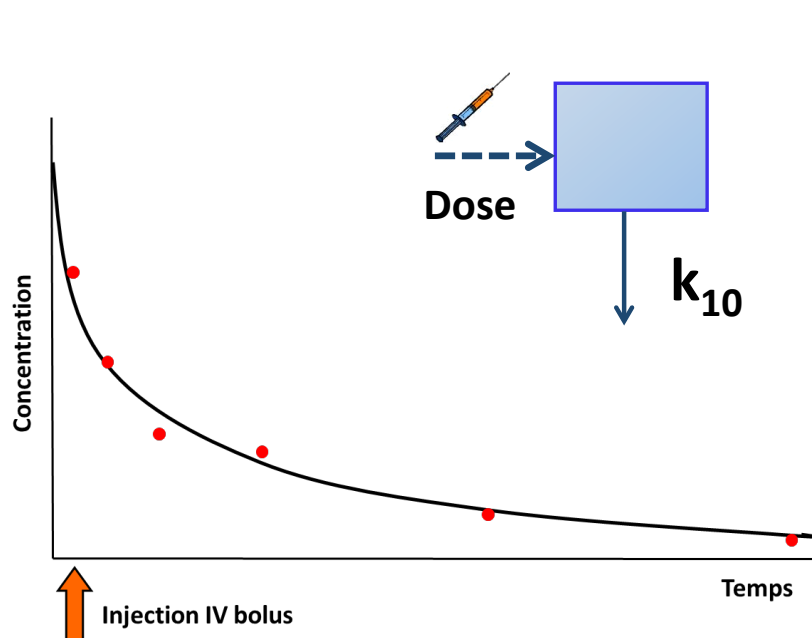
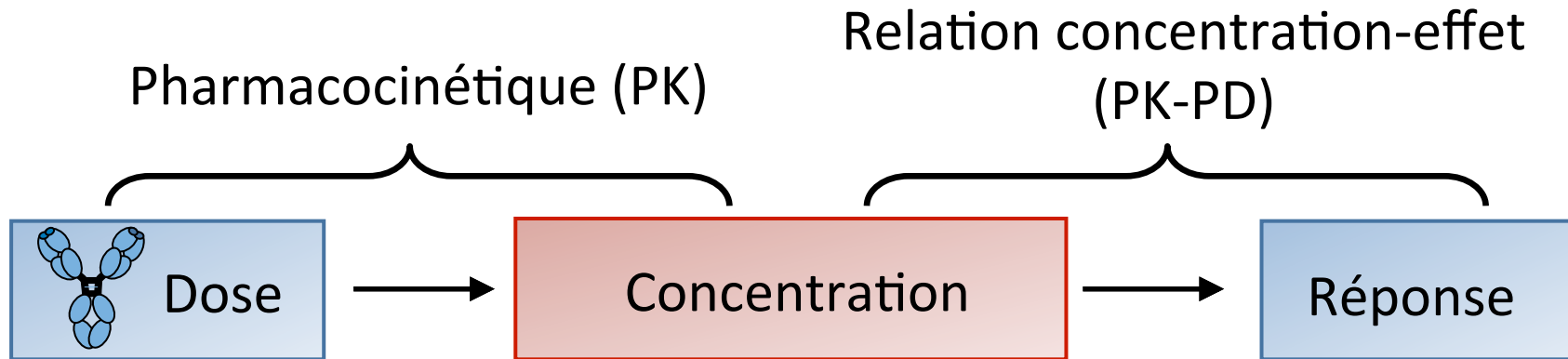
¹UMR CNRS 7292 GICC

²UMR CNRS 7350 LMPT

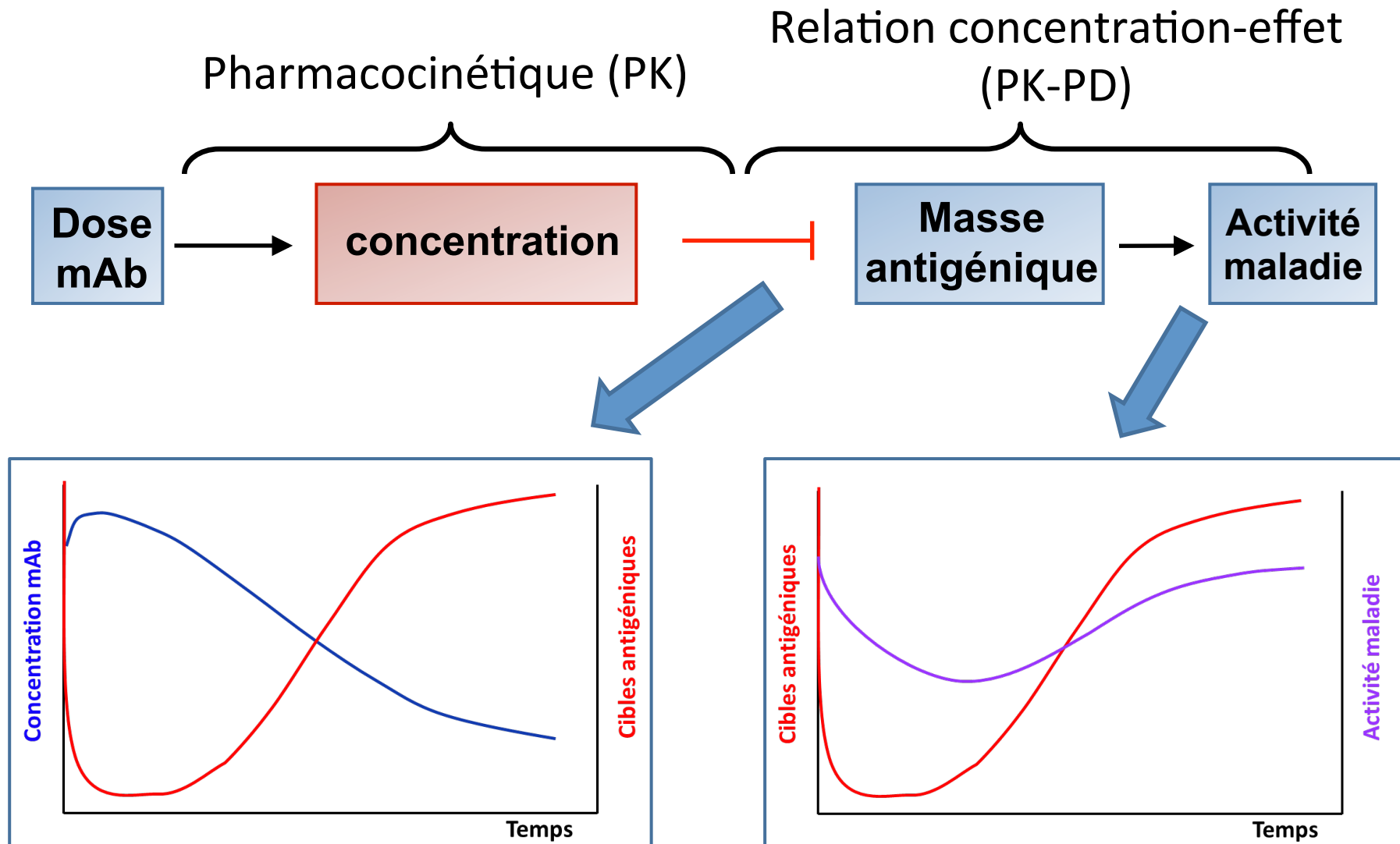
Les anticorps thérapeutiques (mAbs)



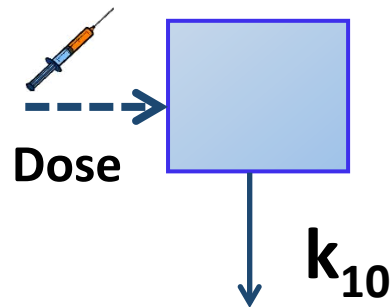
Relation dose-concentration-effet



Relation dose-concentration-effet

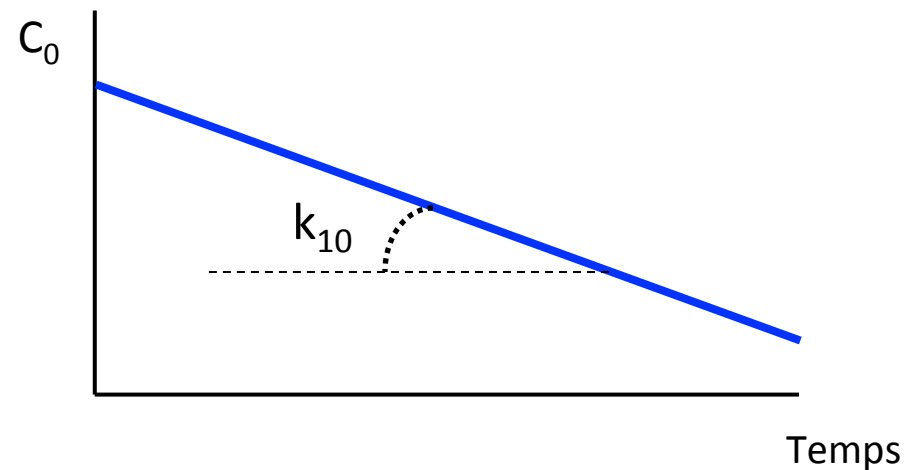


Modèle pharmacocinétique 1 compartiment



$$\frac{dC}{dt} = -k_{10} \cdot C$$

$$C(t) = C_0 \exp(-k_{10} \cdot t)$$

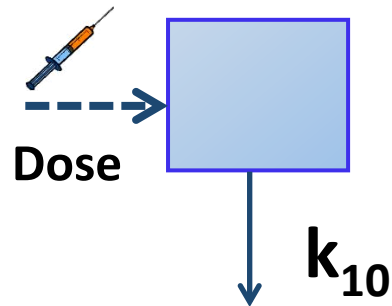


Dose (IV bolus)

k_e : constante d'élimination

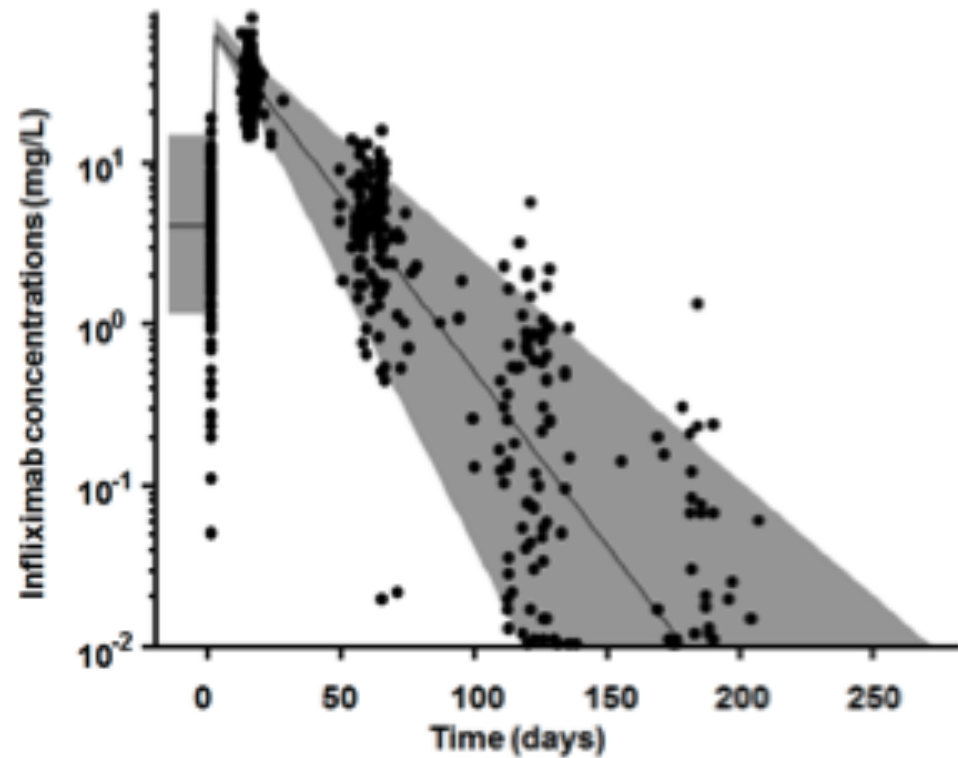
Pharmacocinétique des mAbs

PK infliximab (anti-TNF), maladie de Crohn (n=111)



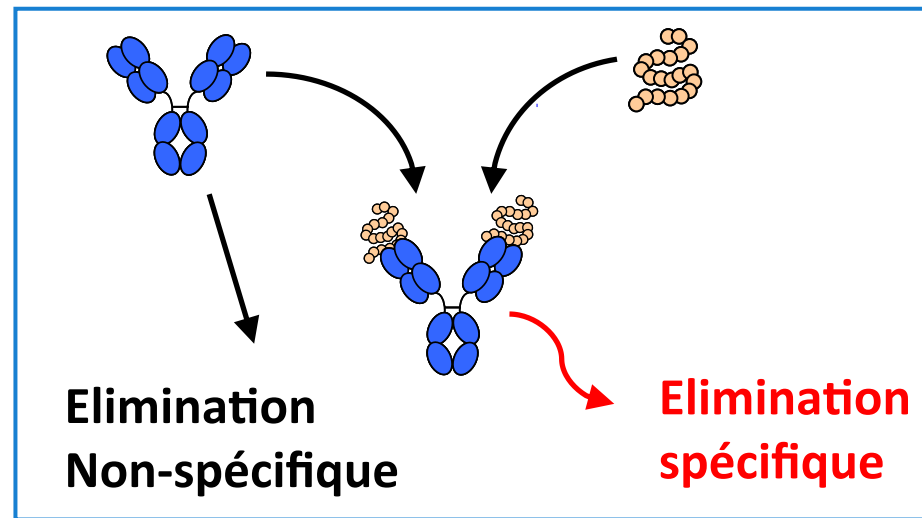
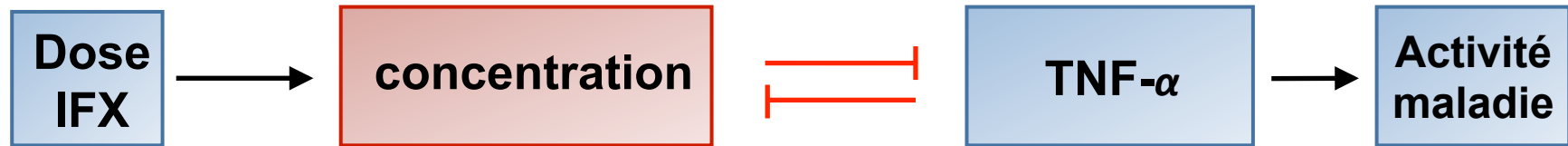
$$\frac{dC}{dt} = -k_{10} \cdot C$$

$$C(t) = C_0 \exp(-k_{10} \cdot t)$$



Ternant, CPK, 2016

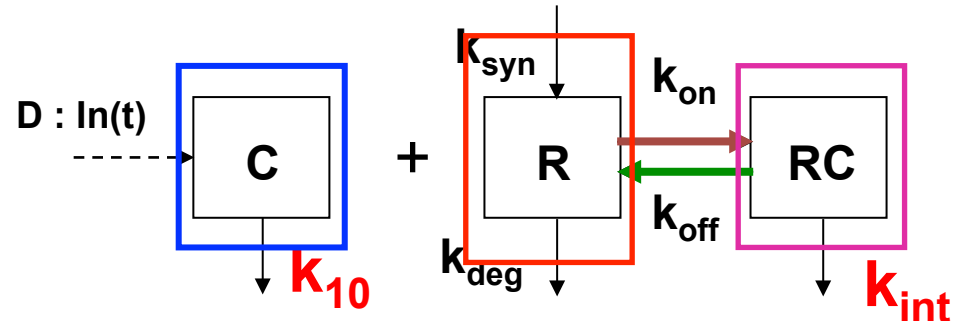
Variabilité PK – masse antigénique



Elimination non-linéaire et masse antigénique

Modèle TMDD

Mager & Jusko, J Pharmacokinet Pharmacodyn, 2001



$$\begin{aligned}
 (1) \quad & \boxed{\frac{dC}{dt} = \ln(t) - k_{10} \cdot C} - k_{on} \cdot R \cdot C + k_{off} \cdot RC \\
 (2) \quad & \boxed{\frac{dR}{dt} = k_{syn} - k_{deg} \cdot R} - k_{on} \cdot R \cdot C + k_{off} \cdot RC \\
 (3) \quad & \frac{dRC}{dt} = k_{on} \cdot R \cdot C - k_{off} \cdot RC + k_{int} \cdot RC
 \end{aligned}$$

$$C(0) = 0, D/V$$

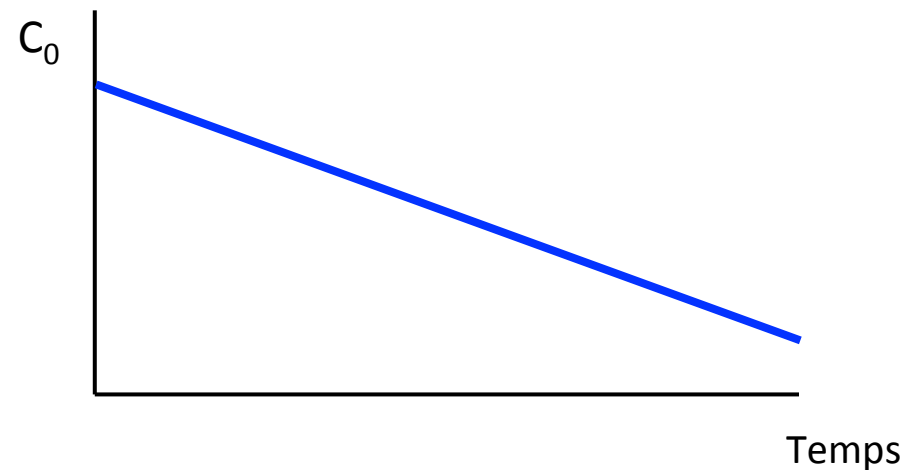
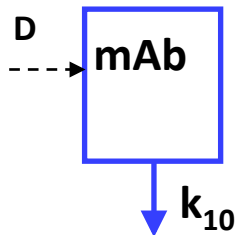
$$R(0) = R_{SS}$$

$$RC(0) = 0$$

- C : concentration (molaire) cpt central
- A_p : quantité (molaire) cpt périphérique
- R : quantité cible, dont récepteur (molaire)
- RC : concentration complexe (molaire)

Elimination non-linéaire et masse antigénique

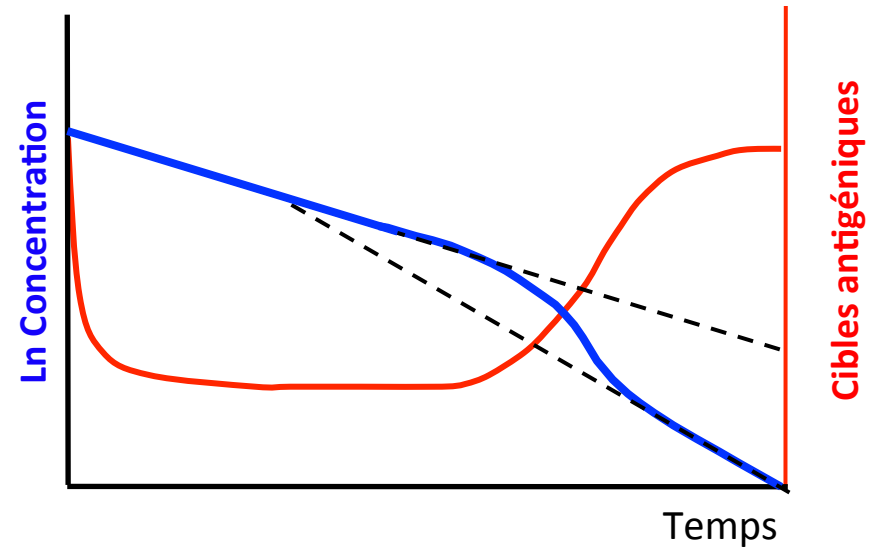
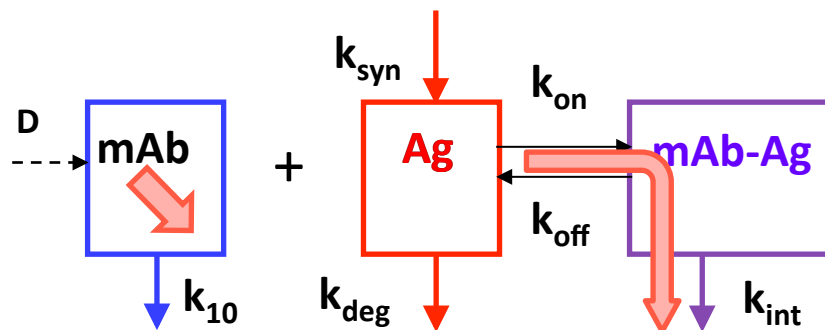
- Elimination médiée par la cible
 - Pas de cible antigénique $\Rightarrow CL_{\text{cible}} = 0$
 - $\Rightarrow \text{Elim}_{\text{totale}} = \text{Elim endogène}$



- mAb libre
- Cible libre
- Complexe mAb-cible

Elimination non-linéaire et masse antigénique

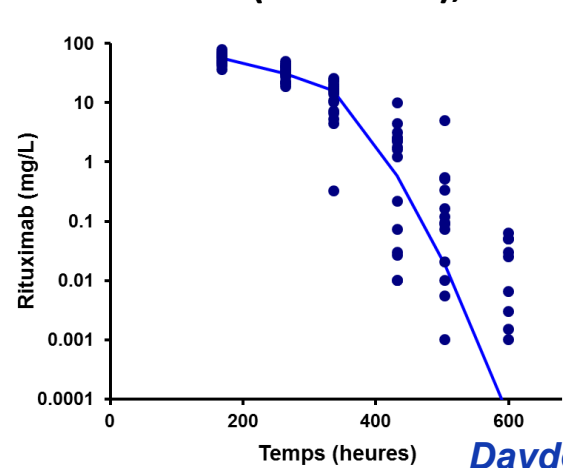
- Elimination médiée par la cible
 - Quantité cibles $\nearrow \Rightarrow \nearrow \text{ELim}_{\text{cible}} \nearrow$
 - $\Rightarrow \text{Elim}_{\text{totale}} \nearrow$



- mAb libre
- Cible libre
- Complexe mAb-cible

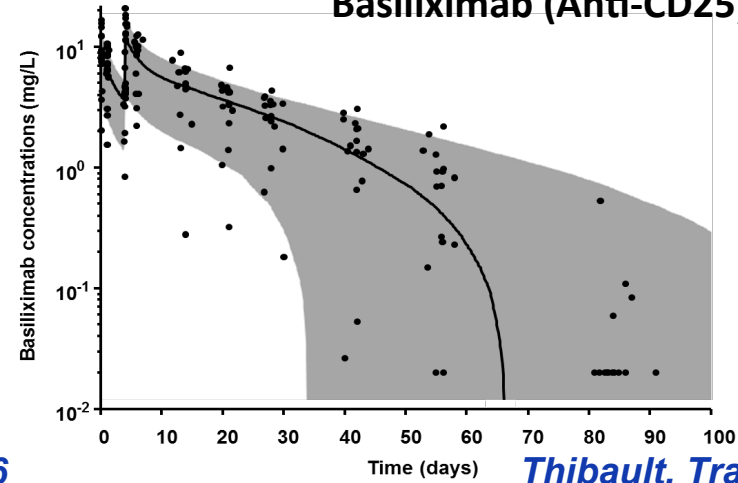
Elimination non-linéaire et masse antigénique

Rituximab (anti-CD20), souris CD20+



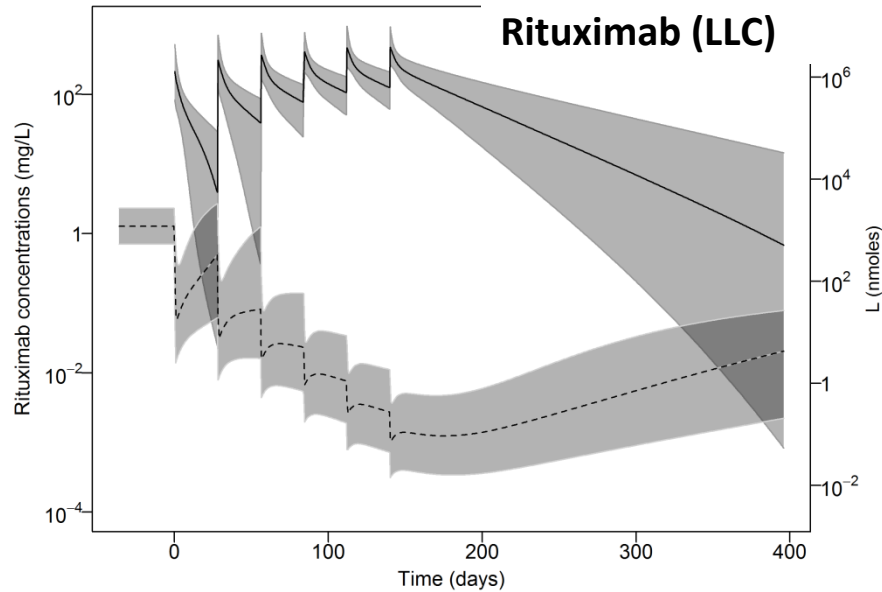
Daydé, Blood, 2016

Basiliximab (Anti-CD25)



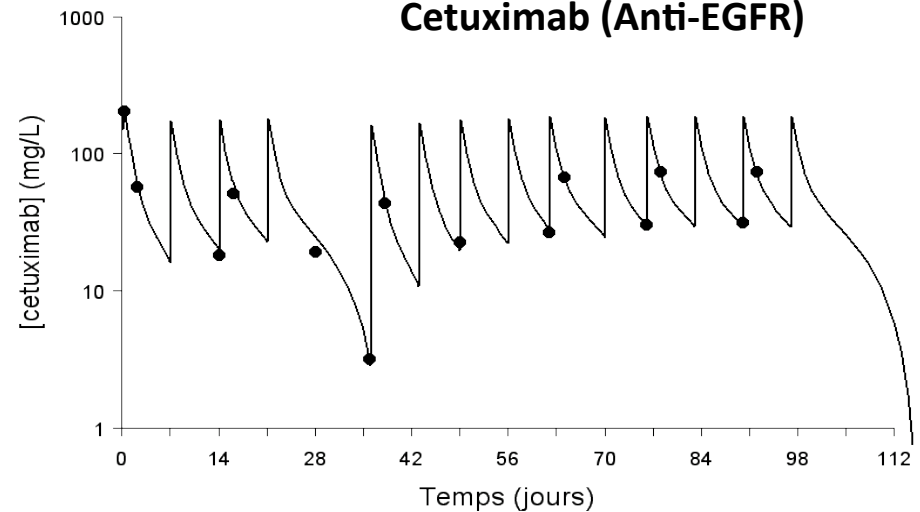
Thibault, Transpl Int, 2016

Rituximab (LLC)



Tout, CPK, 2016

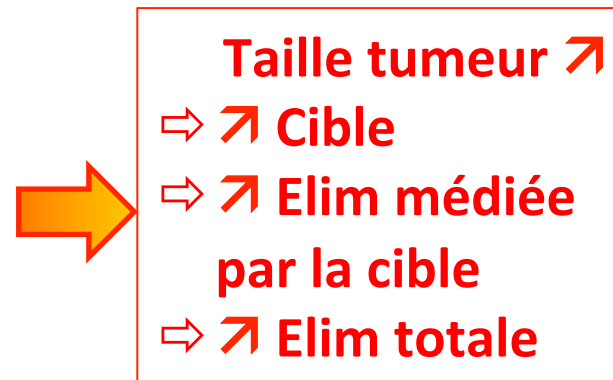
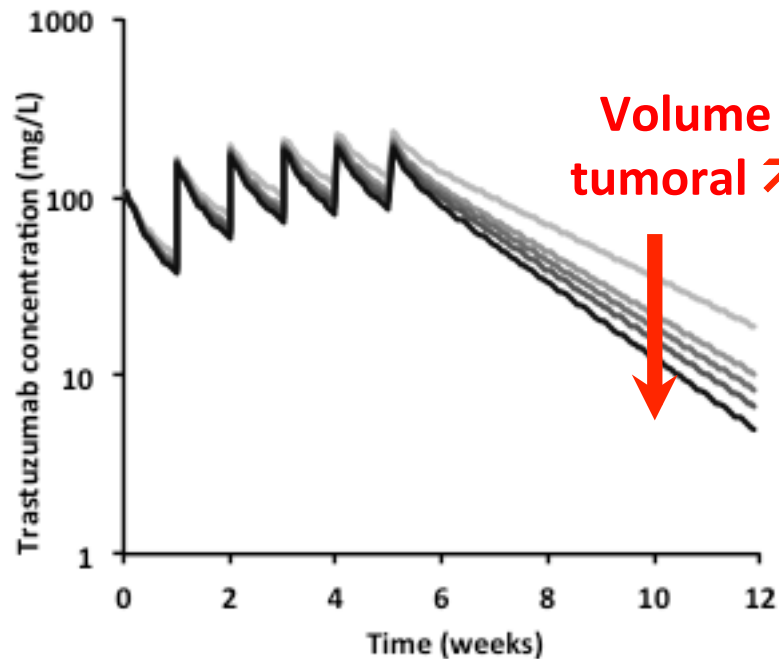
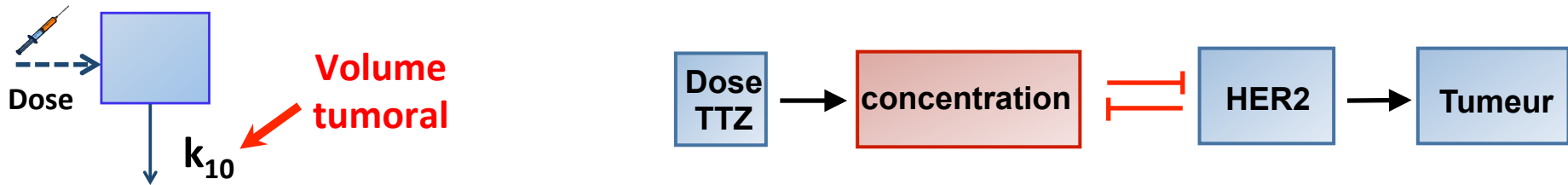
Cetuximab (Anti-EGFR)



Azzopardi, CCR, 2012

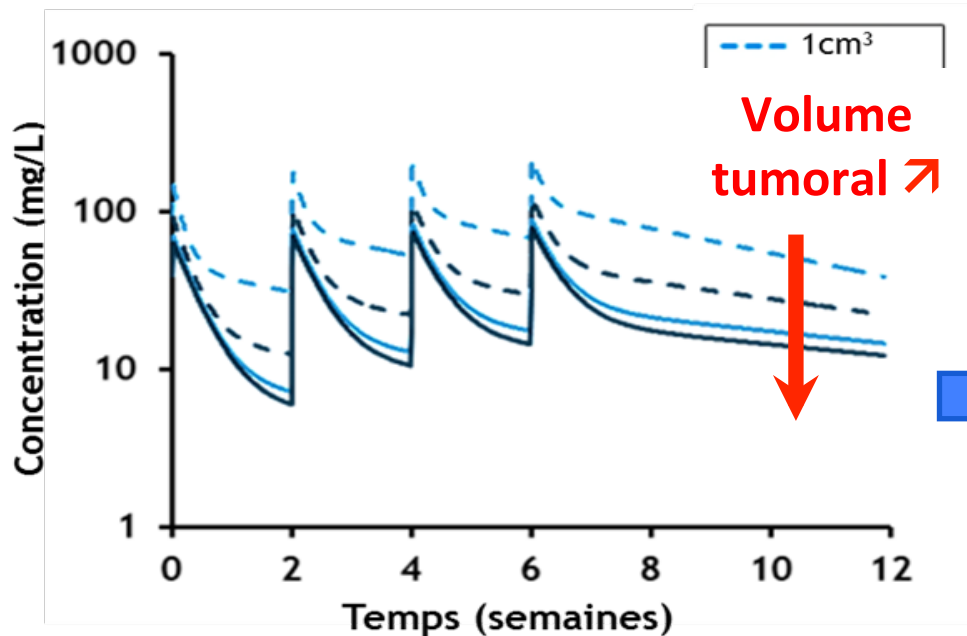
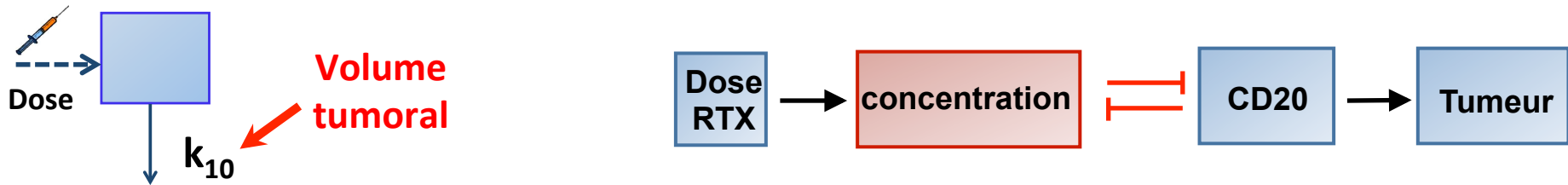
Variabilité PK – masse antigénique

Trastuzumab (Anti-HER2), cancer du sein



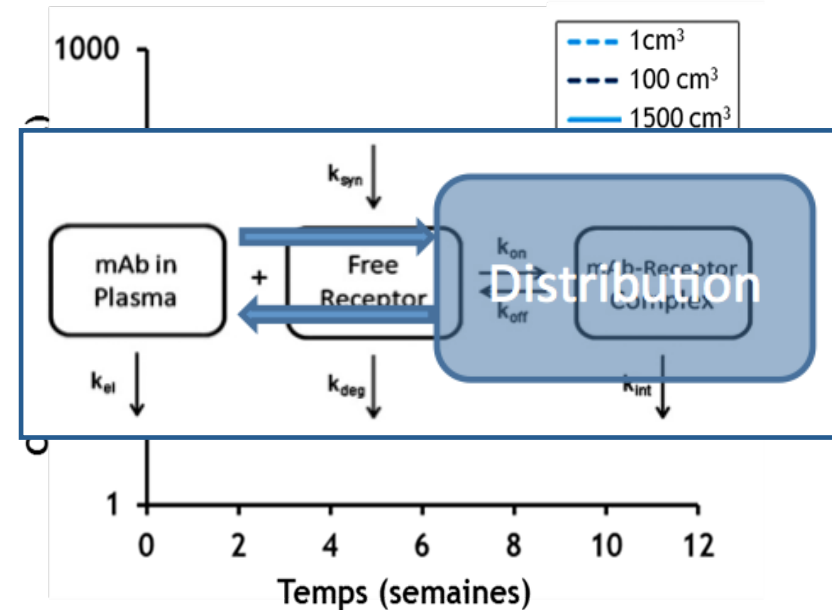
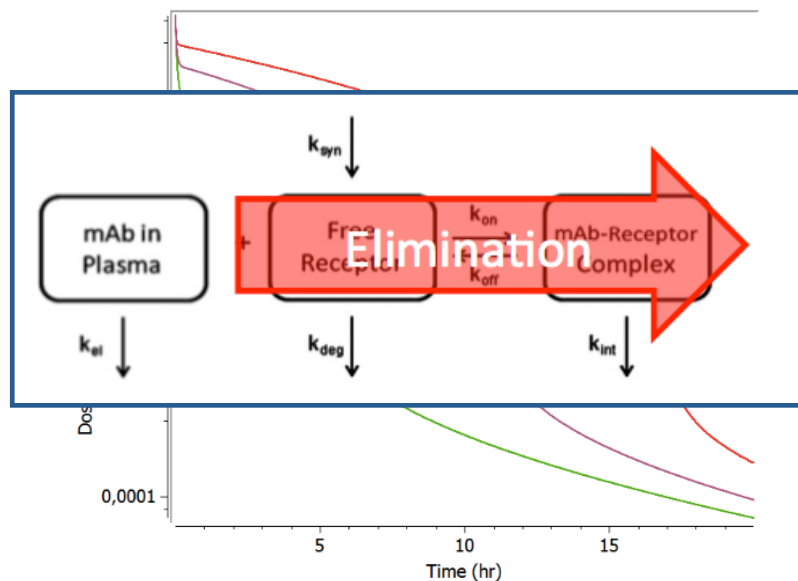
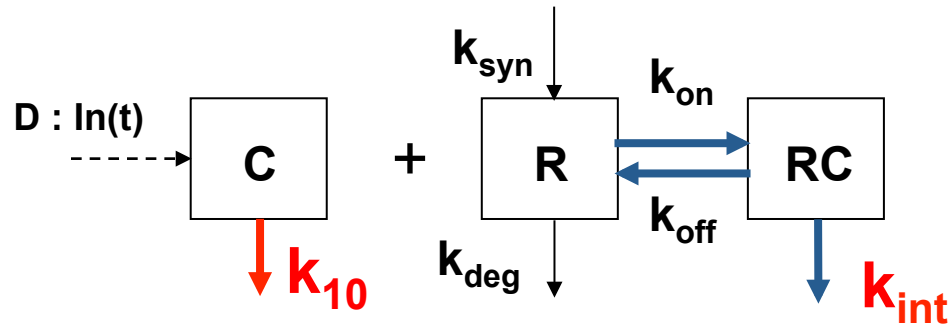
Variabilité PK – masse antigénique

Rituximab (Anti-CD20), lymphomes



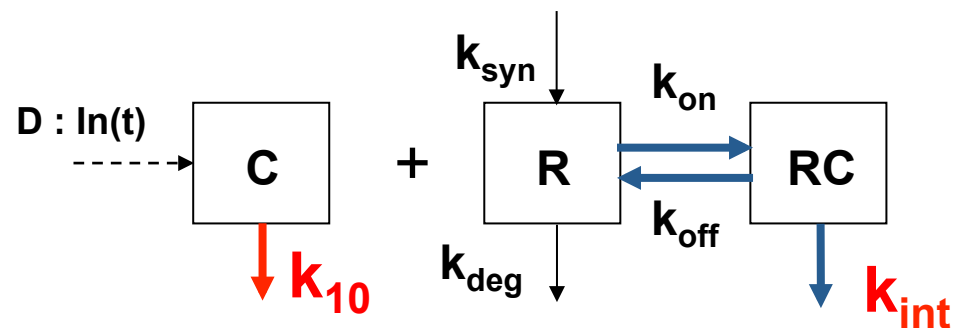
- Taille tumeur ↗
- ⇒ ↗ Cible
- ⇒ ↗ Rétention par cible
- ⇒ ↗ effet « éponge »

Elimination non-linéaire et masse antigénique



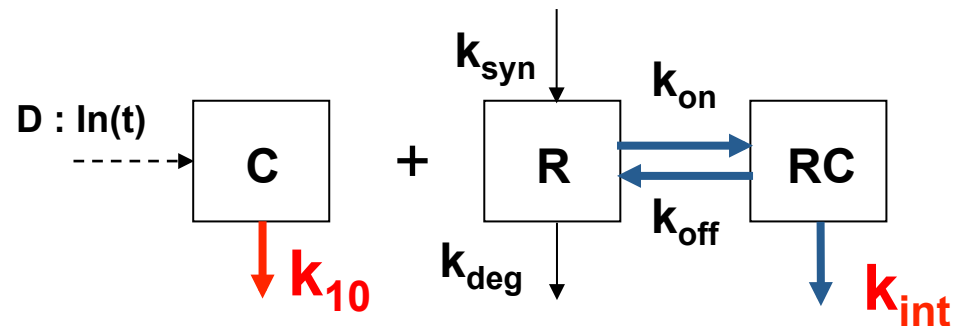
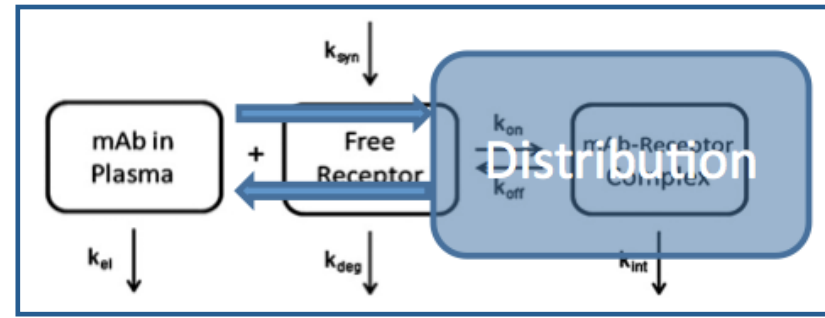
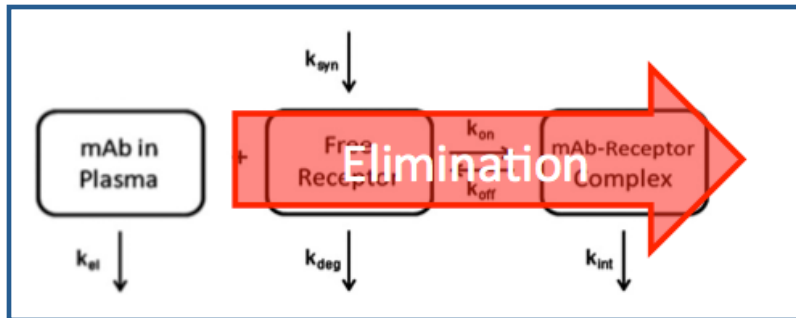
Objectifs

- Questions
 - L'effet « éponge » peut-il être décrit à l'aide de TMDD ?
 - Quelles sont les conditions permettant l'émergence de «sink» ou «sponge» ?
- Collaboration avec UMR CNRS 7350 «LMPT», Tours (V. Perrolaz, S. Madec)
 - Analyse de stabilité : étudier l'association entre masse antigénique (R) et élimination (k_{10}) du système TMDD 3x3



Théorème

- Rapport k_{10}/k_{int} est à l'origine de l'effet «sink» ou «sponge»
 - $k_{10}/k_{int} < 1 \Rightarrow k_{10} < k_{int} \Rightarrow$ «sink»
 - $k_{10}/k_{int} > 1 \Rightarrow k_{10} > k_{int} \Rightarrow$ «sponge»



Simulations

- $k_{10}/k_{int} < 1 \Rightarrow k_{10} < k_{int} \Rightarrow$ «sink» : $R \nearrow \Rightarrow$ vitesse elim \nearrow

param adm

output

kdeg

0.08675 ▼

k10

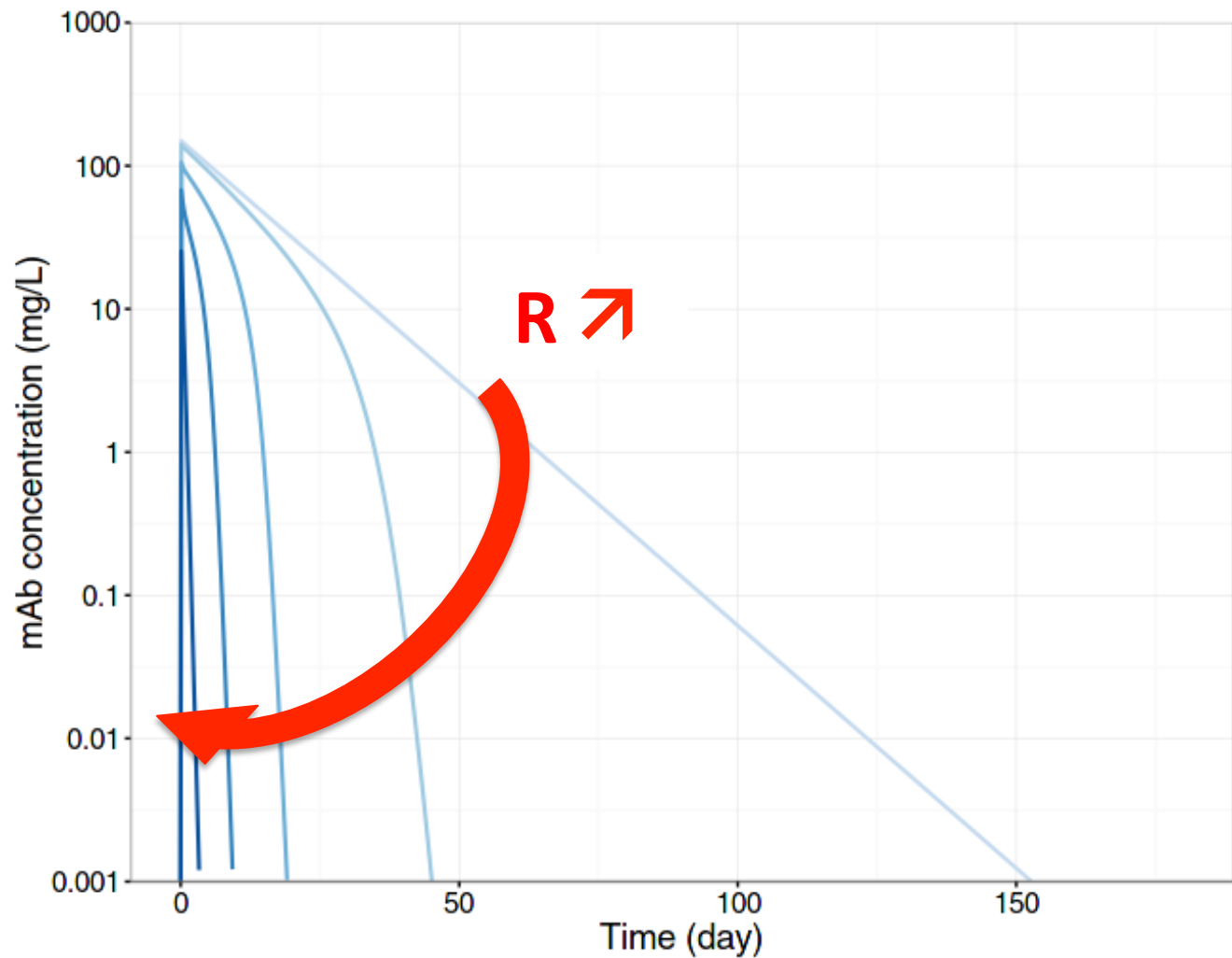
0.078 ▼

kint

3.93 ▼

kD

0.051986301369863 ▼



Simulations

- $k_{10}/k_{int} > 1 \Rightarrow k_{10} > k_{int} \Rightarrow$ «sponge» : $R \nearrow \Rightarrow$ vitesse elim \searrow

param adm

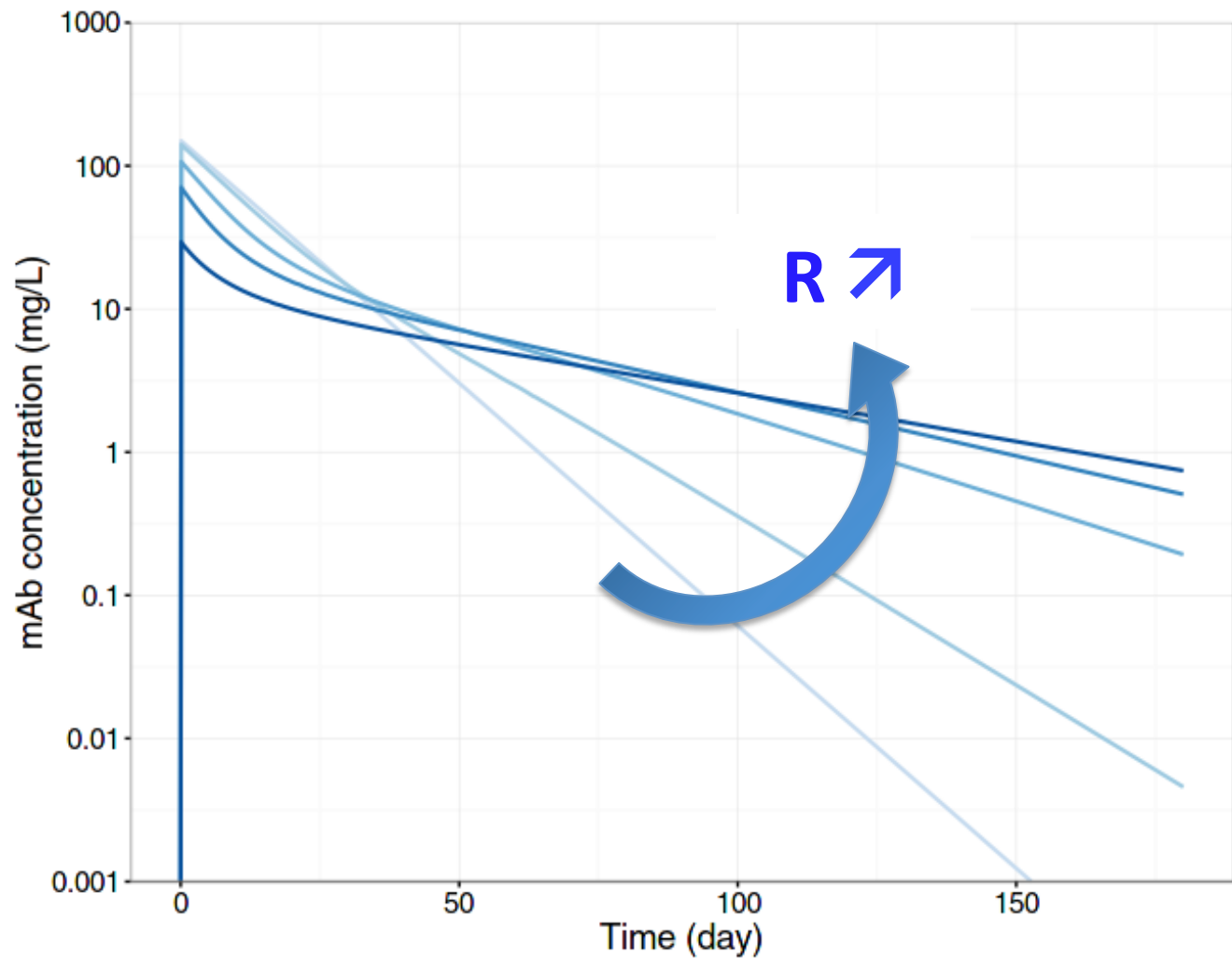
output

kdeg
0.08675

k10
0.078

kint
0.00975

kD
0.051986301369863



Simulations

- $k_{10}/k_{int} = 1 \Rightarrow k_{10} = k_{int} \Rightarrow$ pas d'effet R sur vitesse elim

param adm

output

kdeg
0.08675

k10
0.078

kint
0.078

kD
0.051986301369863

