

Model-based rationale for drug combinations in tuberculosis

Morris Muliaditan
Oscar Della Pasqua

Clinical Pharmacology and Therapeutics Group, UCL,
London, UK
Clinical Pharmacology Modelling & Simulation,
GlaxoSmithKline, Uxbridge, UK

Lewis Sheiner Student Session
PAGE Meeting 2017, Budapest, Hungary



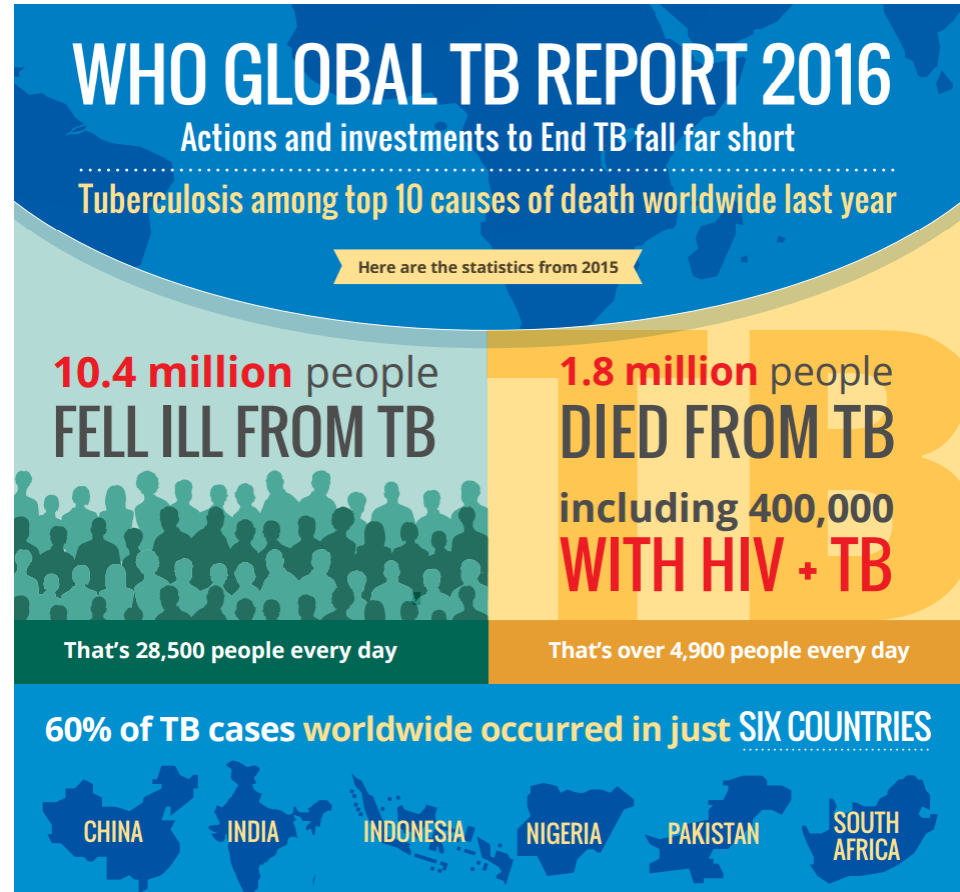
Tuberculosis remains a major burden

Current first-line treatment:

Rifampicin, isoniazid pyrazinamide and ethambutol (2 months) + rifampicin and isoniazid (4 months)

Long, complicated and toxic

Need to replace with shorter regimens



Randomized Clinical Trial of Thrice-Weekly 4-Month Moxifloxacin or Gatifloxacin Containing Regimens in the Treatment of New Sputum Positive Pulmonary Tuberculosis Patients

Mohideen S. Jawahar^{1*}, Vaithilingam V. Rajeswari Ramachandran¹, Perumal Ver Chinnaiyan Ponnuraja¹, Allaudeen S. Ili Dhanaraj Baskaran¹, Santhanakrishnan Sudha Ganapathy¹, Vanaja Kumar¹, Gee Kannivelu Jagannath², Chockalingam C Paranj R. Narayanan¹

ORIGINAL ARTICLE

A Four-Month Gatifloxacin-Containing Regimen for Treating Tuberculosis

Corinne S. M
Martin G
Joseph Odi
Ferdinand Ka
Bouke C. de Jo
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Piero L. I
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ORIGINAL ARTICLE

High-Dose Rifapentine with Moxifloxacin for Pulmonary Tuberculosis

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The NEW ENGLAND
JOURNAL of MEDICINE

ESTABLISHED IN 1812

OCTOBER 23, 2014

VOL. 371 NO. 17

Four-Month Moxifloxacin-Based Regimens for Drug-Sensitive Tuberculosis

Stephen H. Gillespie, M.D., D.Sc., Angela M. Crook, Ph.D., Timothy D. McHugh, Ph.D., Carl M. Mendel, M.D., Sarah K. Meredith, M.B., B.S., Stephen R. Murray, M.D., Ph.D., Frances Pappas, M.A., Patrick P.J. Phillips, Ph.D., and Andrew J. Nunn, M.Sc., for the REMoxTB Consortium*

All shorter regimens **were inferior** to the standard of care regimen

Jawahar et al, 2013
Merle et al, 2014
Jindani et al, 2014
Gillespie et al, 2014



Global Phase 3 “STAND” Trial Launched to Test New Drug Regimen PaMZ to Shorten, Improve Treatment

CANCELLED

Pretomanid-Moxifloxacin-Pyrazinamide

March 17, 2015



Clinical Trial of BPPaMZ Regimen Will Replace Phase 3 STAND Trial

Bedaquiline + Pretomanid-Moxifloxacin-Pyrazinamide

STAND trial will not re-open patient enrollment

December 16, 2016

Situation

Development of novel drug combinations in tuberculosis remains challenging.

Target

More effective use of preclinical data to inform selection of dose and drug combinations prior to clinical development.

Proposal

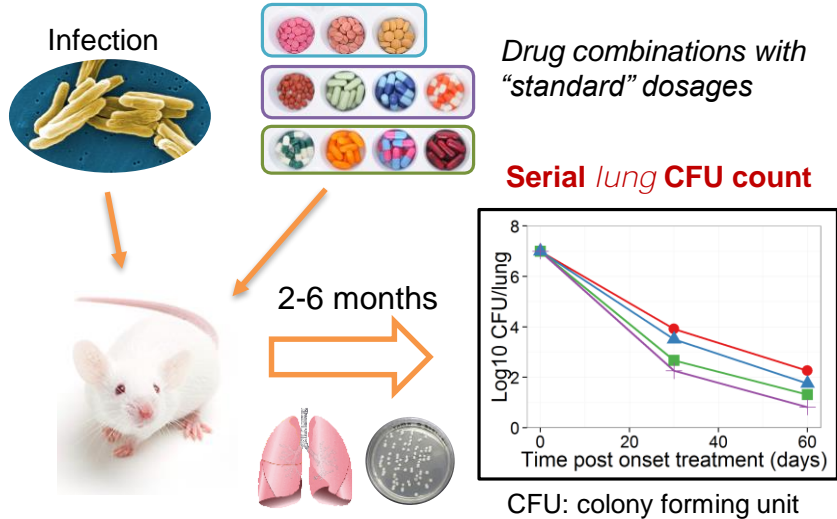
PKPD modelling for integration of preclinical data arising from different experimental protocols.

1. Demonstrate how NLME approach can be used to integrate *in vivo* PKPD data arising from different experimental protocols.
2. Develop a parametric approach to describe the effect of combination treatments on the parameters of interest.
3. Evaluation of different scaling methods for selection of dose and drug combinations in clinical development.

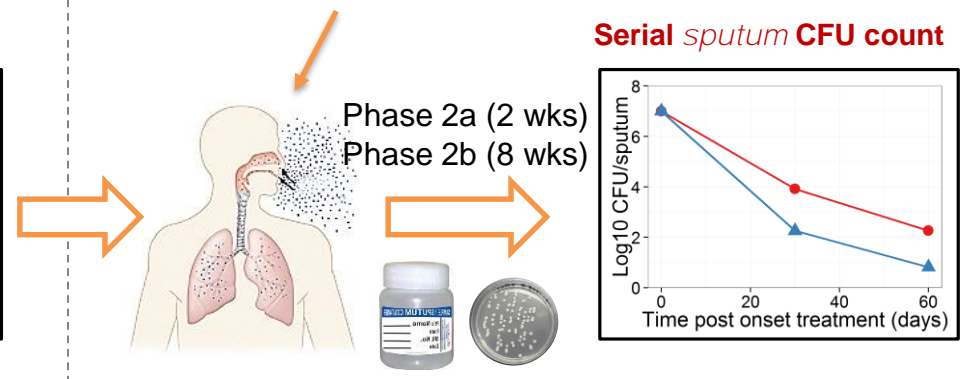
How were novel combinations assessed?

Preclinical stage

Clinical stage (Phase 2)



Select combination with the highest in vivo efficacy
Use currently approved dosages



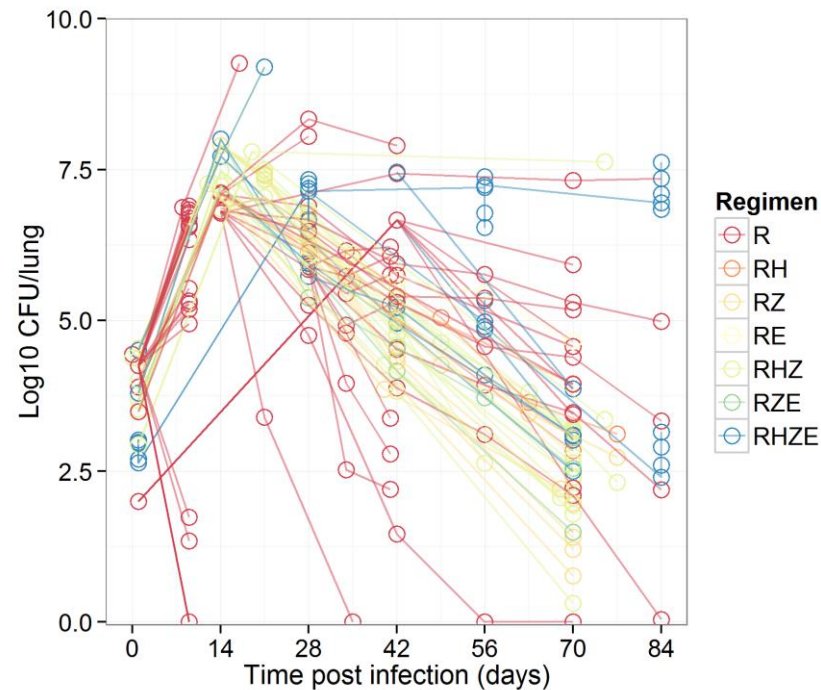
Empirical

*Individual drug contribution to overall treatment effect unclear
Little emphasis on dose optimization based on underlying PKPD relationships*

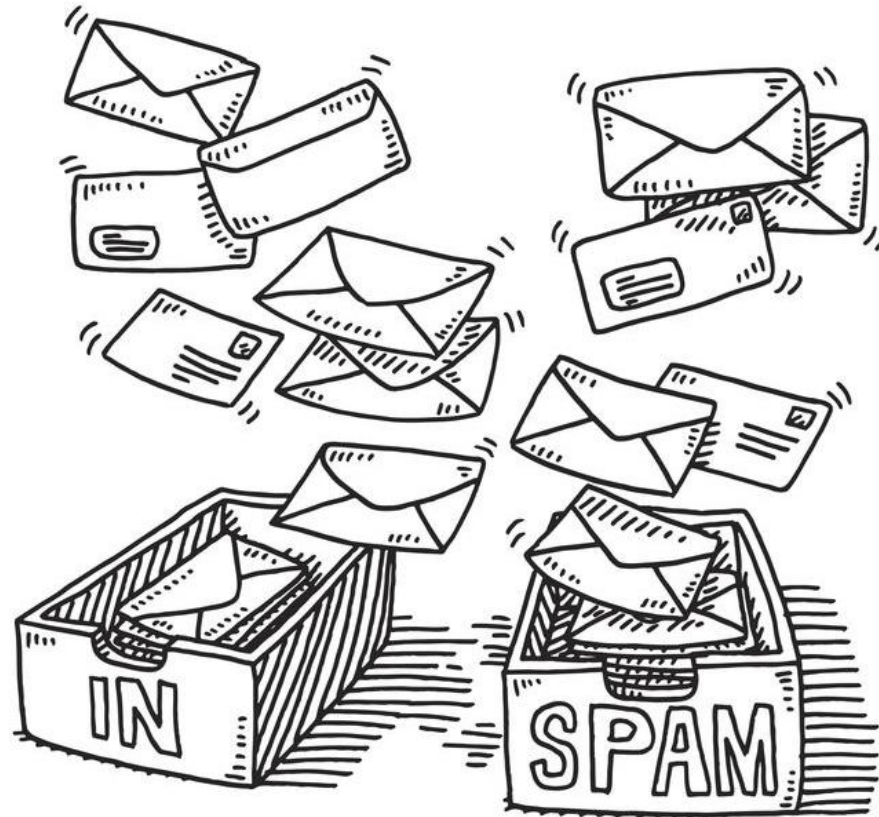
Factorial design to assess drug combinations?

Problems:

1. Large datasets
2. Complex to analyse
3. Results may still not be necessarily translatable to human



How to separate the good from the bad?



Approach: integrated PKPD modelling

Mean generation rate (k_{net})
Carrying capacity (B_{MAX})



Disease

Potency (IC_{50})
Maximum killing rate (E_{max})

PKPD
(backbone drug)

Drug interactions in each
combination

PKPD
(drug combinations)

Predict

Predict

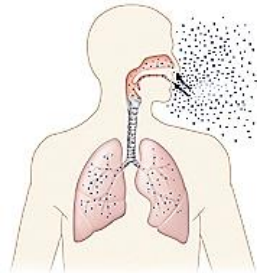
Predict

External validation

Disease

PKPD
(backbone drug)

PKPD
(drug combinations)



In vivo

Literature meta-analysis (CFU only)

Simulations (VPCs) performed without inter-individual variability

PK assumed to be constant across experiments

Human

Individual patient data available (demographics and CFU only)

Published PK models used to simulate exposure in patient population

PK variability assumed to be constant between studies

Approach: integrated PKPD modelling



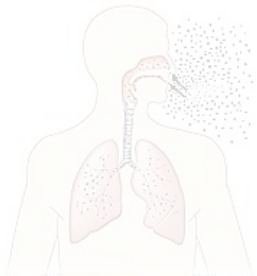
Disease



PKPD
(backbone drug)



PKPD
(drug combinations)



Disease

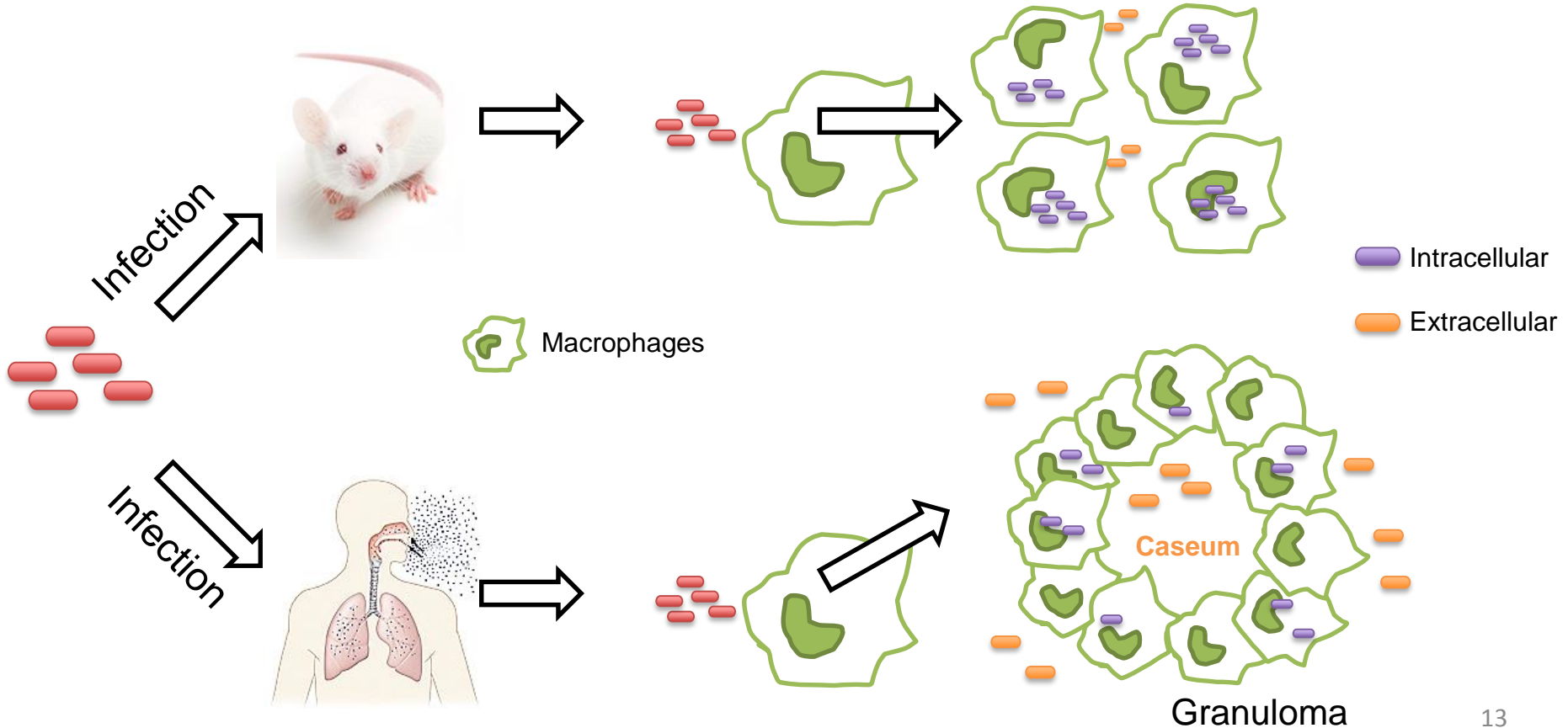


PKPD
(backbone drug)



PKPD
(drug combinations)

Disease progression in tuberculosis

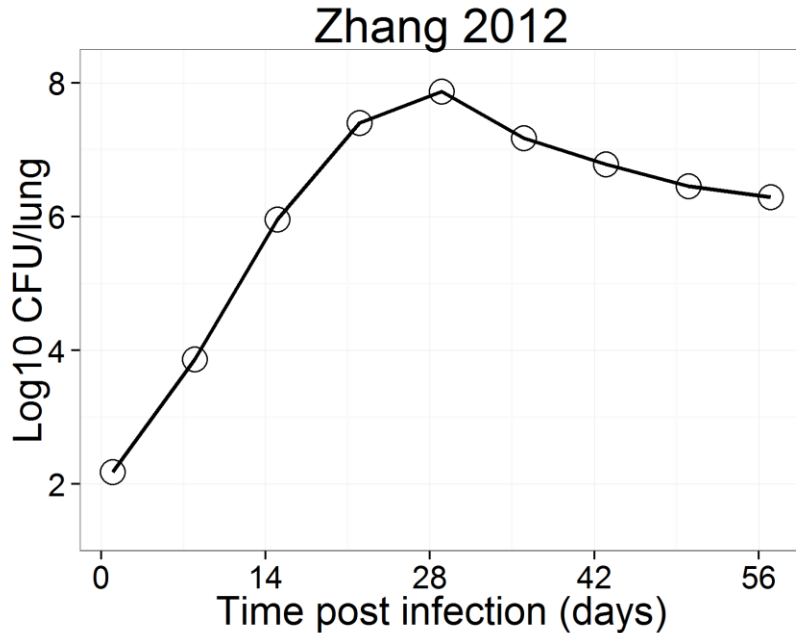


Extracellular and intracellular *M.tuberculosis* were treated as two different populations.

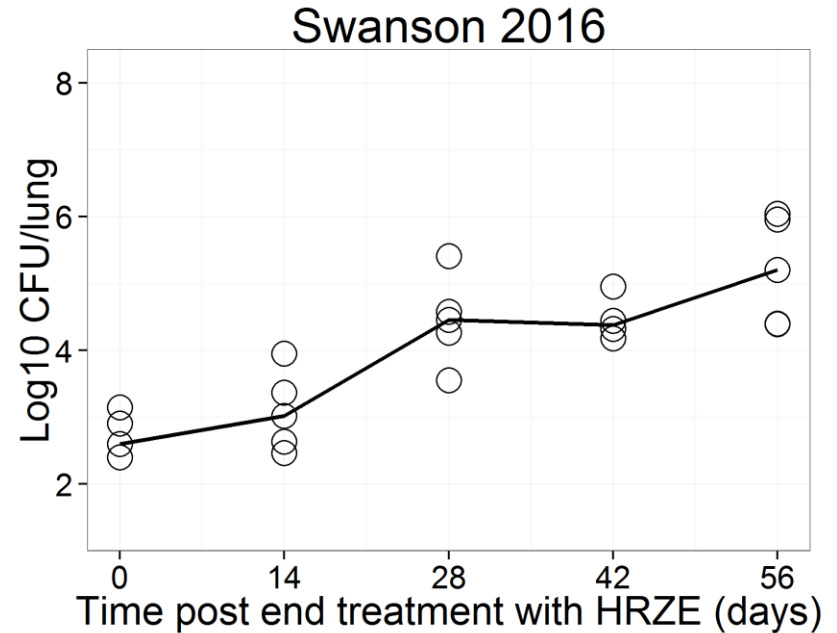
Evidence from preclinical experiments that each population display a different growth rate (fast and slow-growing).^{1,2}

A disease model was subsequently developed aiming to describe the equilibration of both populations over time.

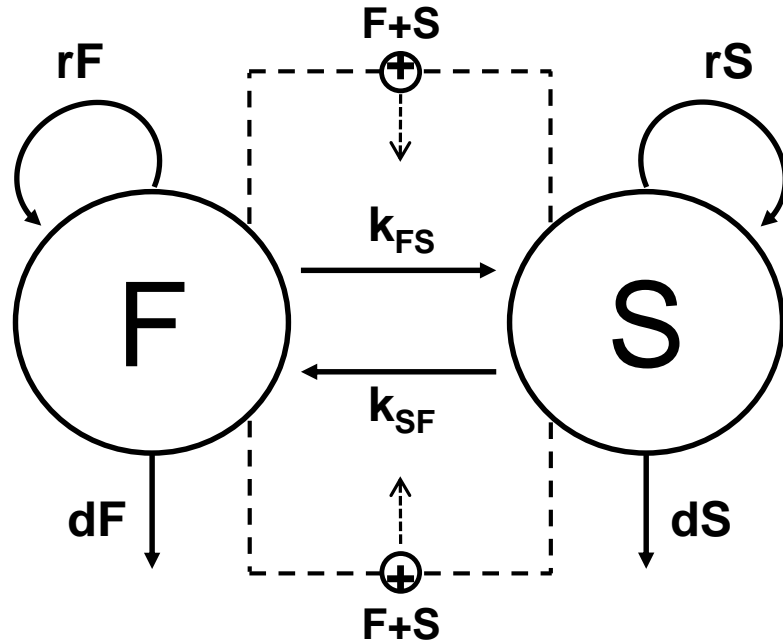
1) Beste et al, 2009; 2) Aljayyussi et al, 2017



CFU count in **untreated**
BALB/c mice



CFU **regrowth** in BALB/c mice
after 2 months of treatment



$$knetF = rF - dF$$

$$knetS = rS - dS$$

$$GROWTH_F = knetF \cdot \left(1 - \frac{(F + S)}{BMAX}\right)$$

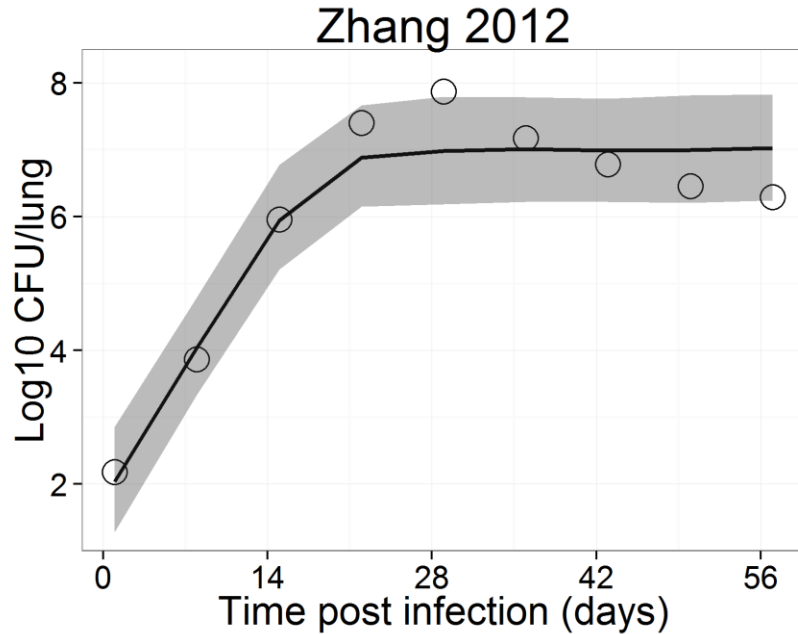
$$GROWTH_S = knetS \cdot \left(1 - \frac{(F + S)}{BMAX}\right)$$

$$kFS = \frac{knetF \cdot (F + S)}{BMAX}$$

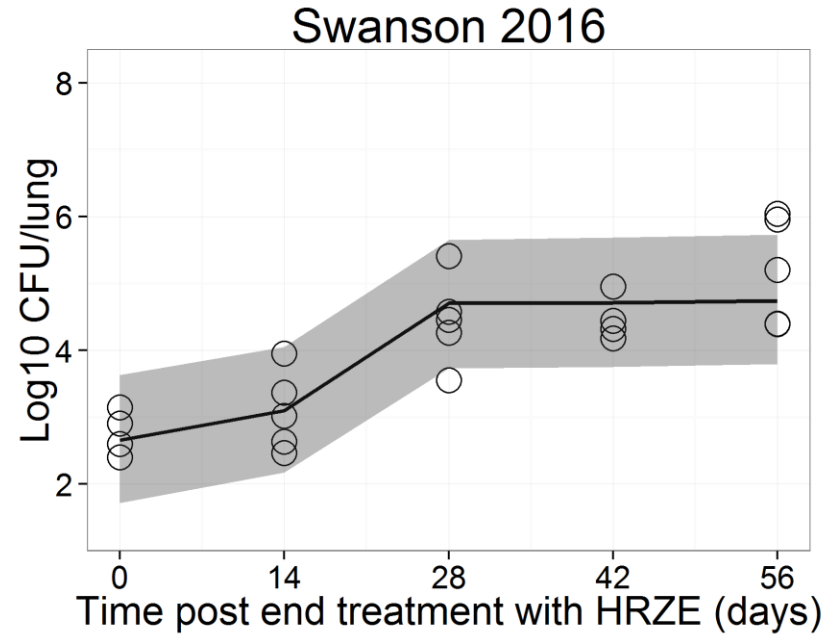
$$kSF = \frac{knetS \cdot (F + S)}{BMAX}$$

$$DADT[F] = GROWTH_F \cdot F - kFS \cdot F + kSF \cdot S$$

$$DADT[S] = GROWTH_S \cdot S + kFS \cdot F - kSF \cdot S$$

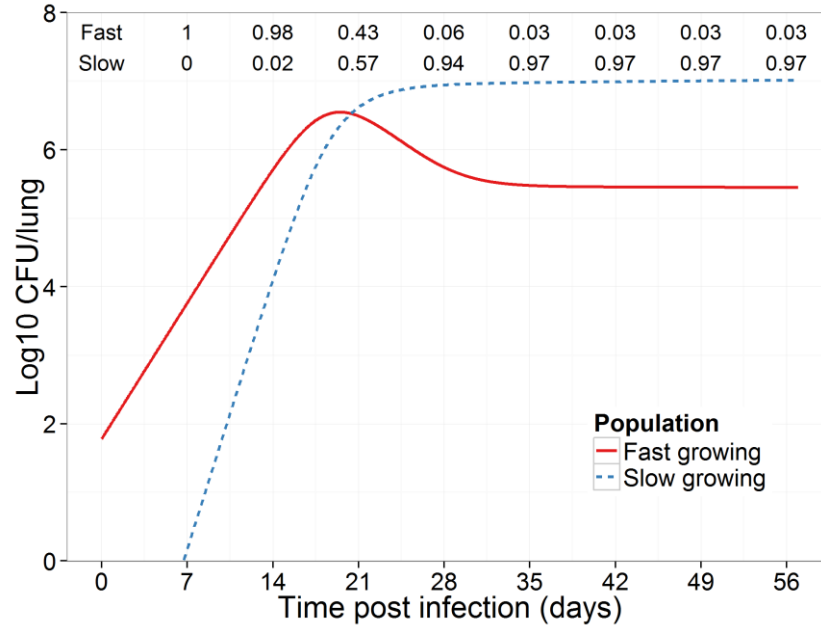


CFU count in **untreated**
BALB/c mice

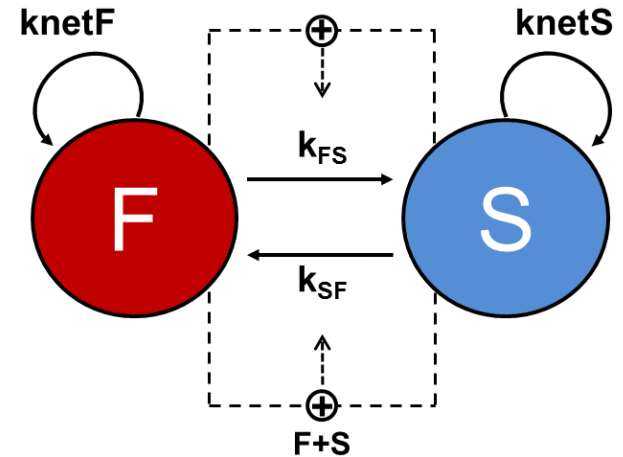


CFU **regrowth** in BALB/c mice
after 2 months of treatment

Predicted in vivo disease progression



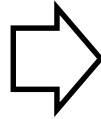
Predicted fraction from total population



Approach: integrated PKPD modelling



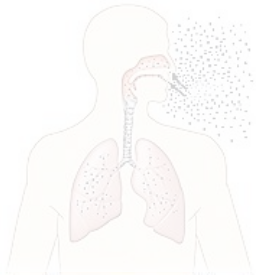
Disease



PKPD
(backbone drug)



PKPD
(drug combinations)



Disease

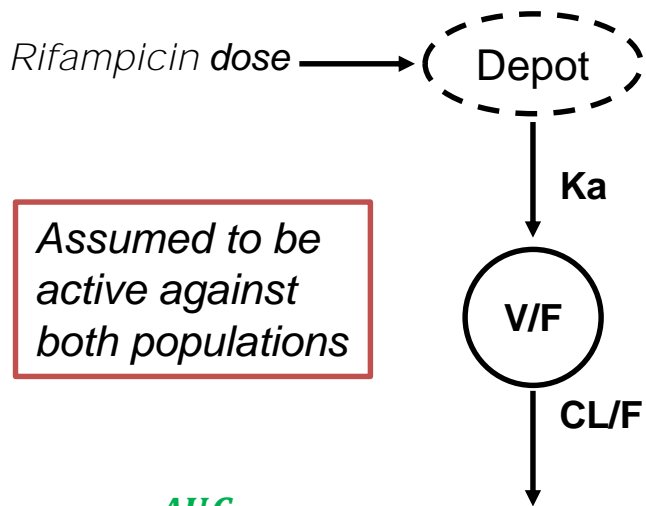


PKPD
(backbone drug)



PKPD
(drug combinations)

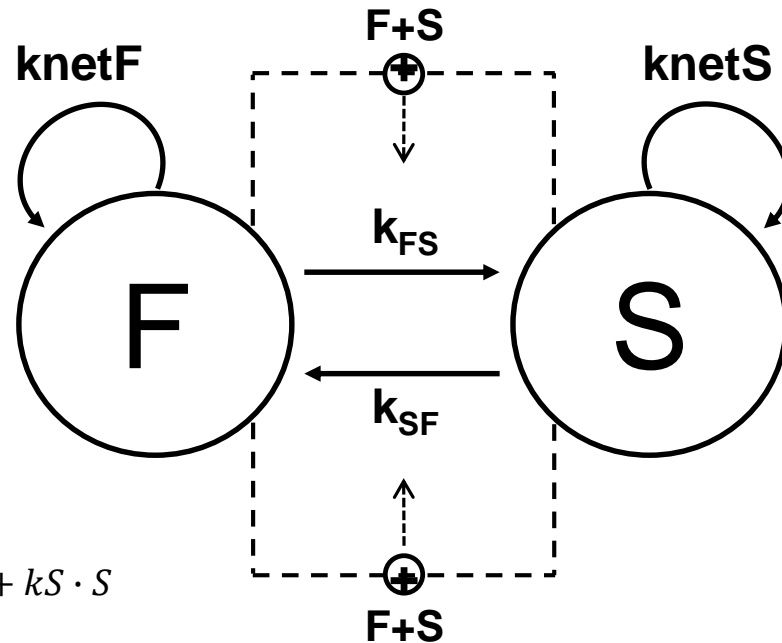
Parameterization of in vivo rifampicin effect



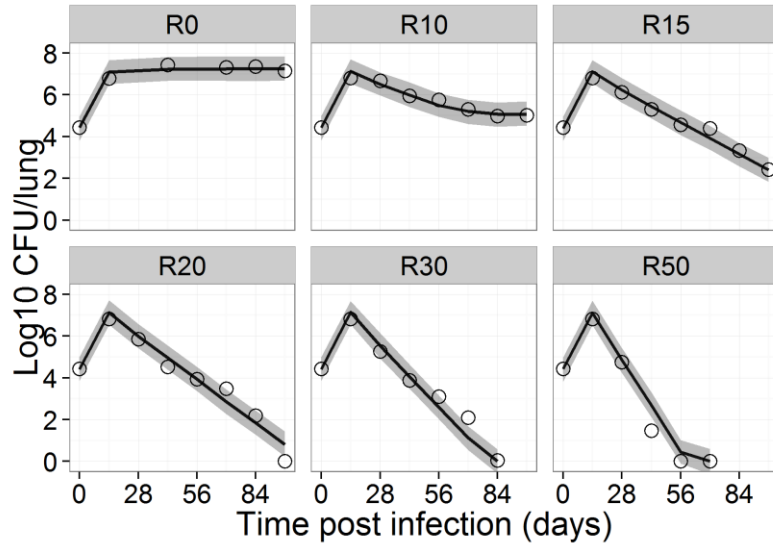
$$C_{ss,av} = \frac{AUC_{0-24}}{24}$$

$$DADT[F] = \left(GROWTH_F - \frac{Emax \cdot C_{ss,av}}{IC50_F + C_{ss,av}} \right) \cdot F - k_{FS} \cdot F + k_{SF} \cdot S$$

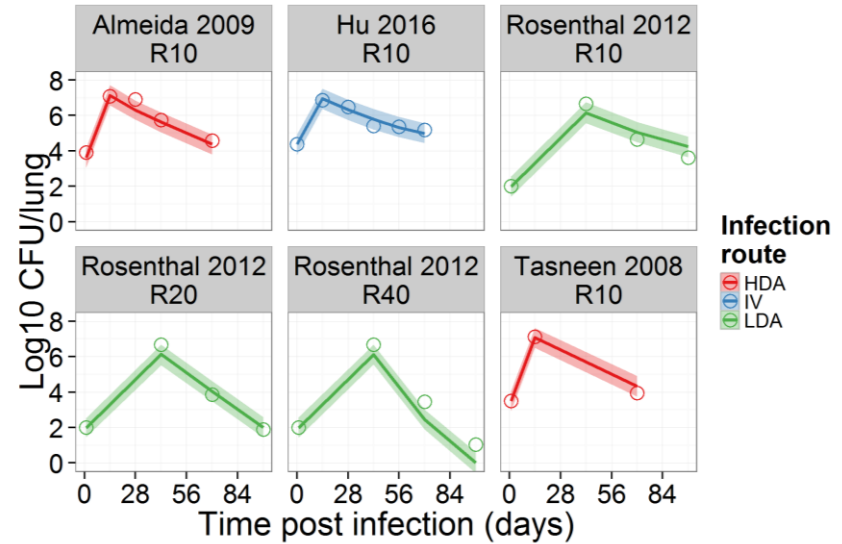
$$DADT[S] = \left(GROWTH_S - \frac{Emax \cdot C_{ss,av}}{IC50_S + C_{ss,av}} \right) \cdot S + k_{FS} \cdot F - k_{SF} \cdot S$$



Model building



External validation



Infection route	IC50, F (mg/L)	IC50, S (mg/L)
Intravenous (IV)	4.87 (reference)	60.2 (reference)
High-dose aerosol (HDA)	3.26	40.3
Low-dose aerosol (LDA)	4.97	61.4

Hu et al 2015

Preliminary conclusions (1)

Longitudinal model to describe growth of fast and slow-growing *Mtb*

Rifampicin IC50 was different between fast and slow growing *Mtb*

Which companion drug(s) for rifampicin?



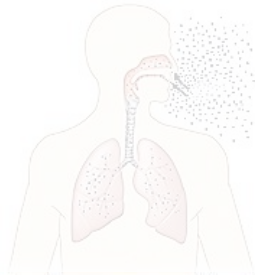
Disease



PKPD
(backbone drug)



PKPD
(drug combinations)



Disease



PKPD
(backbone drug)



PKPD
(drug combinations)

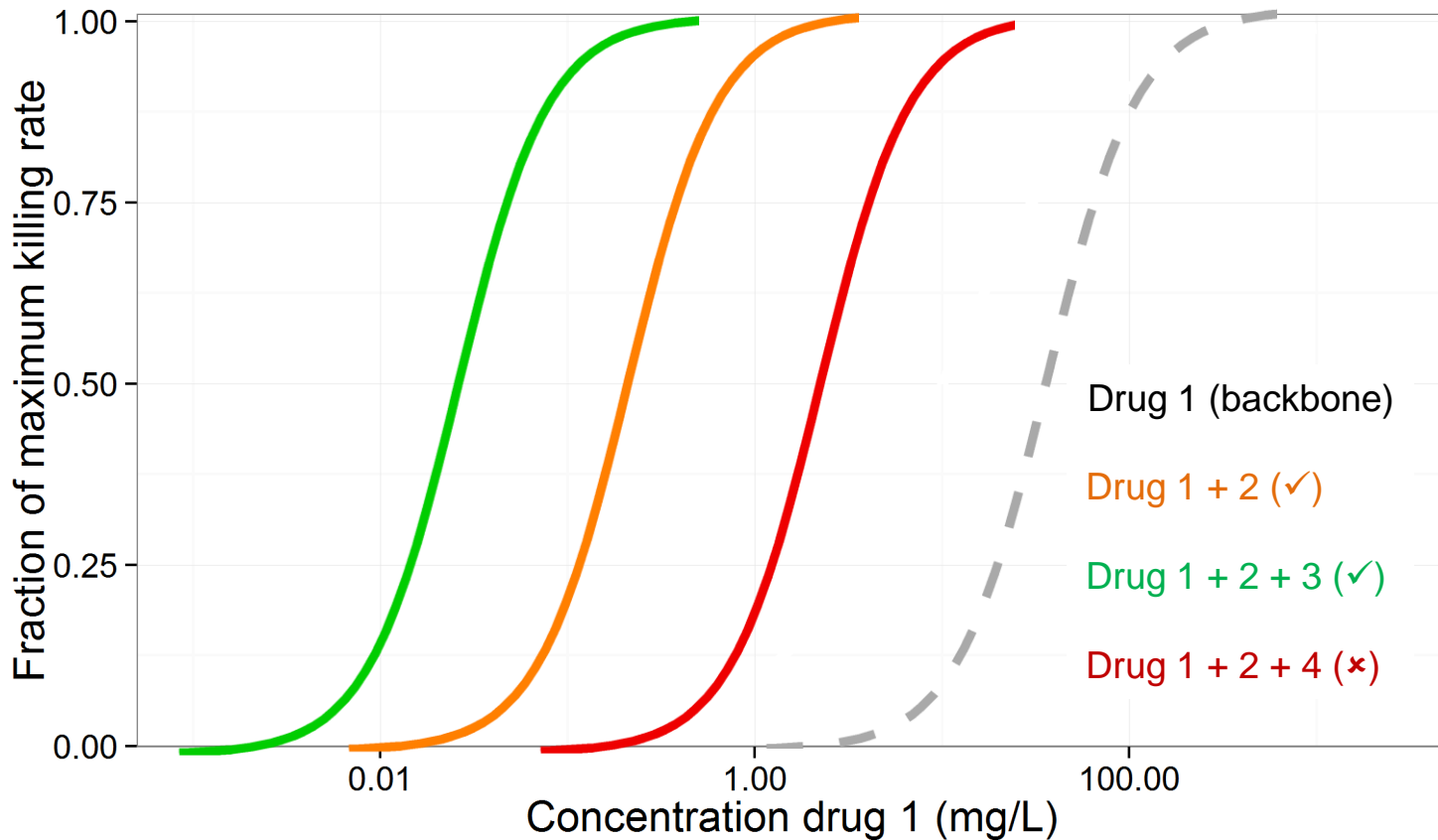
Which partner drug(s) for rifampicin?

Question: how can we capture the contribution of additional drugs to the overall bacterial clearance, despite **limited** experimental data?

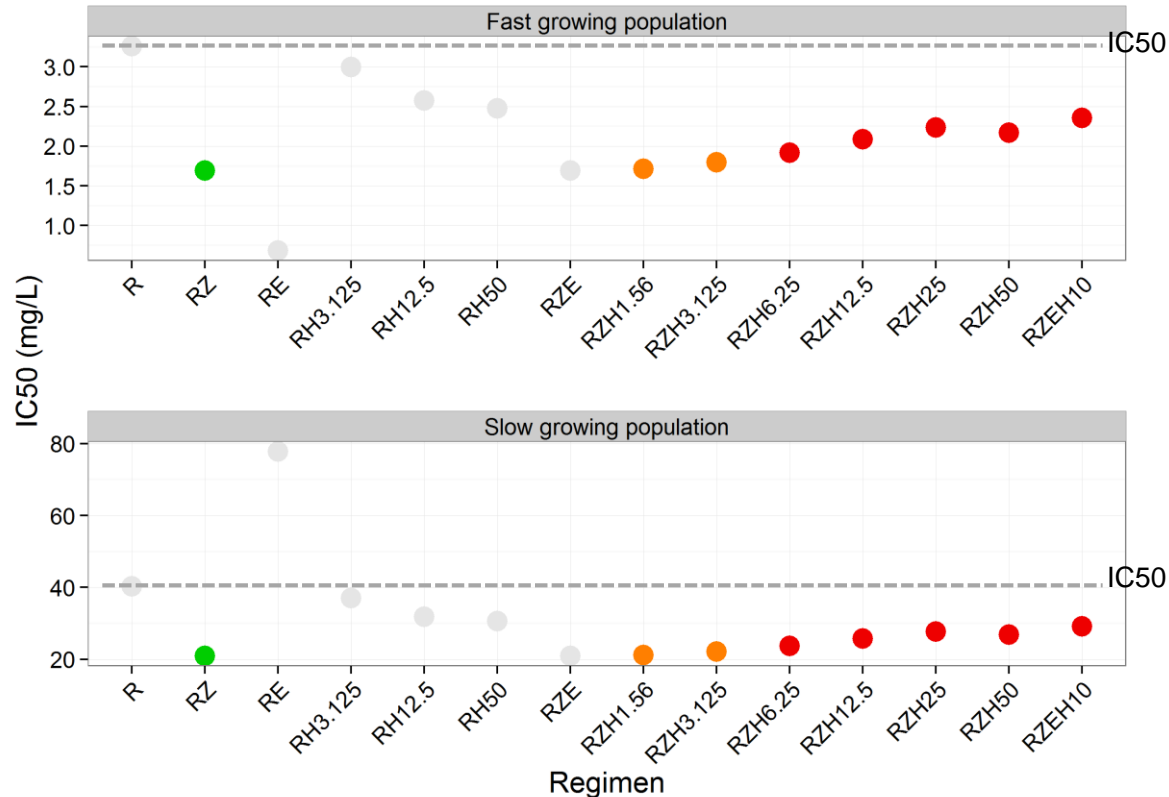
Proposal: treat additional drugs as **discrete covariates** of the potency (IC50) of the backbone drug (rifampicin)



How were drug combinations assessed?



Results with rifampicin as backbone drug



Highest increase in potency with Z

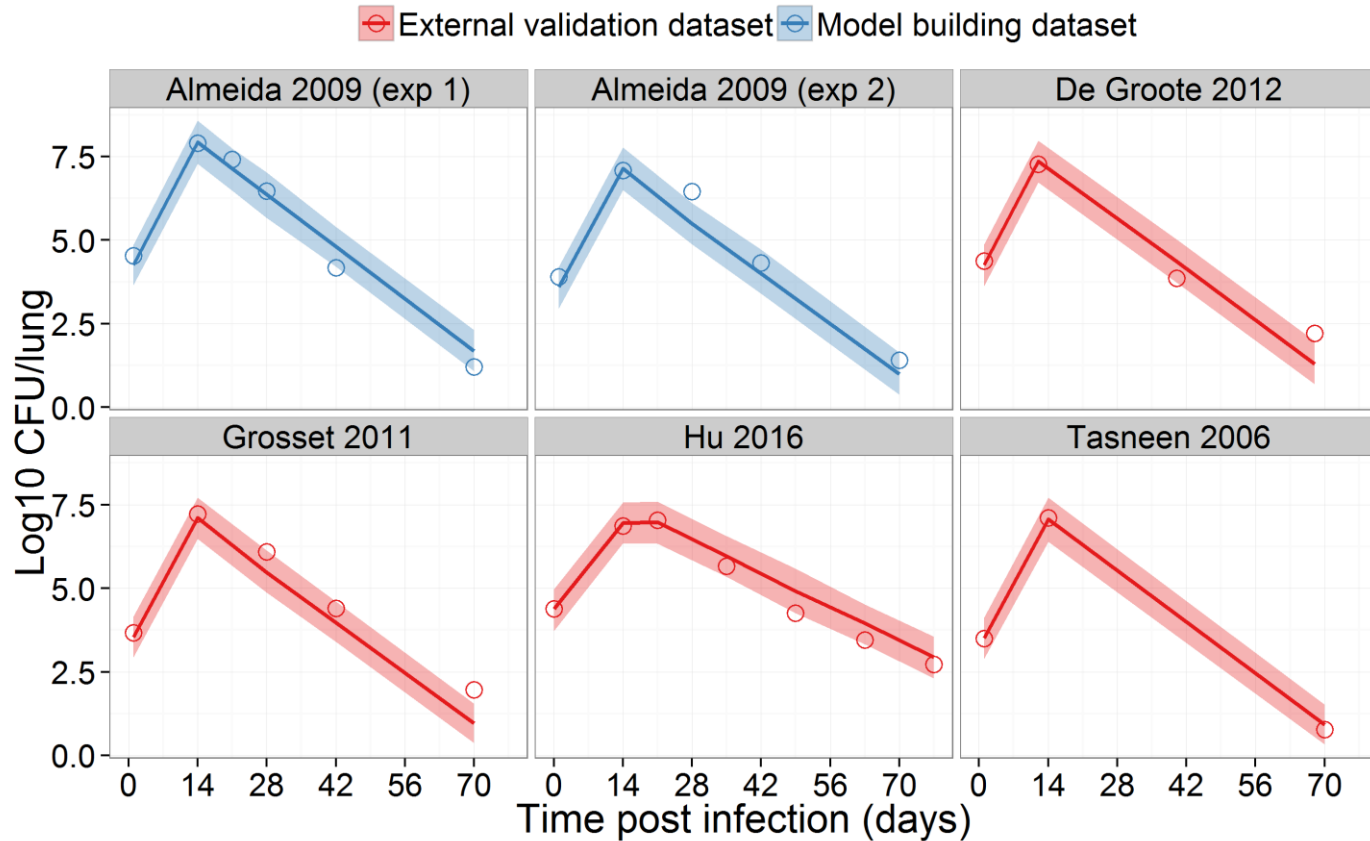
No effect on potency when E added

Reduction in potency if H added

Regimen #1 = RZ

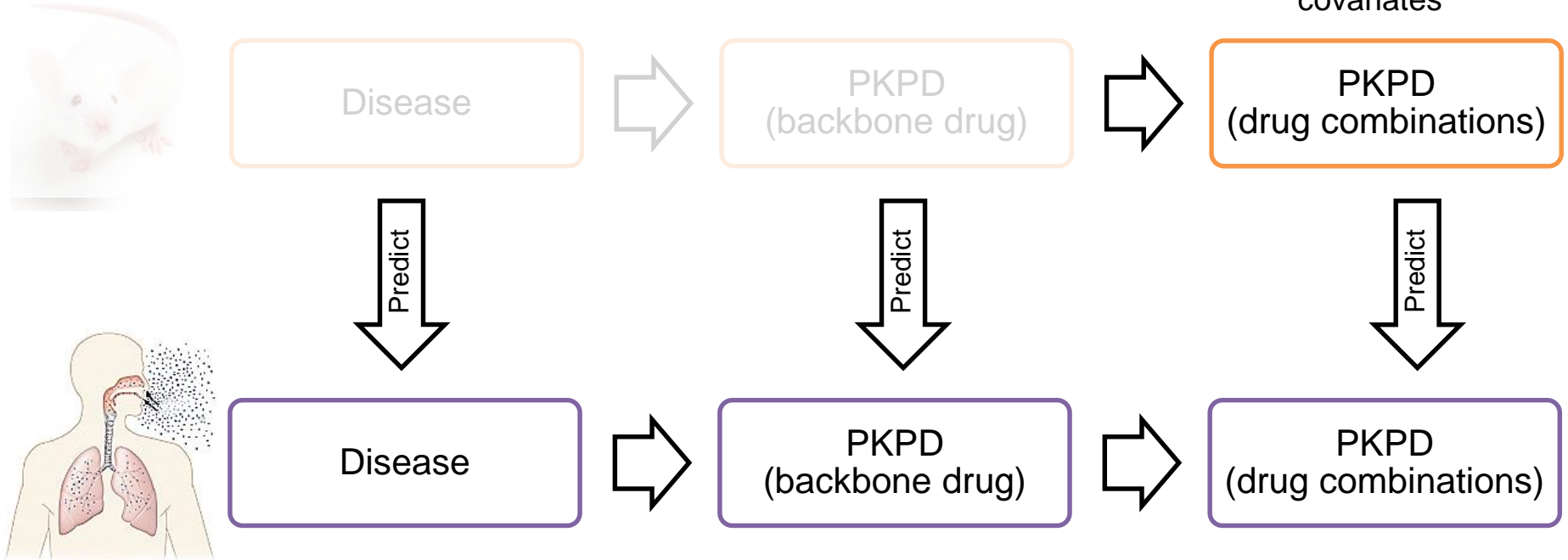
R = rifampicin
H = isoniazid
E = ethambutol
Z = pyrazinamide

Validation of RZ model



Preliminary conclusion (2)

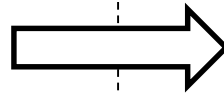
Our approach allowed parameterization of drug combination(s) as discrete covariates



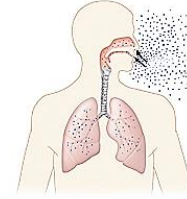


SCALING OF PK

PK model (clearance, volume of distribution, protein binding)



PK model (clearance, volume of distribution, protein binding)



SCALING OF DISEASE

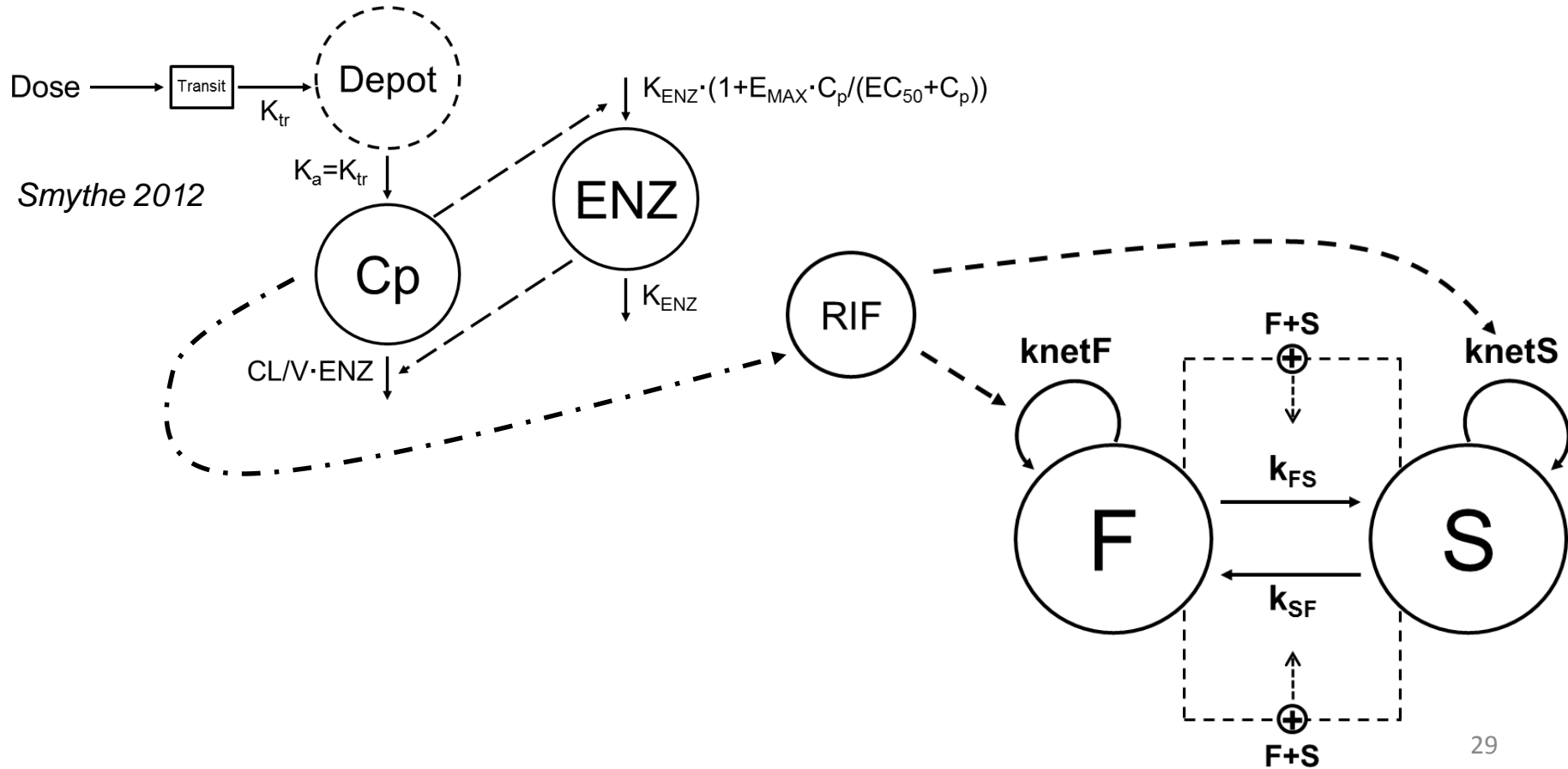
CFU levels and ratio F:S at onset treatment

Disease model (CFU levels)



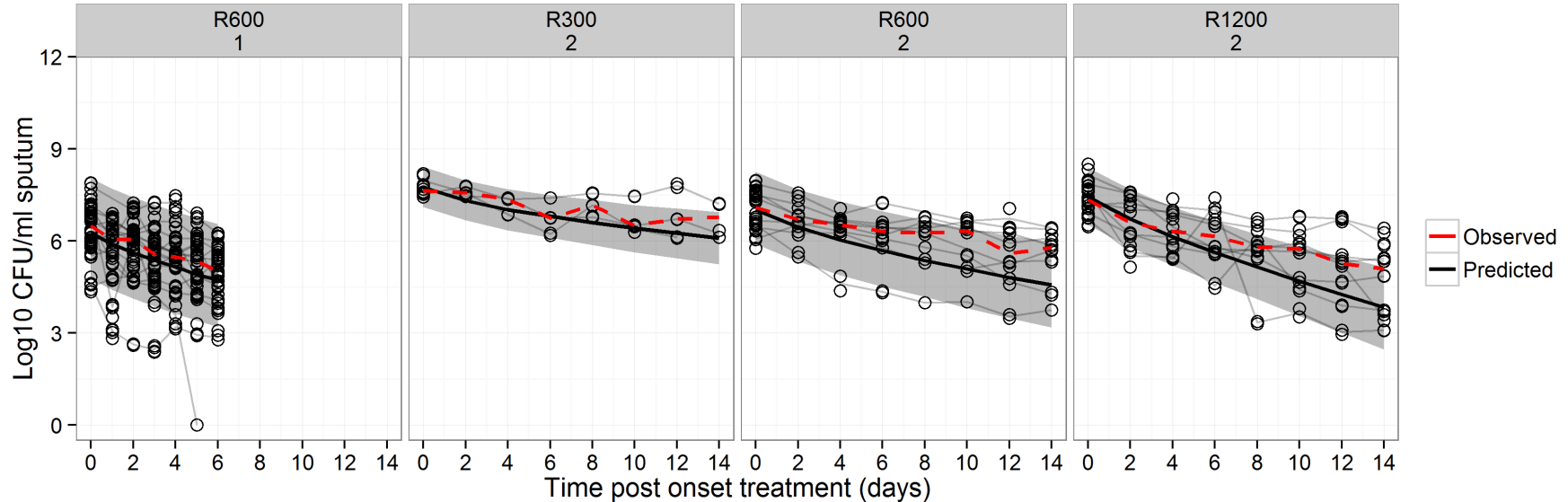
Disease model (CFU levels)

PKPD model of rifampicin in human



Predicted EBA of rifampicin in TB patients

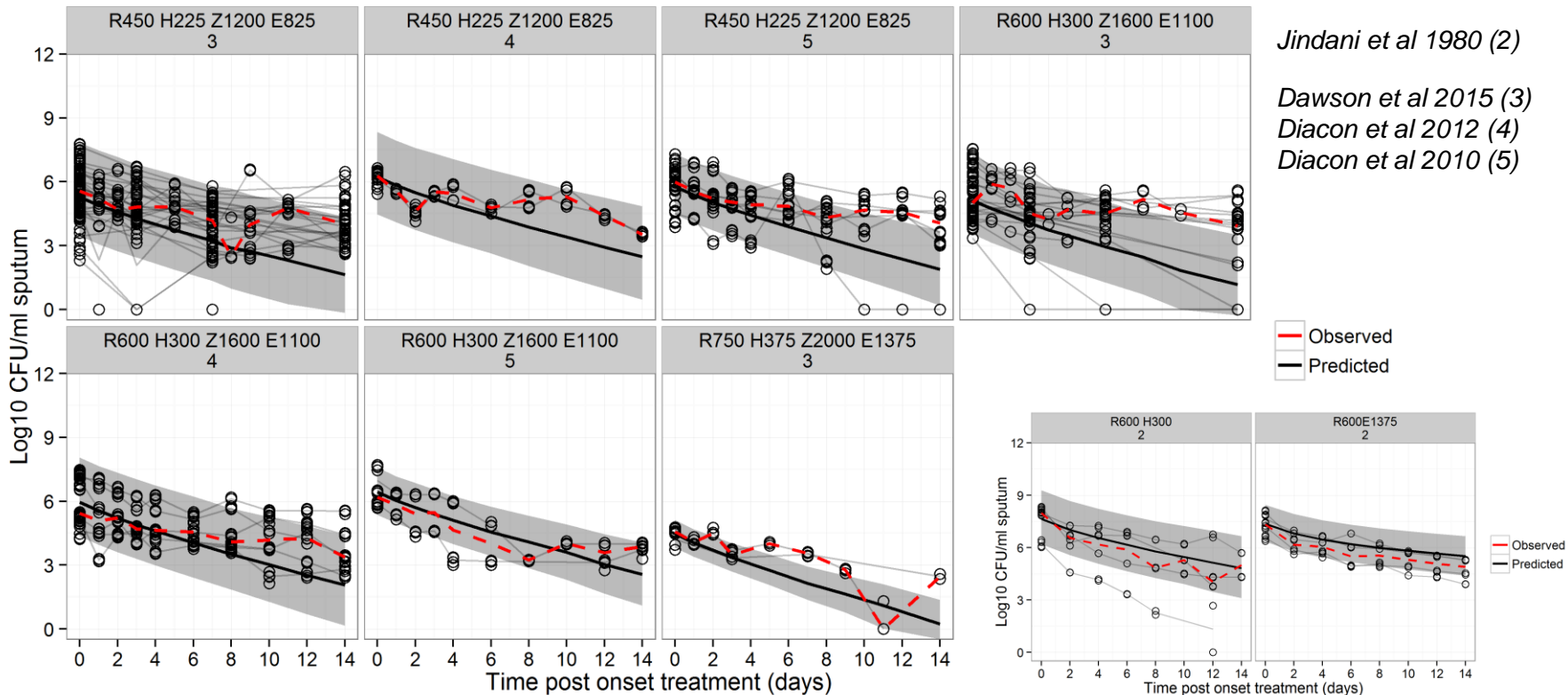
Rustomjee et al 2008 (1)
Jindani et al 1980 (2)



Can we predict EBA following combination treatments too?

EBA = early bactericidal activity

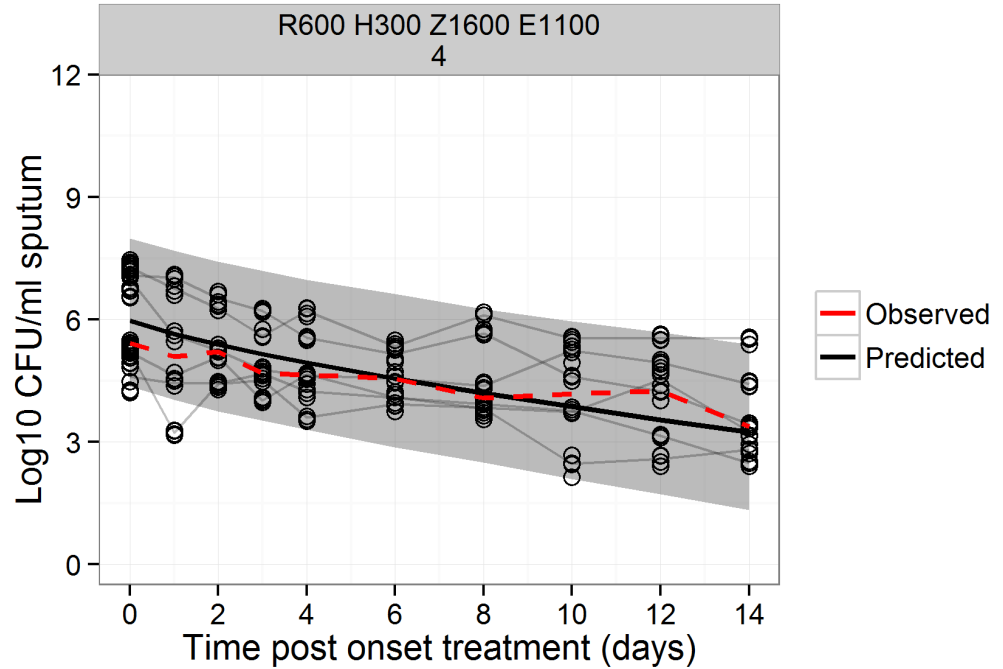
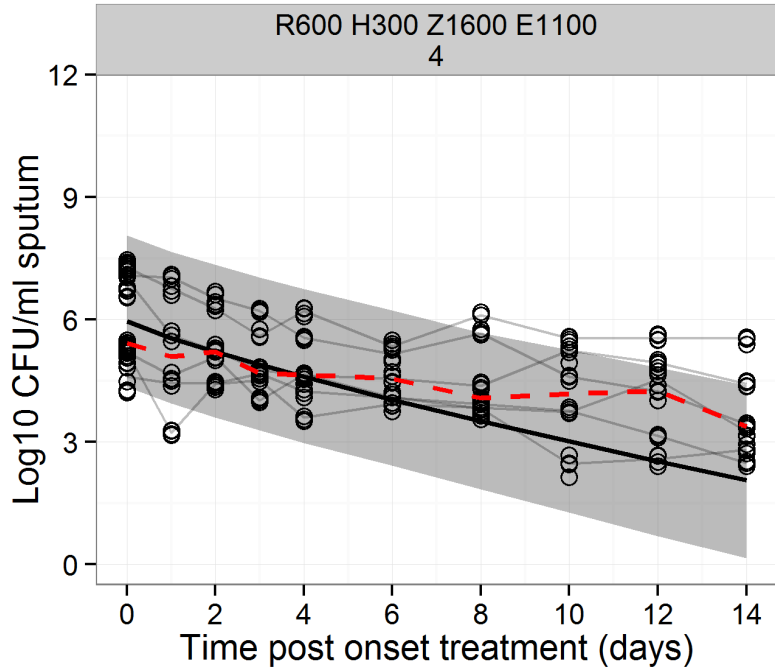
Predicted EBA of combination treatments



EBA = early bactericidal activity

Sensitivity analysis - pharmacokinetics

Diacon et al 2012 (4)



A longitudinal model describing bacterial growth over time provides insight into the dose rationale for the evaluation of drug combinations.

The proposed parameterization of drug combinations as discrete covariates offers a practical solution for the screening of novel compounds.

Accurate predictions of treatment response in humans require scaling of pharmacokinetics and disease characteristics, which often differ across experimental protocols.

Acknowledgments



Gerry Davies
James Kerwin



janssen



Dr. Amina Jindani



Clinical Pharmacology
& Therapeutics group



The research leading to these results has received funding from the Innovative Medicines Initiative Joint Undertaking under grant agreement n°115337, resources of which are composed of financial contribution from the European Union's Seventh Framework Programme (FP7/2007-2013) and EFPIA companies' in kind contribution.

Appendix

VPC of in vivo rifampicin PK model

