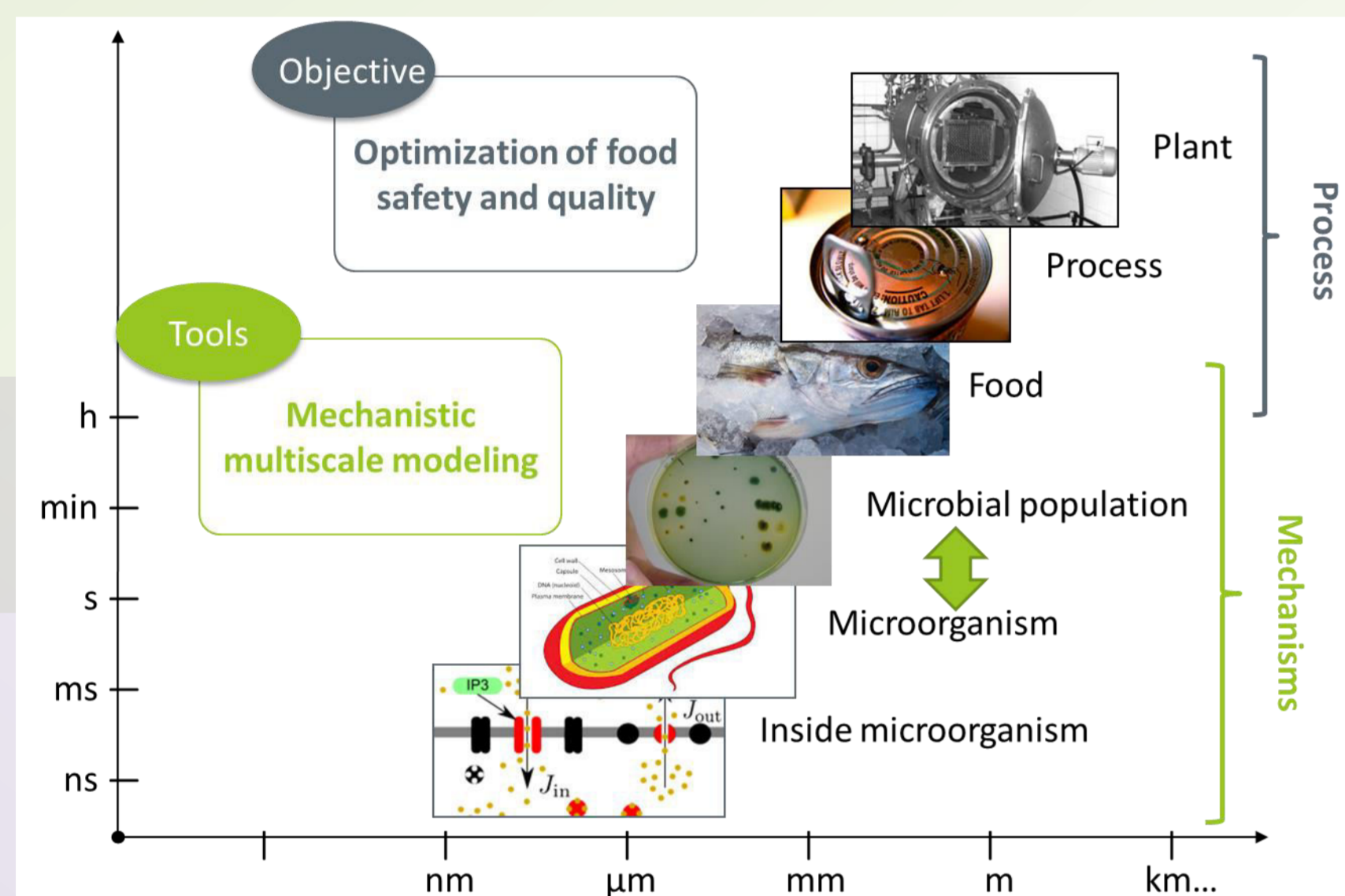


Motivation

Optimisation of antimicrobial treatments using Individual-based modelling (IBM)

- IBM is the natural mathematical formalisms to describe emergence and selection of antimicrobial resistance (AMR)
- In IBM the essential first step is to describe division with simple equations
 - Is size a good descriptor of division? [1]
- IBM needs knowledge of individual parameters
 - Can we extract individual parameters (like division size) from population statistics?

Application: controlling AMR in the food industry

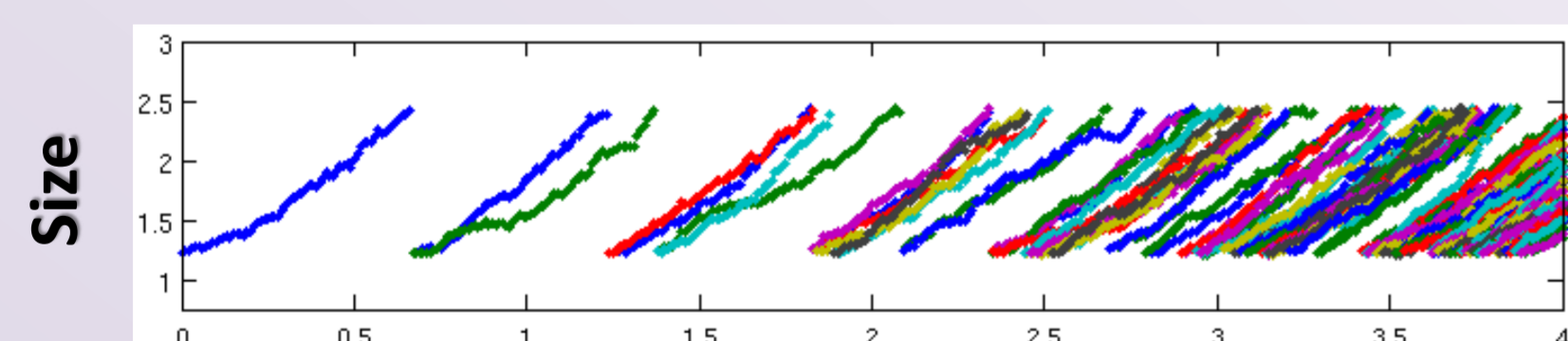


Model: Stochastic size growth

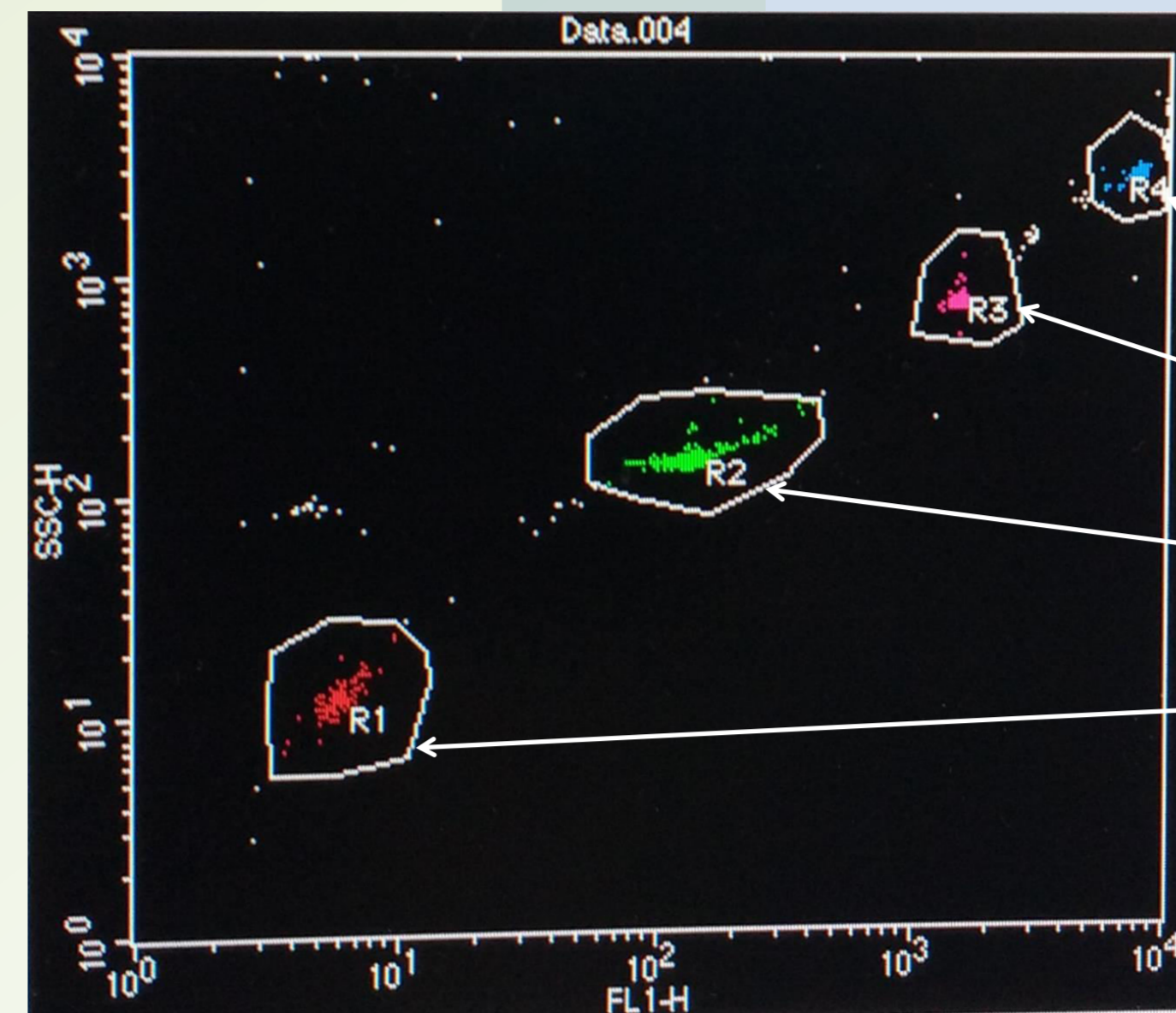
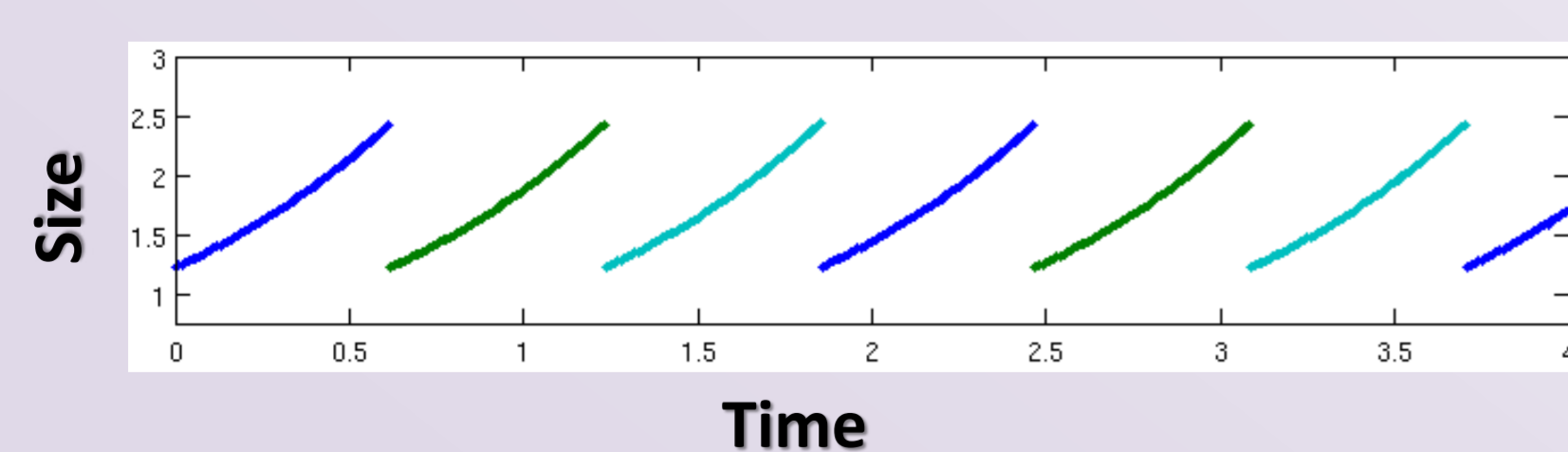
- Assumption:** size is subject to a stochastic fluctuation δW characterized by a Wiener process [3]
- Simulation using stochastic differential equations (SDE)**

$$\begin{aligned} \text{Growth} & \text{ if } y = \log(\text{size}) \quad \delta y = \mu \delta t + \xi \delta W \\ \text{Division} & \text{ if } y \geq y_{div} \quad y \rightarrow y_{son}, y_{son} \text{ with } y_{son} = y_{div} - \log 2 \\ \text{Death} & \text{ if } y \leq y_{min} \quad y \rightarrow \emptyset \end{aligned}$$

- Simulations starting from one bacteria**



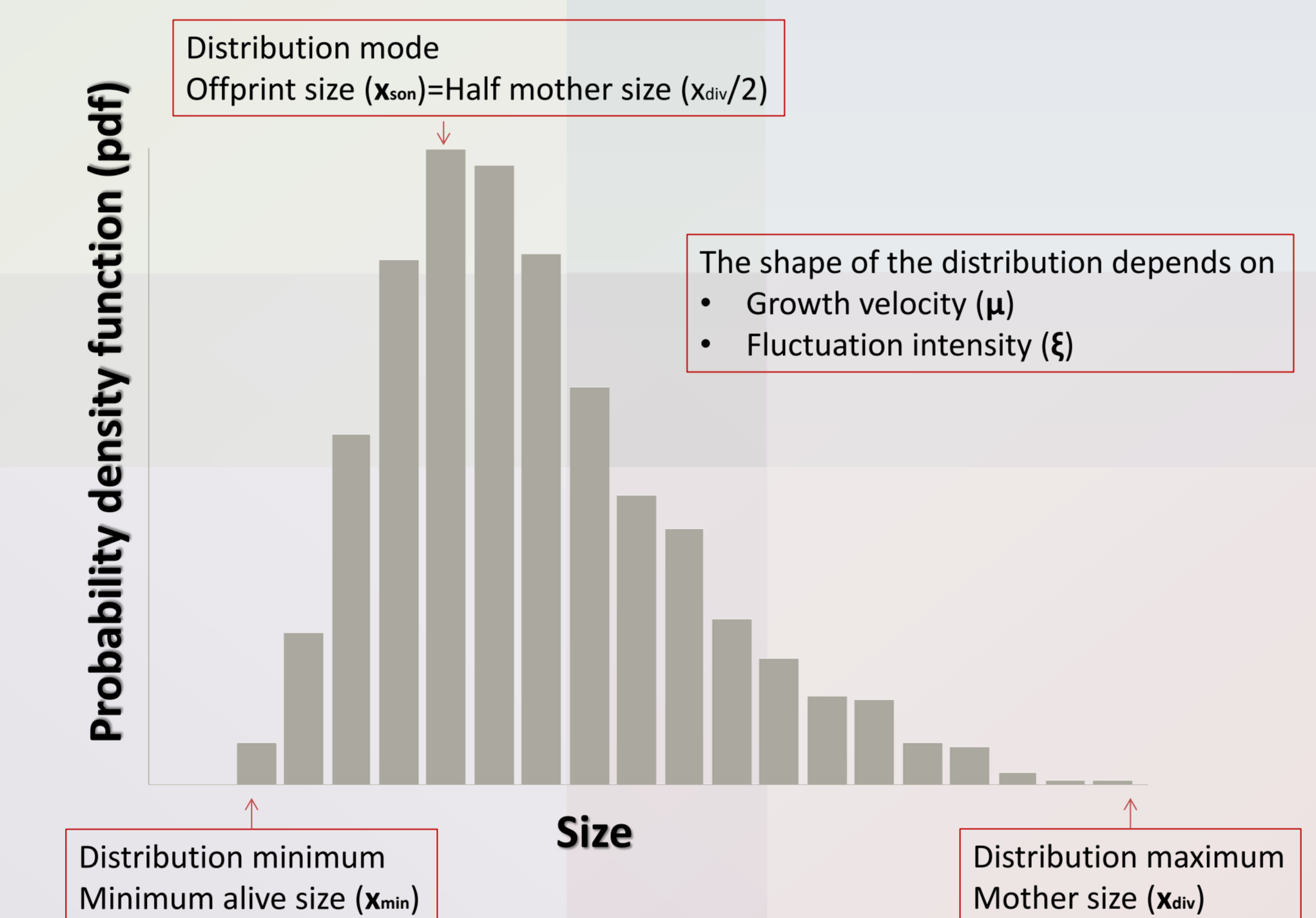
- Comparison with deterministic simulations ($\xi=0$)**



Experiments: Flow cytometry

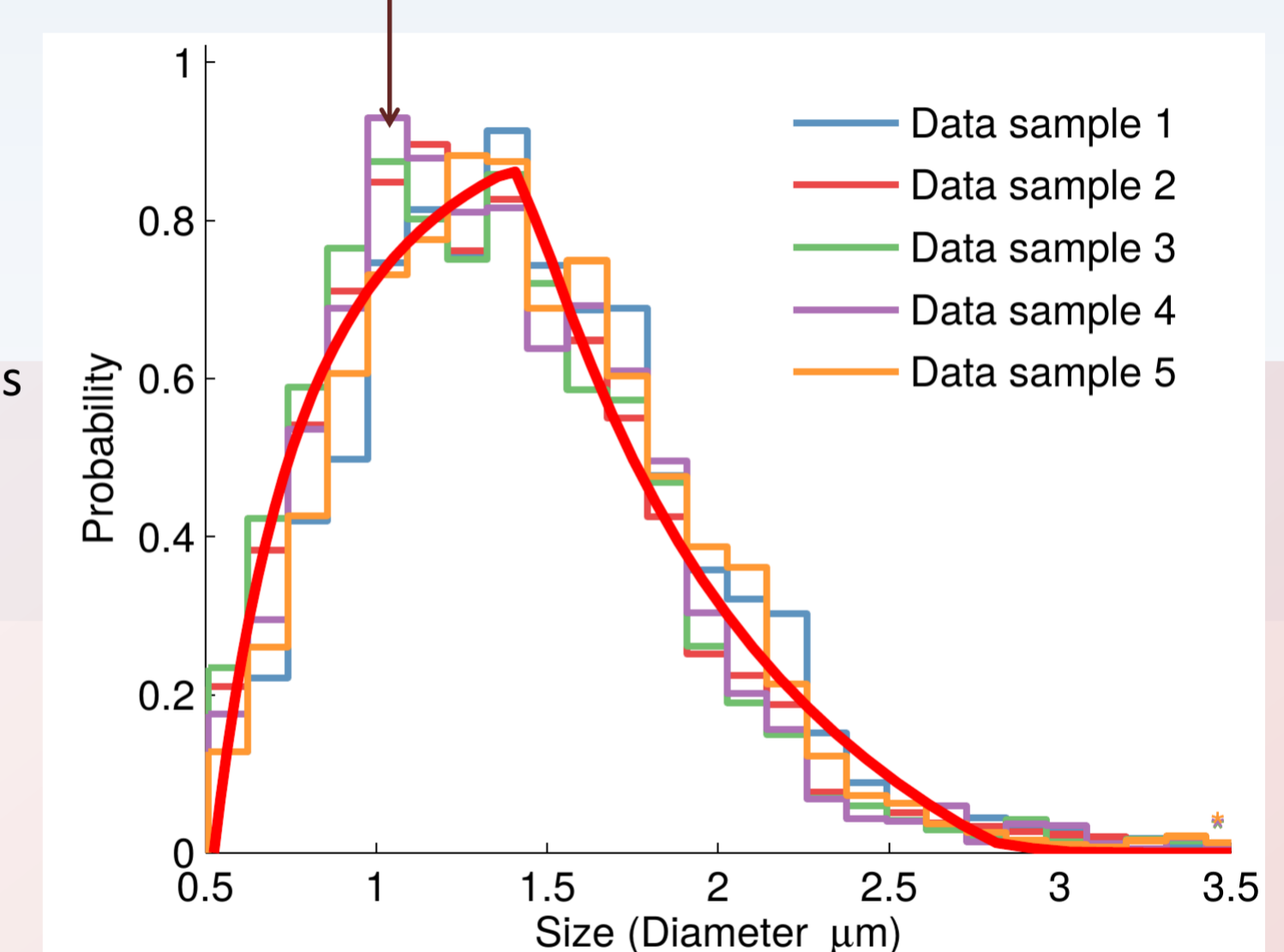
- Light scattering relates with cell size**
 - 0.2 μm (R4) Forward scatter (mainly for big cells)
 - 0.5 μm (R3) Side scatter (mainly for small cells)
 - It requires a calibration with size reference beads [2]
- Flow cytometry data provides population statistics**
 - Shape and time evolution of the probability density function
- Theory is tested using size pdfs of *Pediococcus acidilactici* at different times during the exponential phase (transparent histograms)**

Population size distribution



Pediococcus data
transparent histograms

Fokker-Planck model
Continuous red line



Model: Fokker-Planck eq.

Probability population size (pdf) $\frac{\partial F(t, y)}{\partial t} = -\frac{\partial J(t, y)}{\partial y} + B(t, y) + N(t, y)$

Boundary conditions $\forall t \quad F(t, y_{min}) = F(t, y_{max}) = 0$

Initial conditions $\forall y \quad F(0, y) = \delta(y - y_{son})$

Fluxes $J(t, y) = \mu F(t, y) - \frac{\xi^2}{2} \frac{\partial F(t, y)}{\partial y}$

Division $B(t, y) = -\frac{\partial J(t)}{\partial y}|_{y_{div}} \delta(y - y_{div}) + 2 \frac{\partial J(t)}{\partial y}|_{y_{div}} \delta(y - y_{son})$

Normalization pdf $N(t, y) = -F(t, y) \frac{\partial J(t)}{\partial y}|_{y_{div}}$

- SDEs are transformed into a partial derivative equation**

- allowing simulation of small and large populations
- better estimations of the probability function
- efficient calibrations and validations of the theory

- Validation using *Pediococcus* data showing for example**

- estimated growth velocity of the cell-size ($\mu=0.25 \text{ d}^{-1}$) coincides with population growth velocity ($\mu=0.24 \text{ d}^{-1}$)

CONCLUSIONS:

The proposed model based on stochastic cell size growth shows promising features (efficient, simple) for individual-based modeling.

Single-cell parameters were recover from *Pediococcus* population statistics

Working now on extending the model to include a descriptor of antimicrobial resistance (probably stochastic membrane permeability)

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RESISTANCE

<http://resistance.iim.csic.es/>

REFERENCES:

- Taheri-Araghi, et al. "Cell-size control and homeostasis in bacteria." *Current Biology* 25.3 (2015): 385-391
- Chandler, et al. "A new microparticle size calibration standard for use in measuring smaller microparticles using a new flow cytometer." *Journal of Thrombosis and Haemostasis* 9.6 (2011): 1216-1224.
- Alonso, et al. "Modeling bacterial population growth from stochastic single-cell dynamics." *Applied and environmental microbiology* 80.17 (2014): 5241-5253.