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# Mathematical Modeling of Tumor-Tumor Distant Interactions Supports a Systemic Control of Tumor Growth

S. Benzekry

Inria team MONC, Bordeaux

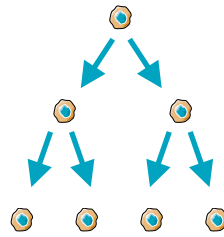
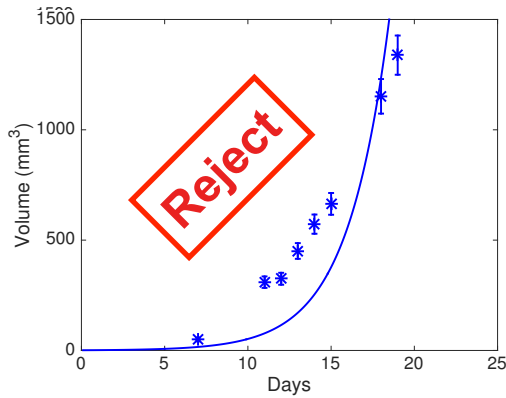
3<sup>rd</sup> Mathematical Biology Modeling days of Besançon

June 22, 2018

# Tumor growth

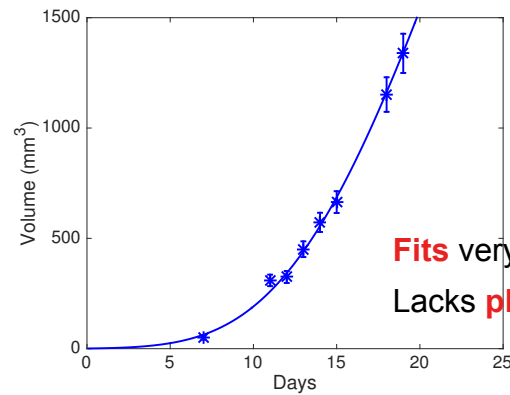
What are **minimal** biological processes able to recover the **kinetics** of (experimental) tumor growth?

## Exponential



$$\frac{dV}{dt} = aV$$

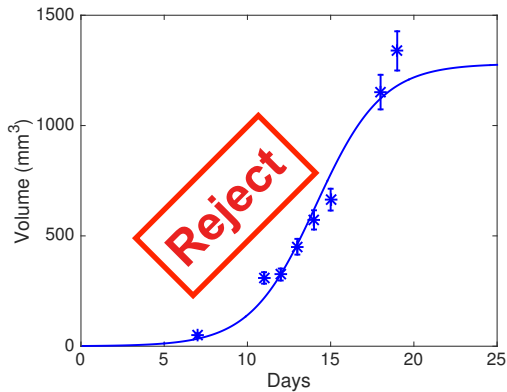
## Gompertz



$$\frac{dV}{dt} = \alpha e^{-\beta t} V$$

**Fits very well**  
Lacks **physiological** interpretation

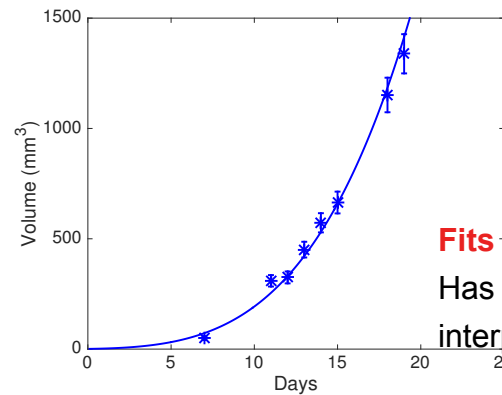
## Logistic



Competition

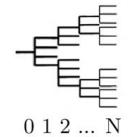
$$\frac{dV}{dt} = aV \left(1 - \frac{V}{K}\right)$$

## Power law



$$\frac{dV}{dt} = \alpha V^\gamma$$

**Fits very well**  
Has **physiological** interpretation

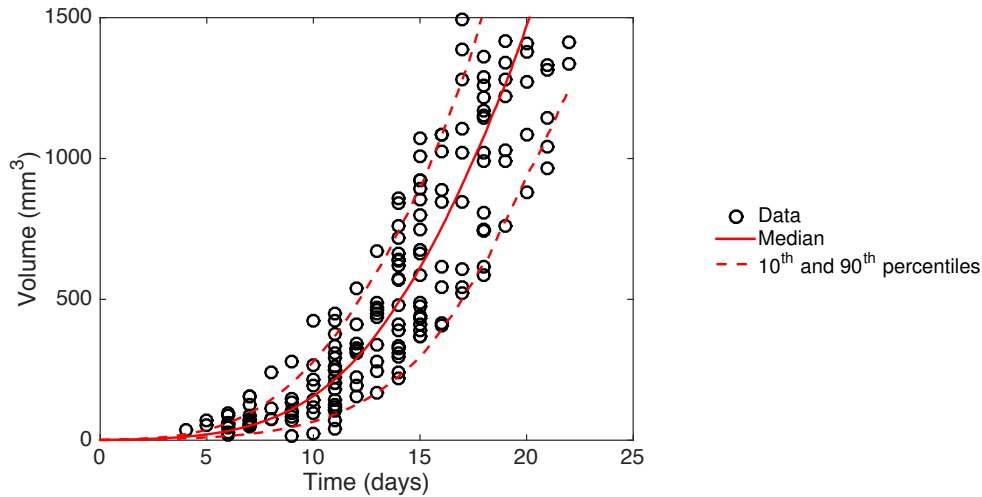


# Population approach and its use for prediction

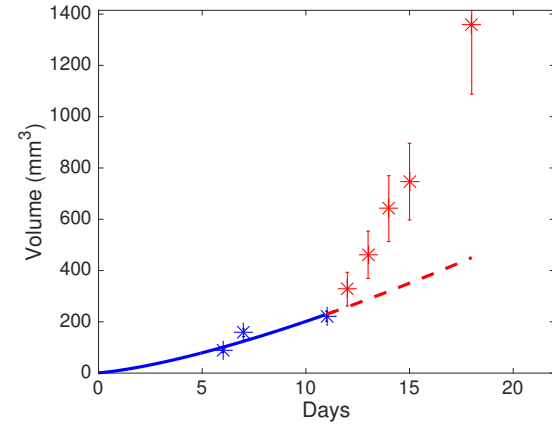
## Nonlinear mixed-effects statistical modeling

$$y_j^i = M(t_j^i, \theta^i) + \varepsilon_j^i, \quad \varepsilon_j^i \sim \mathcal{N}(0, \sigma_j^i)$$

$$\theta^1, \dots, \theta^N \sim \mathcal{LN}(\theta_{pop}, \theta_{\omega}), \quad \theta_{pop} \in \mathbb{R}^P, \theta_{\omega} \in \mathbb{R}^{P \times P}$$

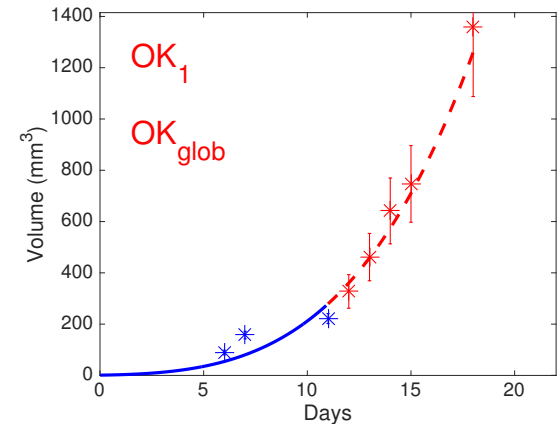


## No a priori



## With a priori

$$l(\theta^i) = \sum_{j=1}^{J^i} \frac{(y_j^i - M(t_j^i, \theta^i))^2}{2\sigma^2} + \sum_{p=1}^P \frac{(\theta_p^i - \theta_{pop,p})^2}{\theta_{\omega,p}^2} + C$$



# Concomitant tumor resistance

- **Inhibition** of secondary **growth** by a primary mass
- Critical clinical implications in terms of **post-surgery metastatic acceleration**

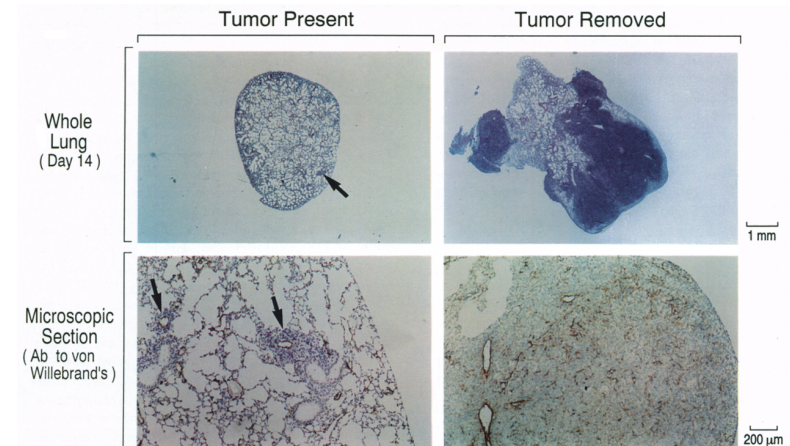
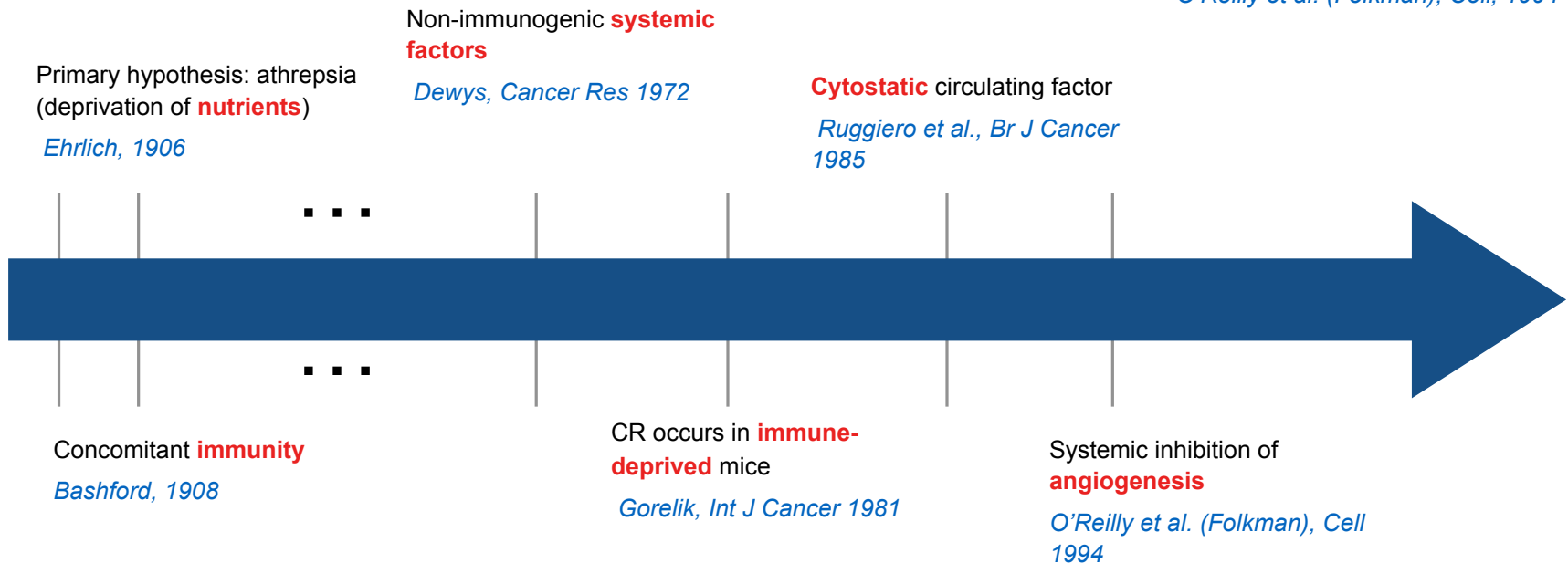


Figure 2. The Presence of a Primary Tumor Is Associated with an Inhibition of Neovascularization and Growth of Its Metastases

*O'Reilly et al. (Folkman), Cell, 1994*



# Questions and experiment

## Questions

- **Quantitatively** distinguish between qualitatively valid **theories** of tumor-tumor interactions
- Establish and validate a **minimal model able to simulate tumor-tumor interactions**

## Experiment

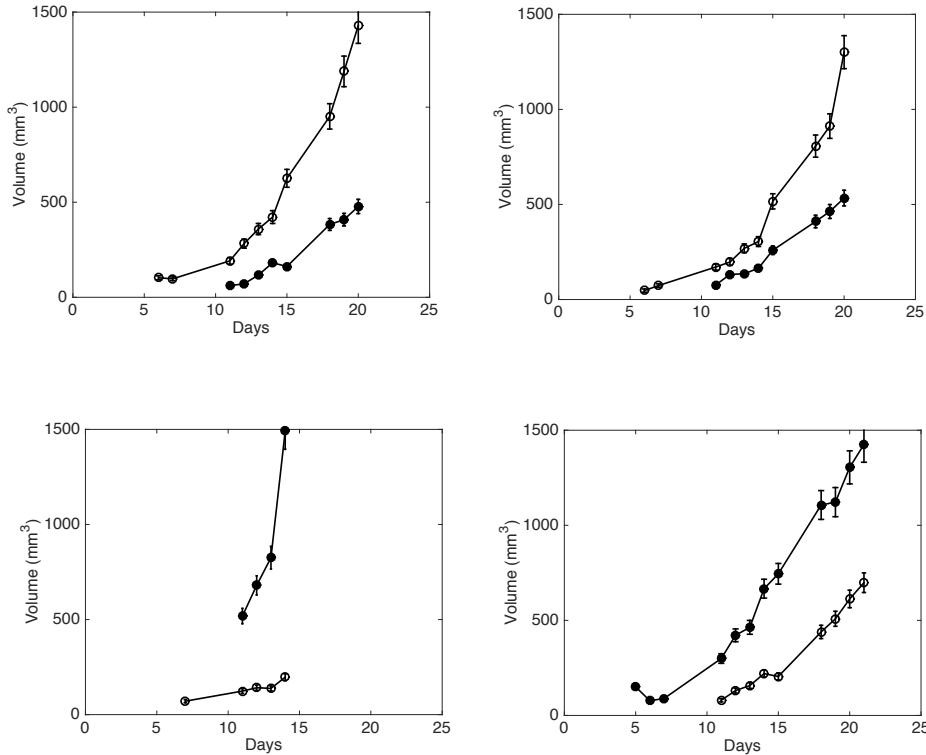
- Injection s.c. of **two tumors** of  $10^6$  LLC cells in C57/BL6 mice
- Two groups
  - Control: only one tumor
  - Group S: **simultaneous** injection of cells in two different sites

# A mouse with two tumors

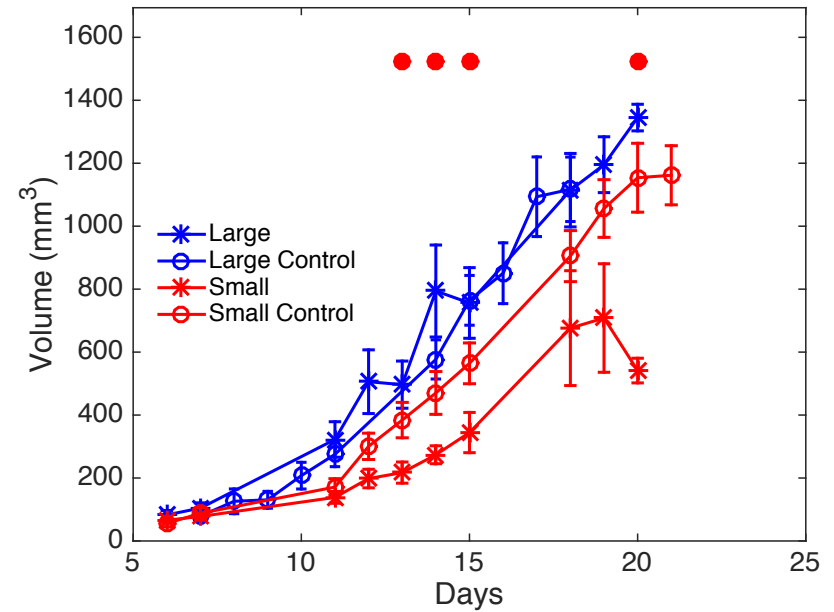


# One tumor has normal growth and the other is suppressed

## Individual growth kinetics



## Small/Large in two-tumor bearing animals VS artificially paired small/large controls

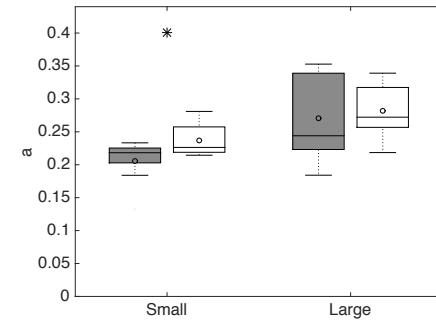
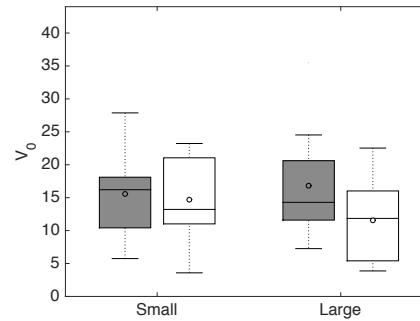




# Single-tumor growth models

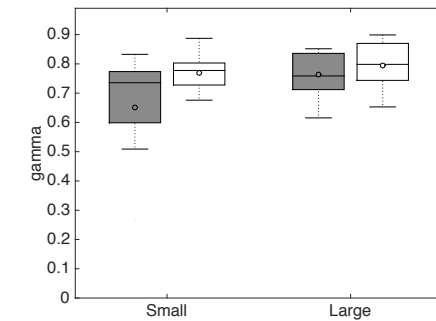
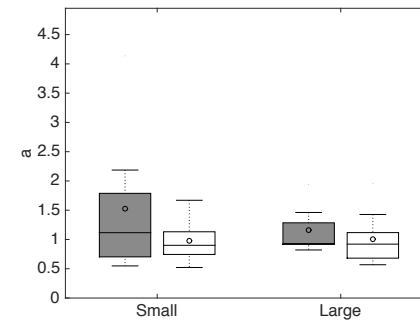
## Exponential V0

$$\begin{cases} \frac{dV}{dt} = aV \\ V(t=0) = V_0 \end{cases}$$



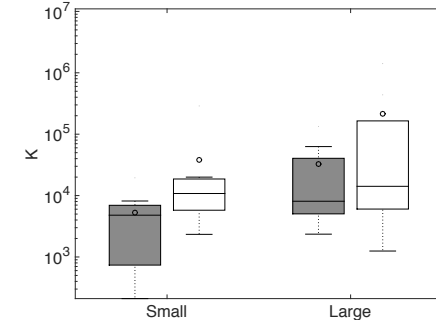
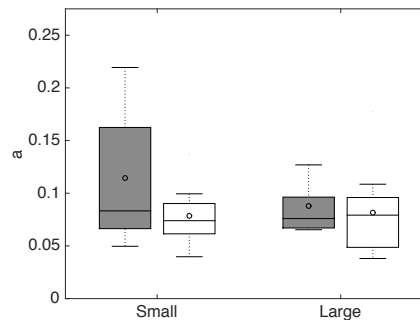
## Power law

$$\begin{cases} \frac{dV}{dt} = aV^\gamma \\ V(t=0) = 1 \text{ mm}^3 = 10^6 \text{ cells} \end{cases}$$



## Gompertz

$$\begin{cases} \frac{dV}{dt} = aV \ln\left(\frac{K}{V}\right) \\ V(t=0) = 1 \text{ mm}^3 = 10^6 \text{ cells} \end{cases}$$



■ Simultaneous  
□ Control

# Two-tumors models

- Requirements:
  - Symmetry:** same parameters for tumor 1 and tumor 2
  - Should resume to **single tumor growth** in the absence of the other tumor
- Main assumption for the difference between the two tumors: difference in **the initial take** ( $V_{0,1} = 1, V_{0,2} = 0.75$ )
- Difference in the growth kinetics should not result from difference in  $V_0$
- Model selection (rejection) criteria: goodness-of-fit + parameter identifiability

## Competition

$$\begin{cases} \frac{dV_1}{dt} = aV_1 \ln\left(\frac{K}{V_1 + V_2}\right), & V_1(t=0) = V_{0,1} \\ \frac{dV_2}{dt} = aV_2 \ln\left(\frac{K}{V_1 + V_2}\right), & V_2(t=0) = V_{0,2} \end{cases}$$

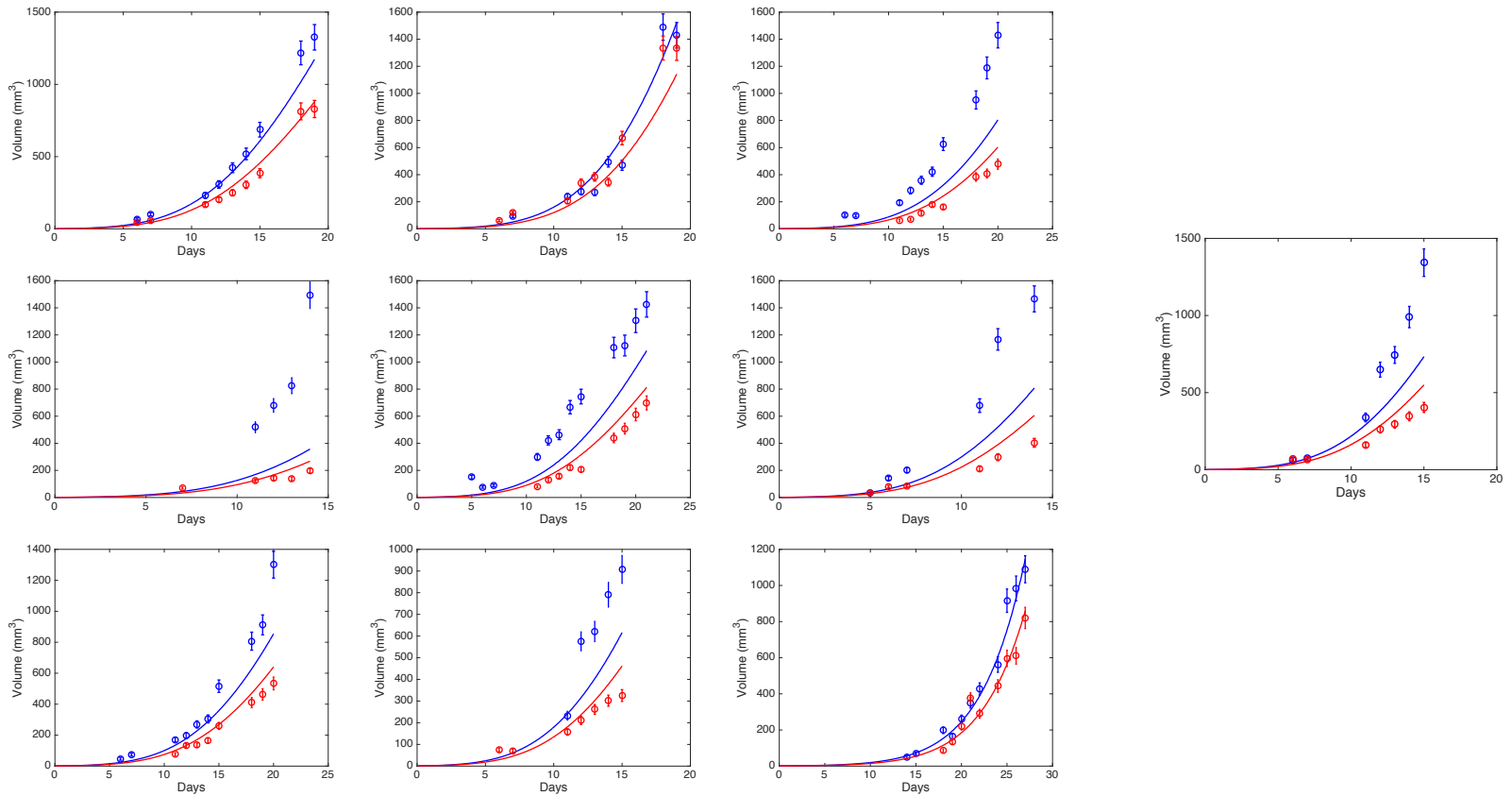
## Angiogenesis inhibition

$$\begin{cases} \frac{dV_1}{dt} = aV_1 \ln\left(\frac{K_1}{V_1}\right), & V_1(t=0) = V_{0,1} \\ \frac{dK_1}{dt} = bV_1 - dV_1^{\frac{2}{3}}K_1 - eV_2 1_{K_1 > K_0}, & K_1(t=0) = K_0 \\ \frac{dV_2}{dt} = aV_2 \ln\left(\frac{K_2}{V_2}\right), & V_2(t=0) = V_{0,2} \\ \frac{dK_2}{dt} = bV_2 - dV_2^{\frac{2}{3}}K_2 - eV_1 1_{K_2 > K_0}, & K_2(t=0) = K_0 \end{cases}$$

## Proliferation inhibition

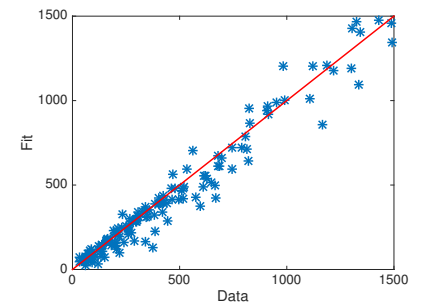
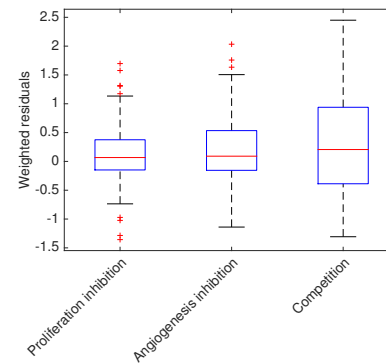
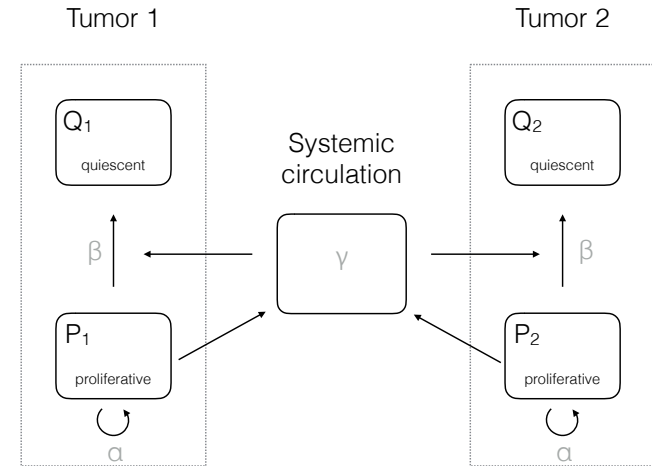
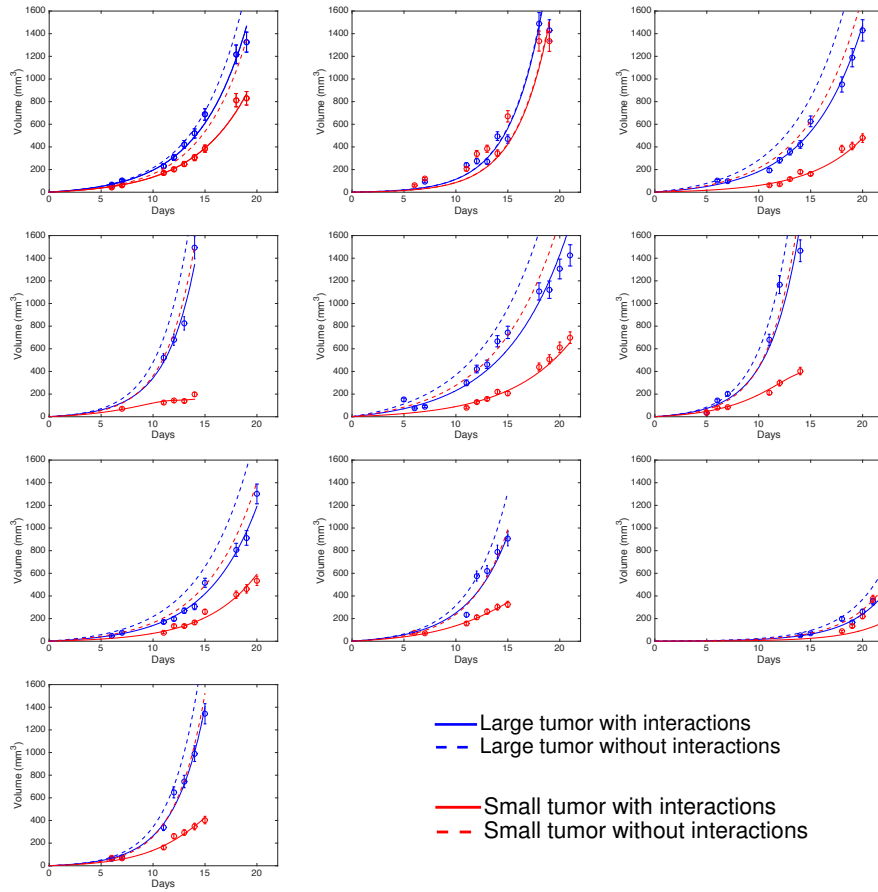
$$\begin{cases} \frac{dP_1}{dt} = \alpha P_1 - (\beta P_1 + \gamma(P_1 + P_2)) 1_{P_1 > 0}, & P_1(t=0) = V_{0,1} \\ \frac{dQ_1}{dt} = \beta P_1 + \gamma(P_1 + P_2), & Q_1(t=0) = 0 \\ \frac{dP_2}{dt} = \alpha P_2 - (\beta P_2 + \gamma(P_1 + P_2)) 1_{P_2 > 0}, & P_2(t=0) = V_{0,2} \\ \frac{dQ_2}{dt} = \beta P_2 + \gamma(P_1 + P_2), & Q_2(t=0) = 0 \end{cases}$$

# The competition model did not fit



$$\begin{cases} \frac{dV_1}{dt} = aV_1 \ln\left(\frac{K}{V_1 + V_2}\right), & V_1(t=0) = V_{0,1} \\ \frac{dV_2}{dt} = aV_2 \ln\left(\frac{K}{V_1 + V_2}\right), & V_2(t=0) = V_{0,2} \end{cases}$$

# The « inhibition of proliferation » model fitted best



Model	Par.	Unit	Median value (CV)	RSE (%)
Proliferation inhibition	$\alpha$	day <sup>-1</sup>	5.77 (67.4)	17.5
	$\beta$	day <sup>-1</sup>	5.07 (49.3)	21.2
	$\gamma$	-	0.074 (2.69e+03)	2.47

Model	SSE	AIC	RMSE	R2	#
Proliferation inhibition	0.204(0.0319 - 0.461)[1]	-14.2(-54 - -8.28)[1]	0.453(0.182 - 0.688)[1]	0.961(0.902 - 0.987)[1]	3
Angiogenesis inhibition	0.336(0.154 - 0.772)[2]	-5.07(-27.5 - 5.67)[2]	0.588(0.4 - 0.891)[2]	0.957(0.645 - 0.986)[2]	3
Competition	0.666(0.141 - 2.2)[3]	0.71(-33.2 - 13.1)[3]	0.828(0.383 - 1.5)[3]	0.694(-0.0757 - 0.964)[3]	2

# Summary

- « Proliferation inhibition » model was able to adequately fit the data and provides with a **simple** (3 parameters), **identifiable, biologically grounded model**.
- « Angiogenesis inhibition » model was **also able** to fit the data, but to a lesser extent.
- « Competition model » was not able to fit the data, thus allowing to **reject this theory/model** as being sufficient to explain the data.
- Our model gives a dynamical valid explanation of the **CR paradox** (= if a tumor is able to inhibit the growth of a distant one, how can it grow at the same time?)

**Perspective:** integrate this model for tumor-tumor interactions into the **organism-level** for the dynamics of the metastatic population

# Conclusion

- A general modeling framework for **modeling metastases**
- Simplified model (growth + dissemination) able to describe available clinically relevant **preclinical data** of dynamics of total metastatic burden
- **Quantitative** exploration of classical theories for metastatic colonization and **tumor-tumor interactions** and st
- A **patient-specific key parameter  $\mu$**  was critical in the quantification of patient-specific metastatic aggressiveness

# Acknowledgements

- Preclinical data of ortho-surgical animal models of metastases

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- One and two-tumors study

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C. Lamont, P. Hahnfeldt, L. Hlatky**

- Biology of the kidney metastases to the lung

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RMSB, CNRS**

**Thank you for your attention!**