

# Quantifying adaptive resistance in bacteria

## using well-designed dynamic time-kill curve experiments

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### Background

*In vitro* time-kill curve experiments allow to study the concentration-effect relationship of antimicrobial treatments. Mathematical models leverage the experimental data by allowing to simulate microbial growth under clinically relevant concentration-time profiles and under combination therapy.

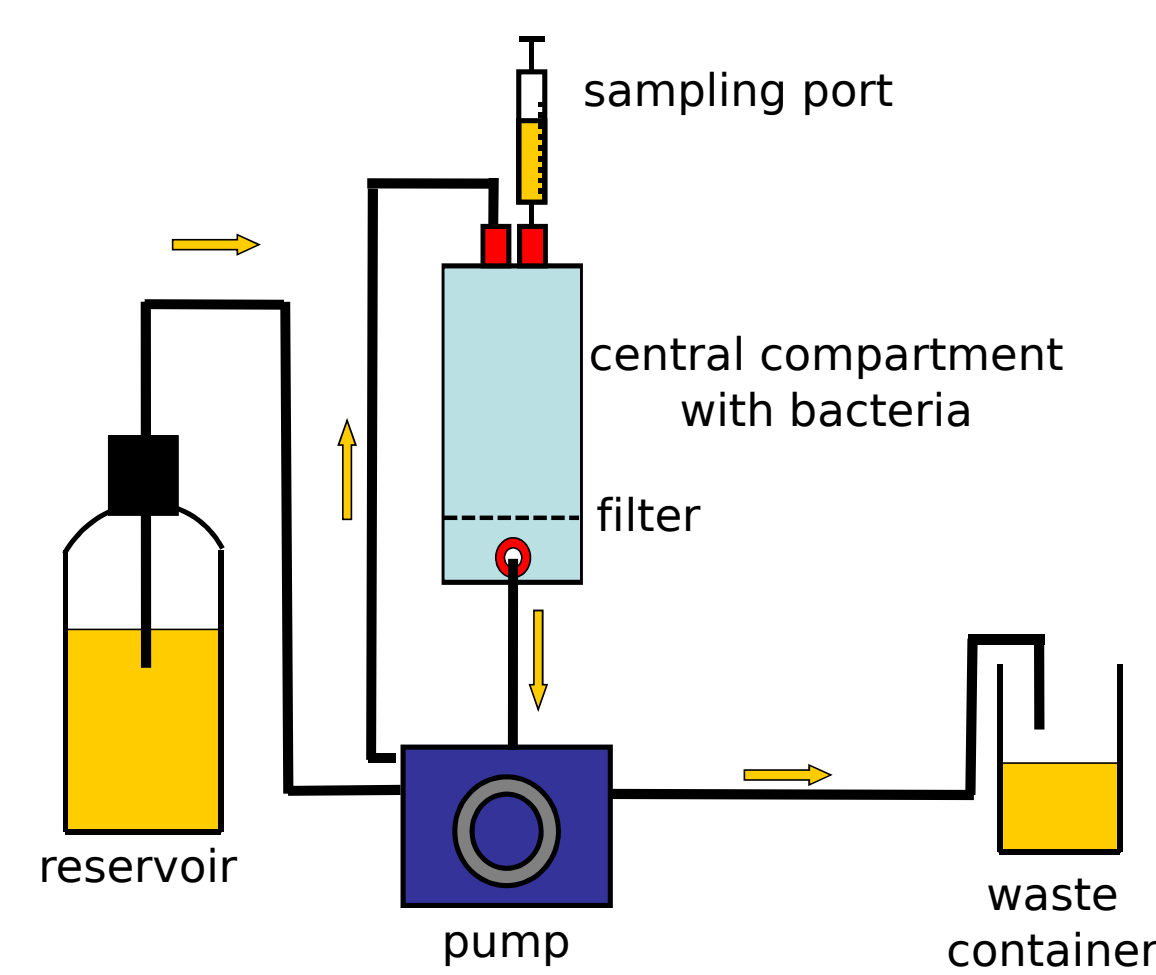
However, some dynamic processes such as **adaptive resistance** and persister formation (dormant state), both stress-triggered phenotypic changes, are **difficult to quantify reliably from these experiments** [1].

### Objective

Propose **tailored time-kill curve experiments** to differentiate adaptive resistance and persister formation using **Optimal Design** theory.

### Time-kill curve experiments

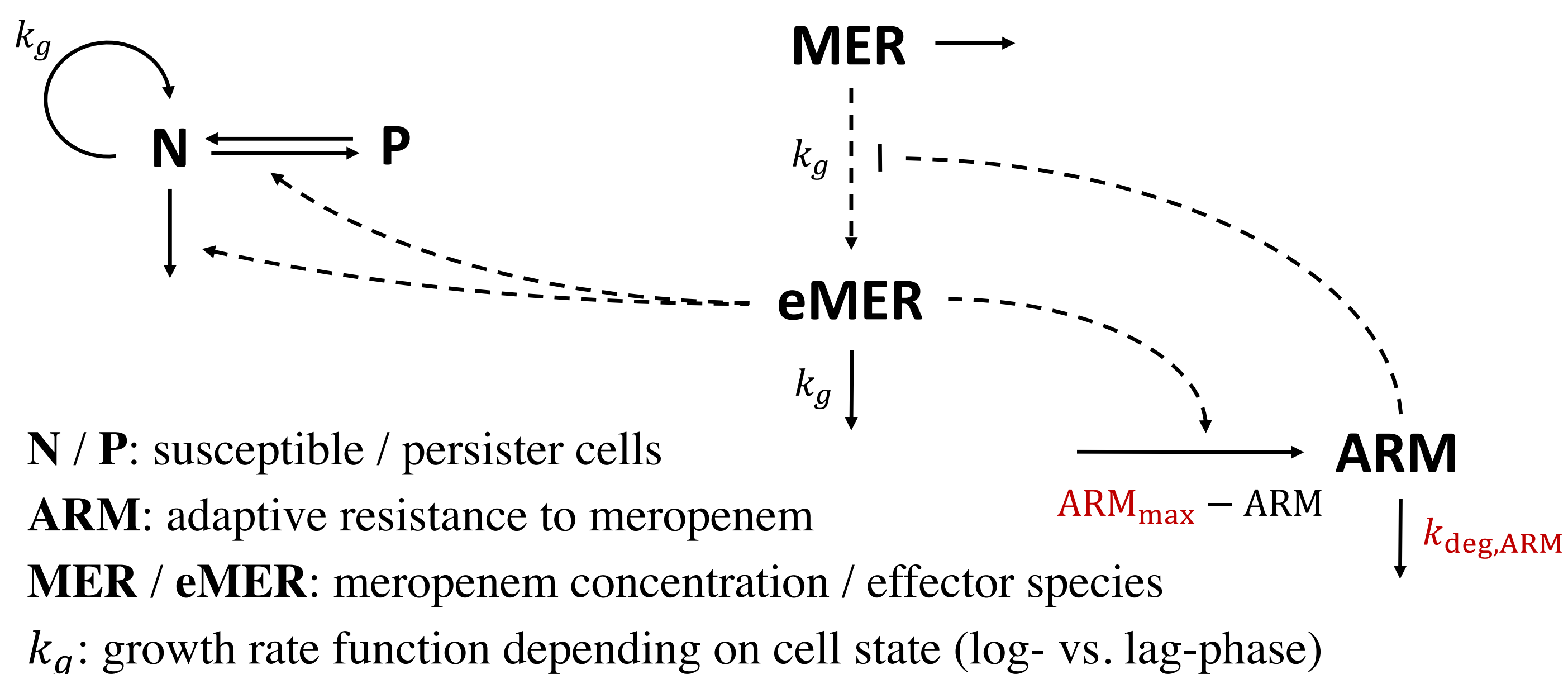
- Bacteria in a culture flask are exposed to antibiotics in an *in vitro* infection model (IVIM)
- IVIM can be **static** (no change in drug concentrations; no exchange of culture medium) or **dynamic** (pumping system allows for time-varying drug concentrations; see Figure)
- Time-kill curves (TKC)**: obtained by repeated sampling from an IVIM and quantifying bacterial concentrations



Sketch of a dynamic *in vitro* infection model (adapted from [2])

### Bacterial growth model

Model for antibiotic combination therapy, developed previously from static TKC data and mechanistic understanding [3,4]; only meropenem effect is considered here.



**Assumptions on adaptive resistance** during model development:

- Adaptive resistance does not wear off:  $k_{deg,ARM} = 0 \text{ h}^{-1}$
- Adaptive resistance can inhibit meropenem effect completely:  $ARM_{max} = 1$

*Could these parameters have been determined from dynamic time-kill curve experiments?*

### Design of time-kill curve experiments

$D_S$ -optimality

- Maximise information on **interesting** parameters ( $I$ )
- Account for correlations ( $C$ ) with nuisance parameters ( $N$ )
- Robust variant:  $\log D_S$  averaged over parameters

Here: **interesting**  $\hat{=}$   $k_{deg,ARM}$  and  $ARM_{max}$

$$FIM = \begin{pmatrix} I & C \\ C^T & N \end{pmatrix}$$

Optimality criterion [5]:  
 $D_S = \det(I - CN^{-1}C^T)$

Idea for dynamic TKC experiments:

- Adaptive resistance has to be triggered (high drug concentration),
- For positive  $k_{deg,ARM}$ , adaptive resistance can wear off in a drug-free rest phase
- Reduction of adaptive resistance manifests in a decrease of bacterial load after a second exposure (possibly lower) to antibiotics

→ we consider **intermittent antibiotic exposure experiments** (and for comparison, static conditions and dynamic 1-compartment kinetics)

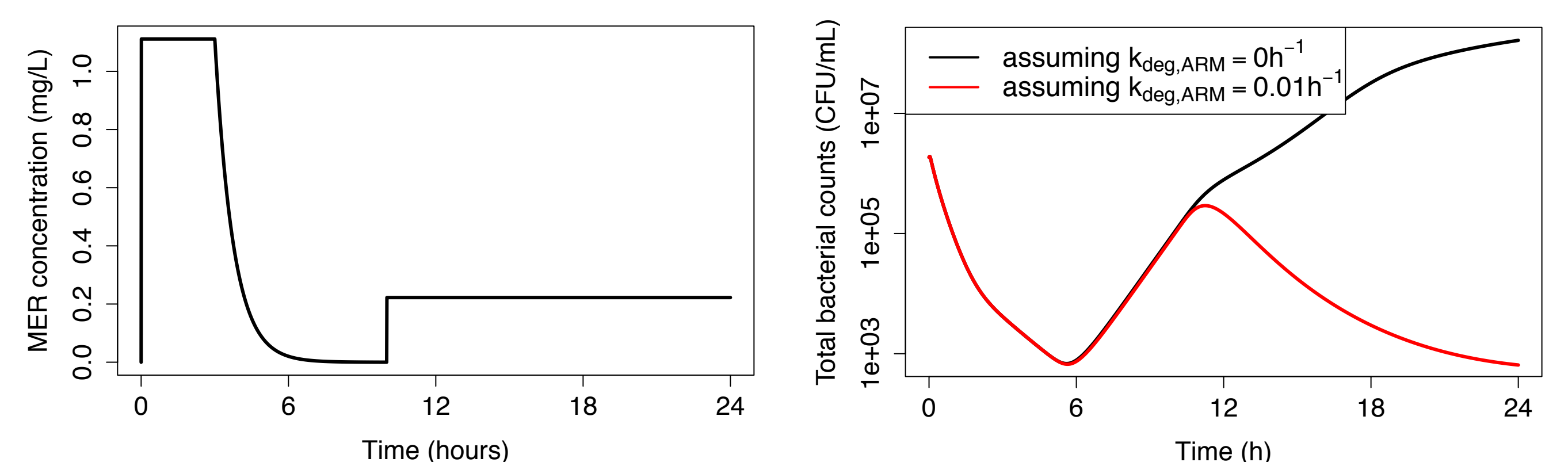
Prior information:

$FIM_{static}$  (from modelling static TKC data)

$$FIM = \underbrace{FIM_{static}}_{\text{performed experiment}} + \underbrace{FIM_{dynamic}}_{\text{planned experiment}}$$

### Results

Intermittent exposure experiment discriminating  $k_{deg,ARM}$  values



Optimal design for different experimental setups

Assumed true parameters		Predicted standard errors (SE) for optimal design					
$k_{deg,ARM}$	$ARM_{max}$	SE ( $k_{deg,ARM}$ )			SE ( $ARM_{max}$ )		
		static	1-cmt	intermittent	static	1-cmt	intermittent
0	1	0.003	0.004	0.003	0.03	0.04	0.03
0.01	1	0.02	0.01	0.02	0.2	0.2	0.1
0.1	1	1.3	0.2	0.02	6.8	1.2	0.1
0	0.9	0.03	0.02	0.03	0.2	0.2	0.3
0.01	0.9	0.04	0.03	0.02	0.3	0.3	0.2
0.1	0.9	2.0	0.3	0.06	8.7	1.3	0.2

good precision with intermittent exposure design

optimality criterion ( $E \log D_S$ ) for best **robust** design

static	1-cmt	intermittent
9.09	11.17	11.47

→ benefit of intermittent exposure design less prominent

### Conclusions

- Static TKC data can be leveraged for designing dynamic TKC experiments
- Tailored experiments contribute to elucidating bacterial resistance mechanisms
- Robust simultaneous characterisation of several resistance mechanisms remains challenging

### References

- [1] Jacobs et al.: Distinguishing Antimicrobial Models with Different Resistance Mechanisms via Population Pharmacodynamic Modeling. PLoS Comput Biol (2016).  
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 [3] Hethey et al.: Impact of the intracellular ribosomal concentration on in vitro bacterial growth kinetics and the antibacterial effect of linezolid on *S. aureus* in

time-kill assays. PAGE 25 (2016).

[4] Wicha et al.: Pharmacodynamic and response surface analysis of linezolid or vancomycin combined with meropenem against *Staphylococcus aureus*. Pharm Res (2014), 32(7):2410-8.

[5] Studden: Ds-Optimal Designs for Polynomial Regression Using Continued Fractions. The Annals of Statistics (1980) 8(5):1132-41.

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