



# A SYSTEMS PHARMACOLOGY MODEL FOR Understanding Bug-Host-Regimen Interplay

TRESSOPPENCOLUE

Natasha Strydom

## Connecting the **Network**

### Regimen





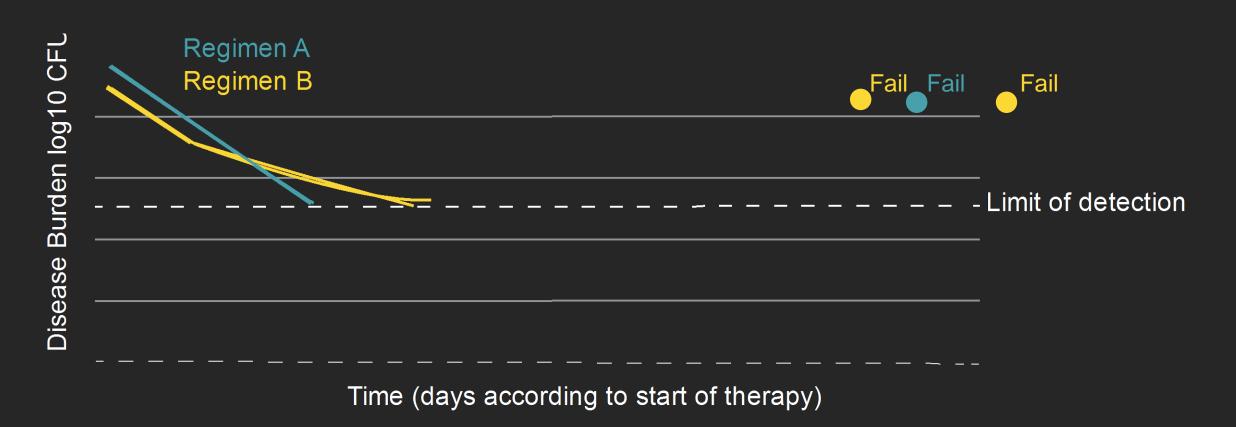


## Systems Pharmacology



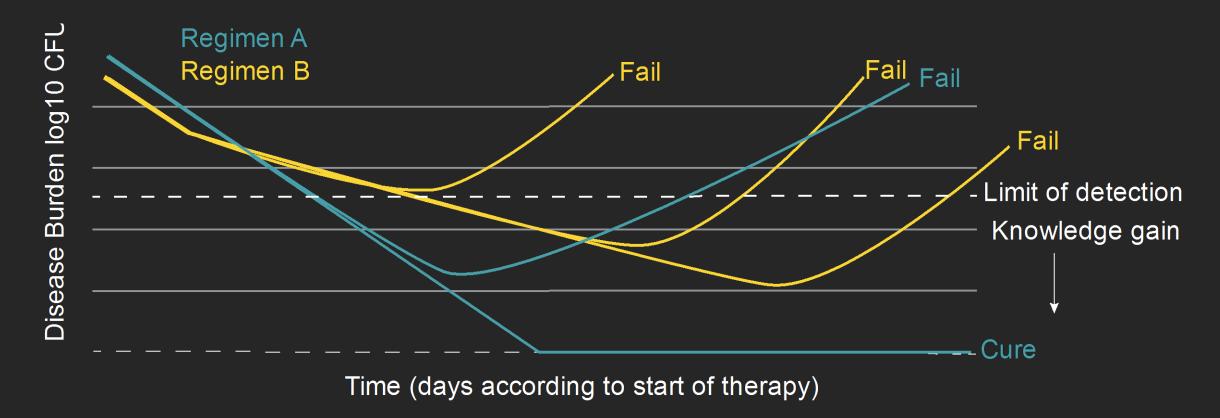
## Current limit in measuring tuberculosis cure

Our current knowledge of tuberculosis treatment failure vs cure is limited by our assays.

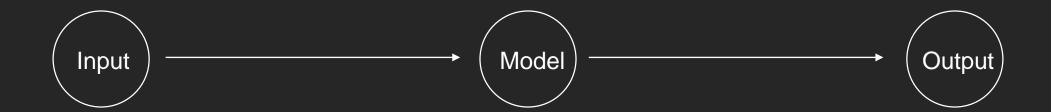


## Current limit in measuring tuberculosis cure

Our current knowledge of tuberculosis treatment failure vs cure is limited by our assays. Through the use of **modelling**, **diagnostics** and emerging **biomarker data**, we can gain "depth" in understanding clearance of tuberculosis. Using this gained knowledge we're able to better predict treatment outcome success and failure.



## Model Overview

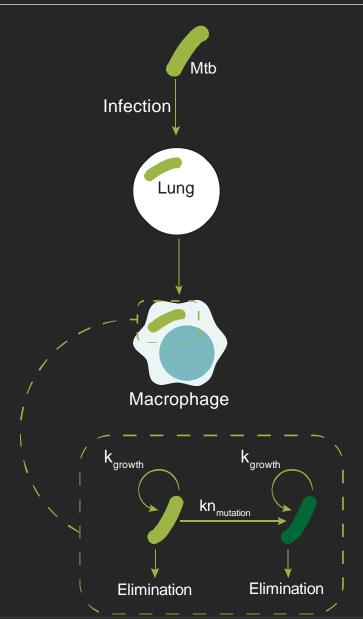


## Systems Model

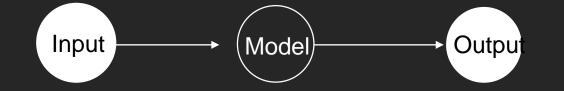










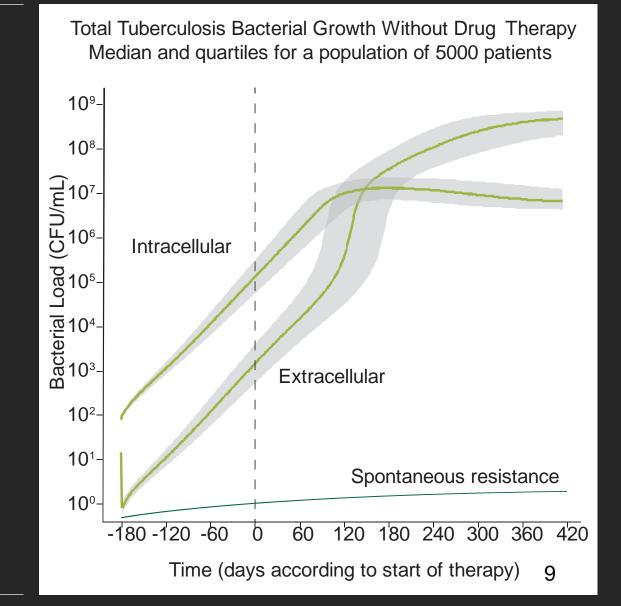


### **Model Parameters**;

Growth Rate
Natural resistance
Intracellular bacteria

#### Source

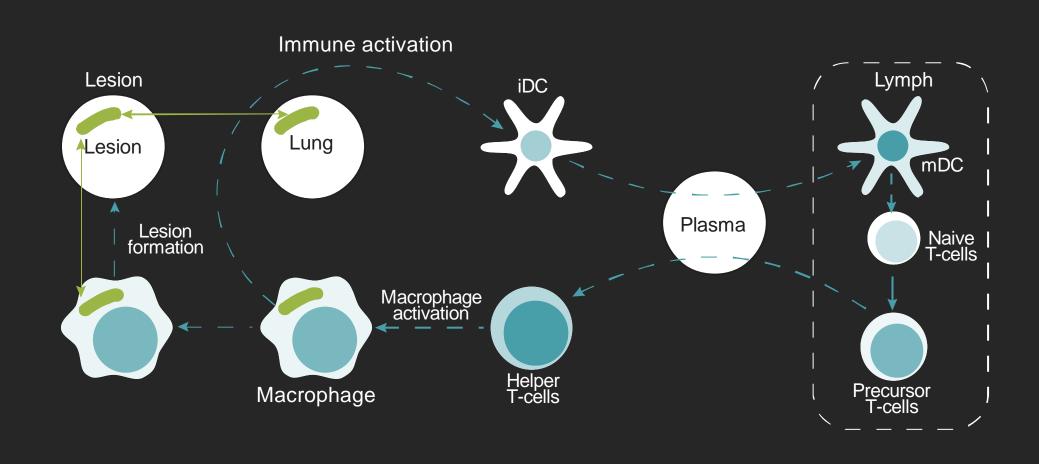
Mouse model - Ahmad Z, et al. (2011) Antimicrob Agents Chemother 55: 1527-1532. Clinical - Menzies D, et al. (2009) PLoS Med 6(9)





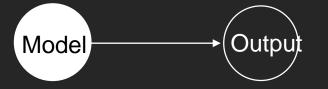
## Host Immune Responsengut

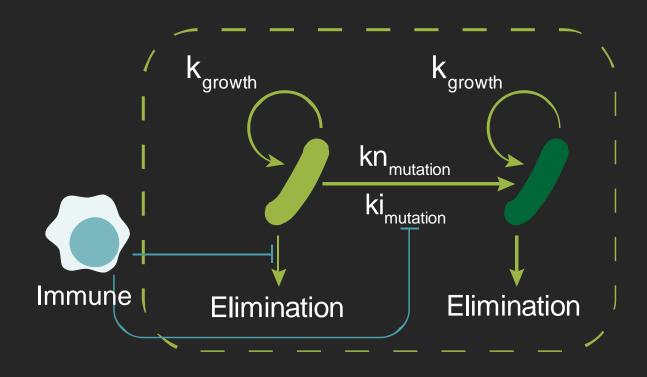






## Host Immune Response Puput







## Host Immune Response Input



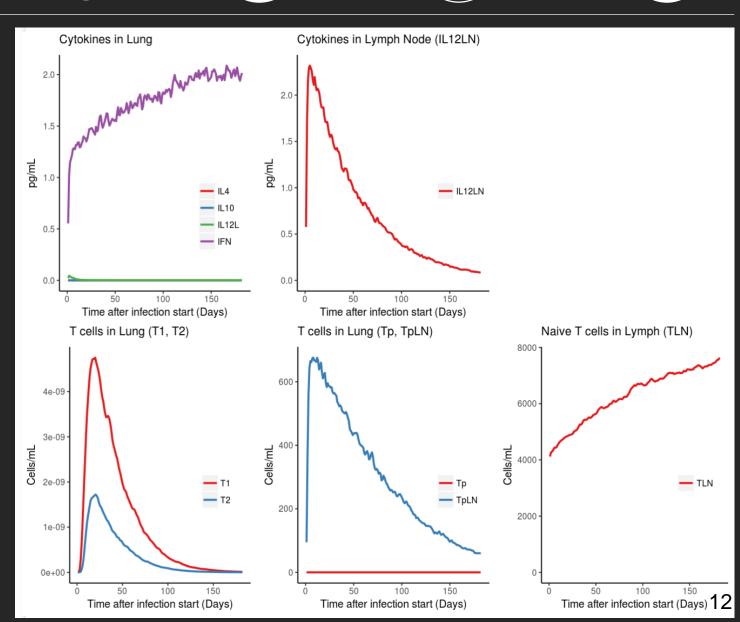
Output

### **Model Parameters**;

Maximal T-cell killing rate
Rate of Th1 differentiation
Rate of Th2 differentiation
Extracellular bacterial growth rate
Intracellular bacterial growth rate
Bacterial uptake by IDC in lung
Half-sat, Be on IDC activation

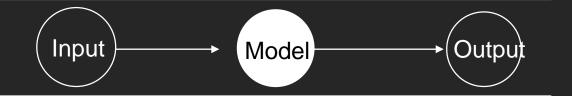
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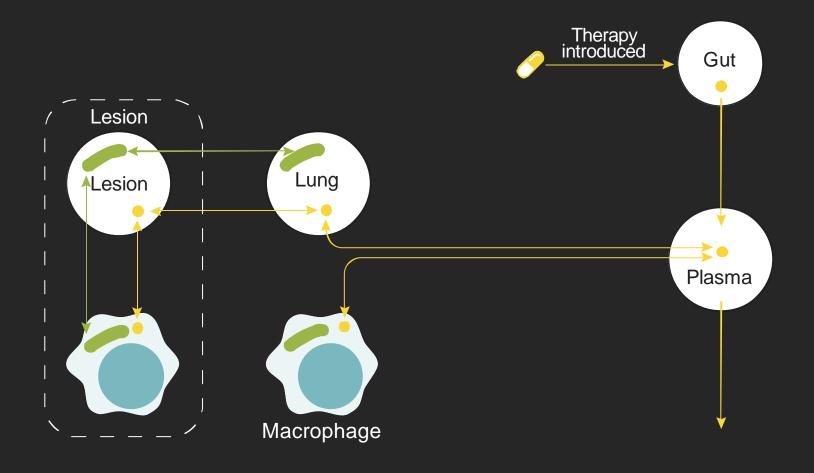
Marino S, Kirschner DE. (2004) *J Theor Biol* 227: 463-486.



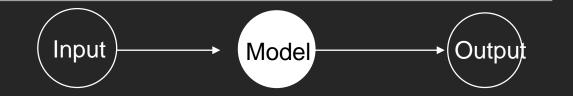


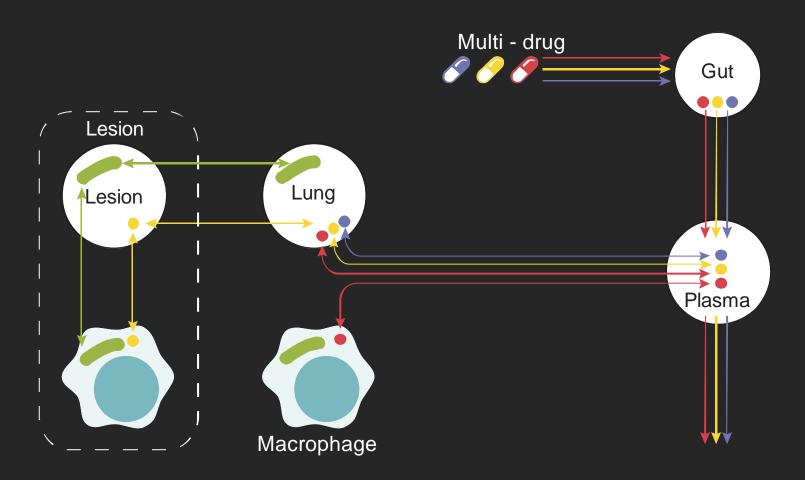
## Mono-therapy PK



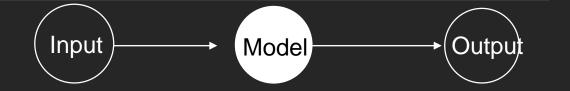


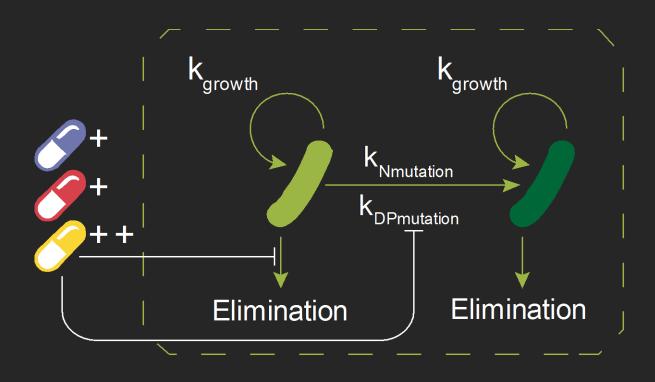




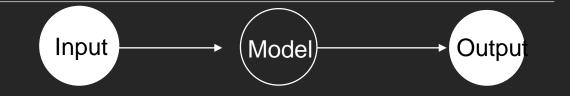








## Multi-drug PK

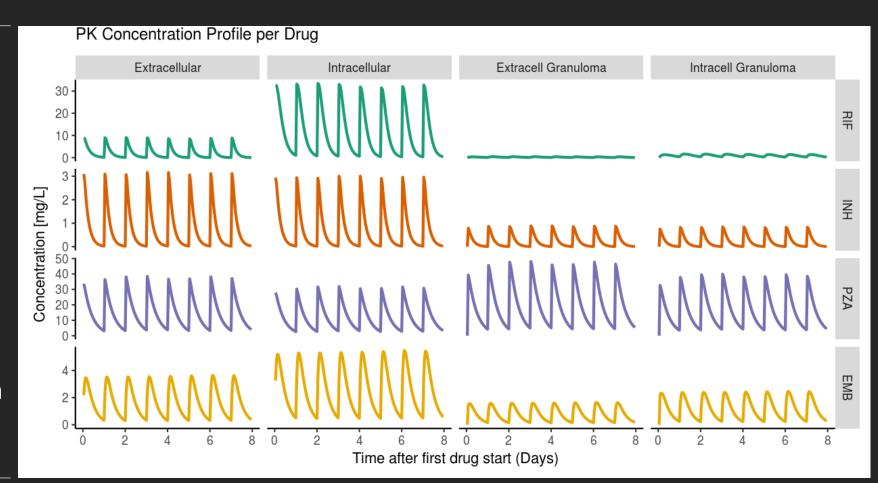


## Model Parameters & Sources

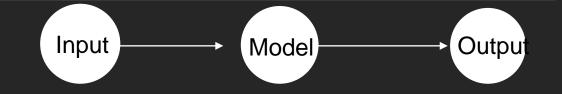
Absorption, clearance, elimination (human volunteers & patients)

Auto-induction & acetylation rate (human subjects)

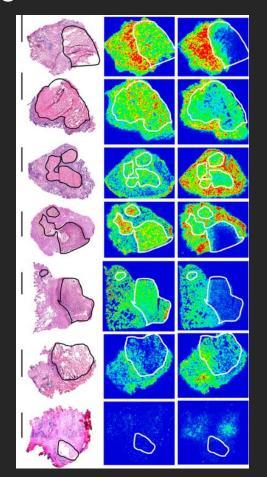
Intra-macrophage accumulation (in-vitro, mouse, rabbit)

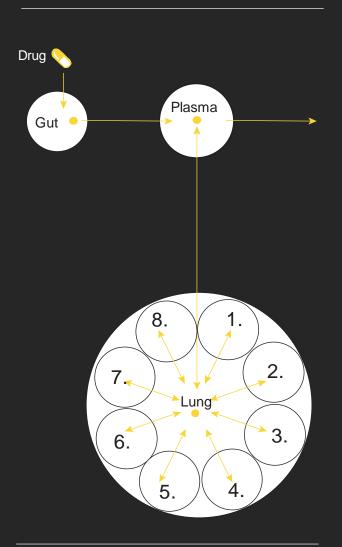


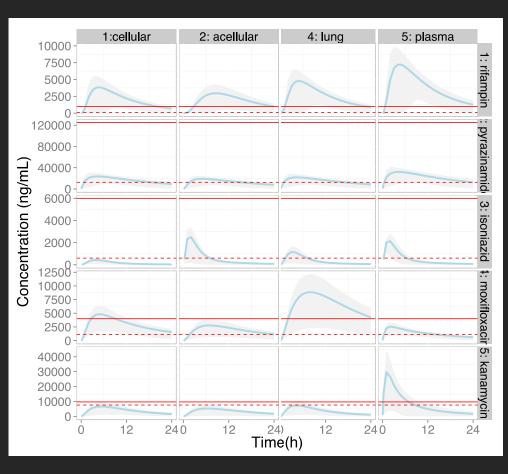




### Rutgers MALDI-MS data

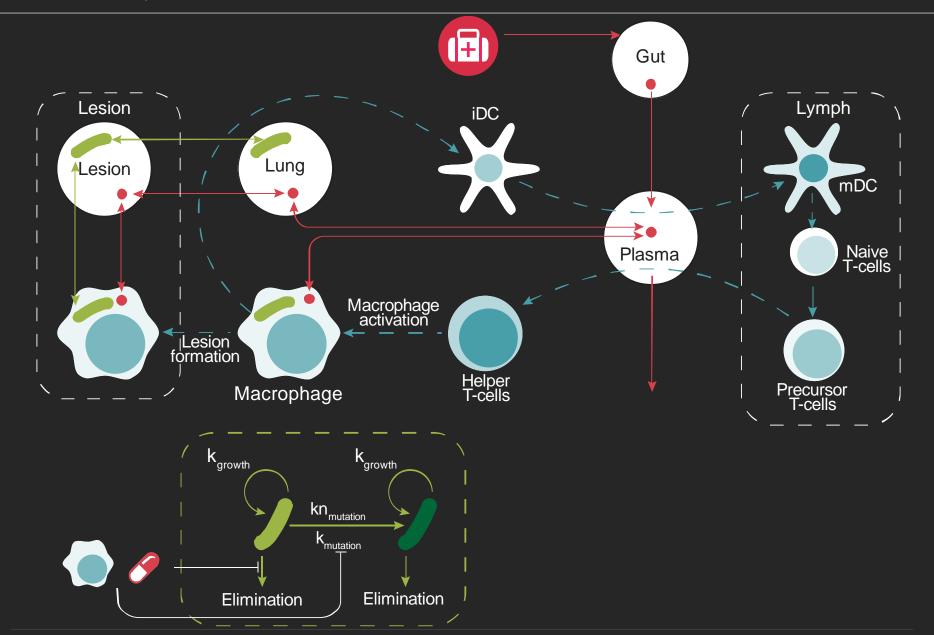






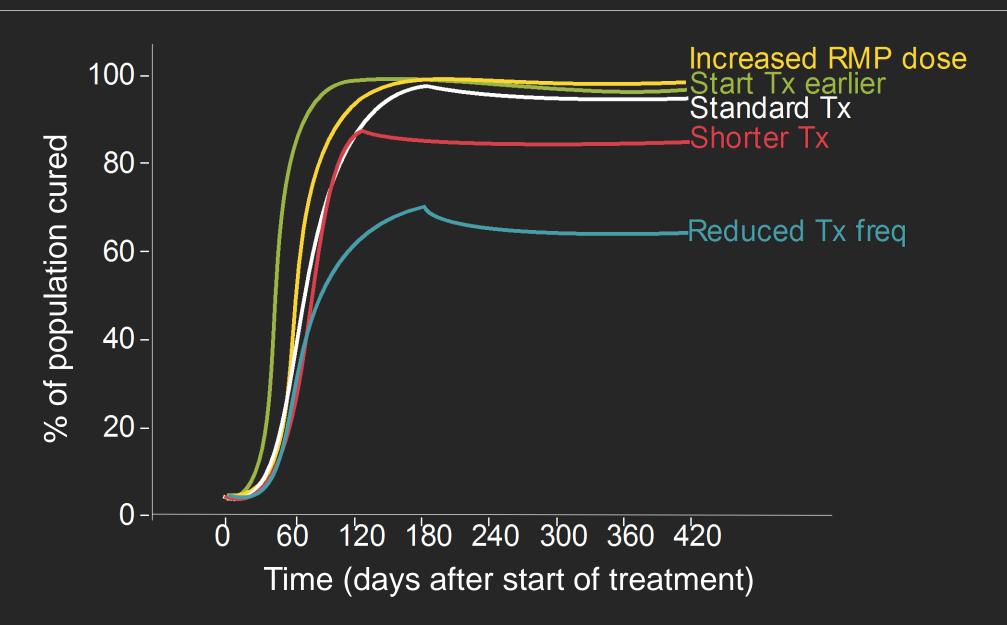


## Full QSP model



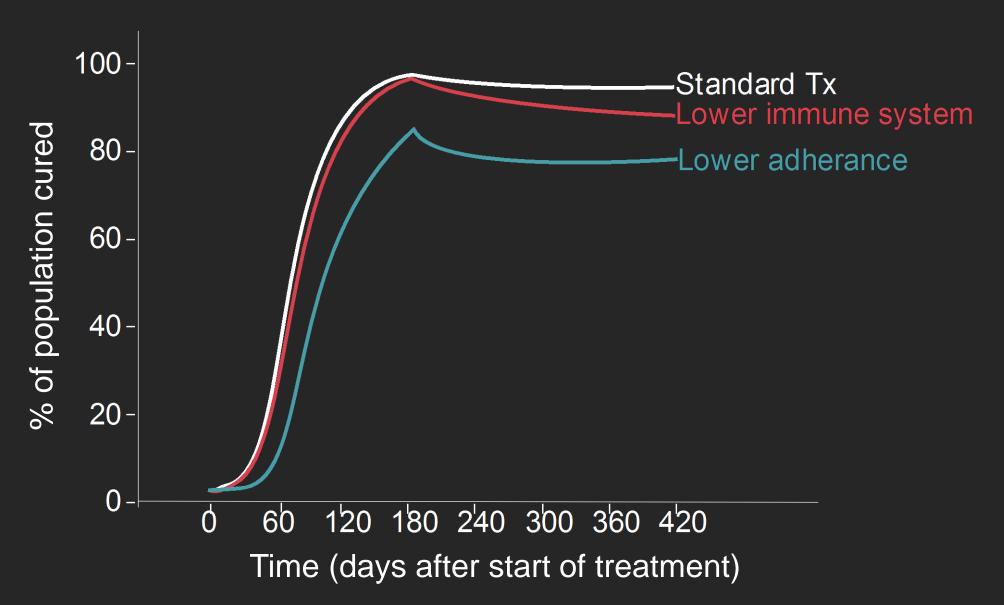


## Exploring drug therapies



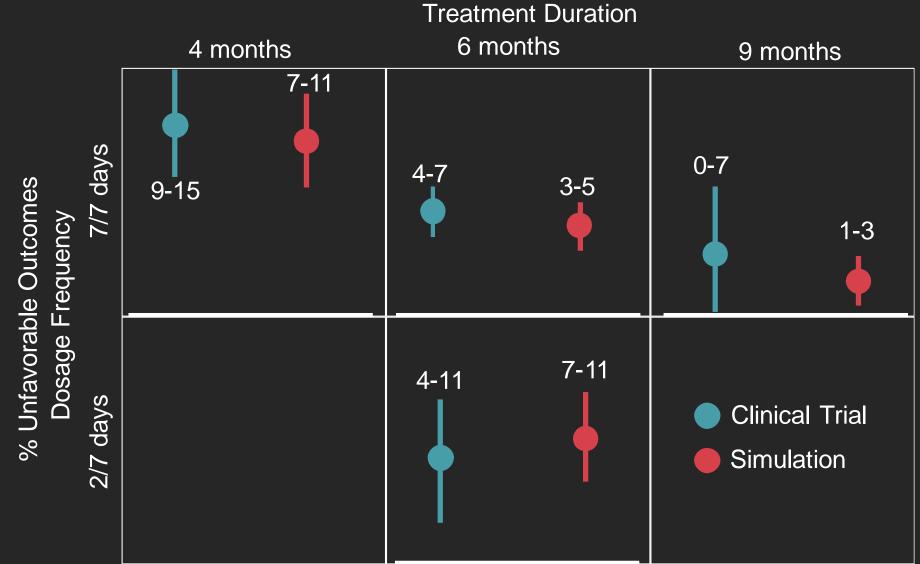


## Exploring drug therapies



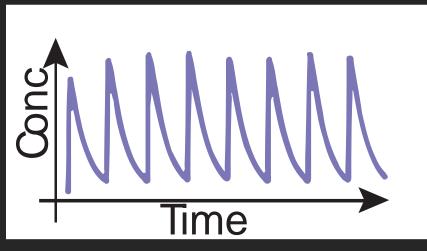


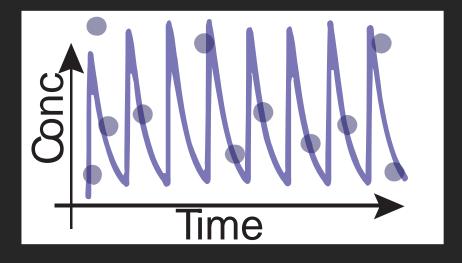
### Simulated Data vs Clinical Trials

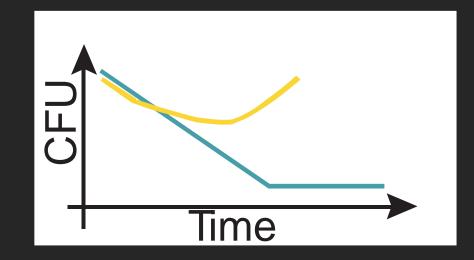


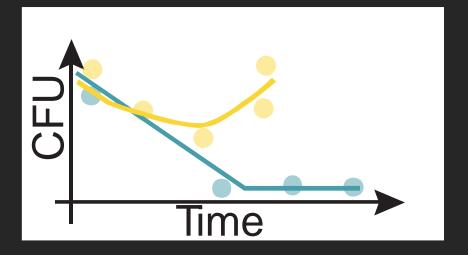


### Simulation -> Estimation

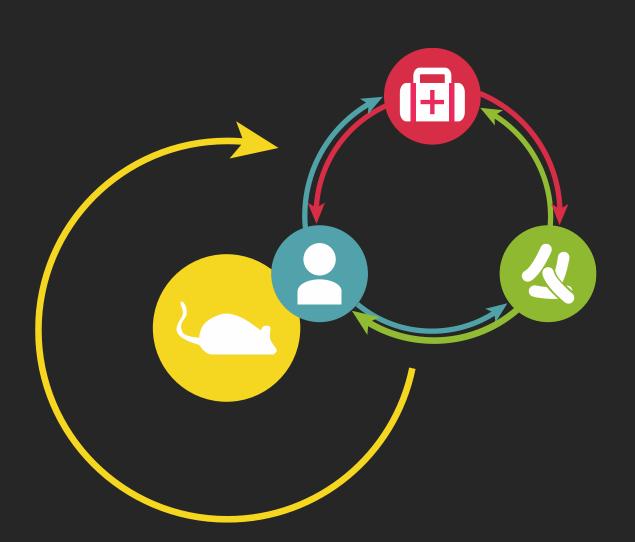








## **Preclinical Translation**

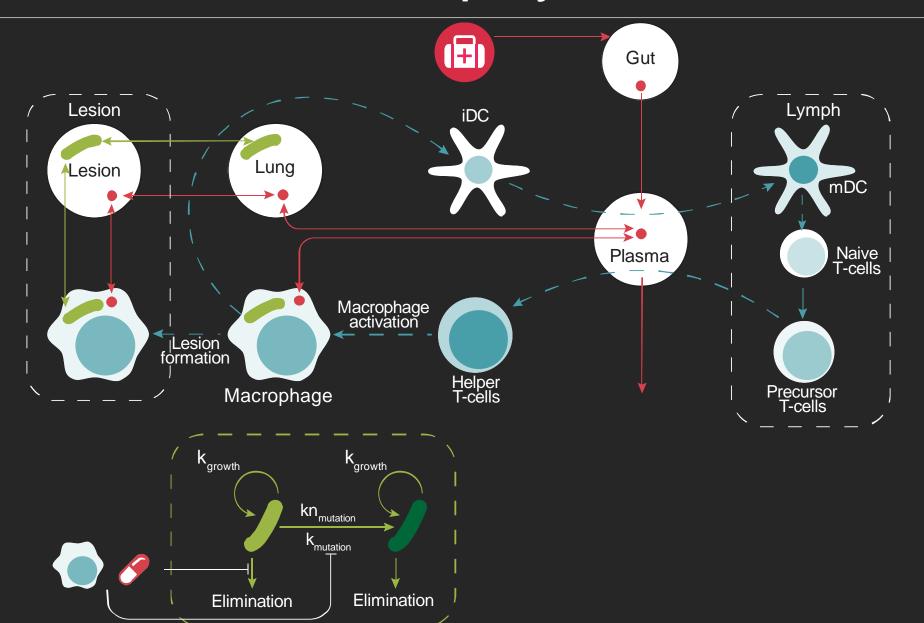


## Scaling Limitations



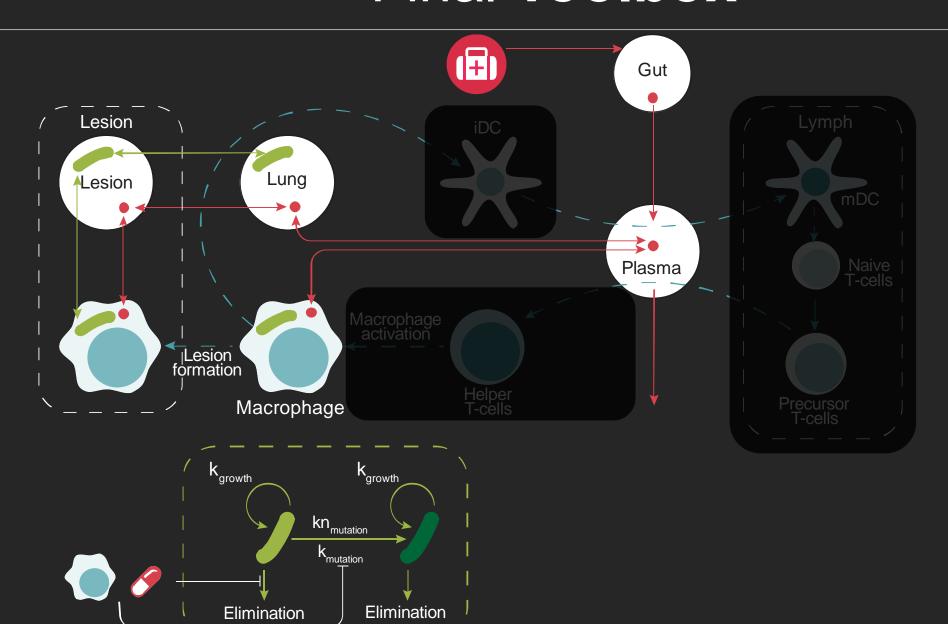


## Simplify





## Final Toolbox

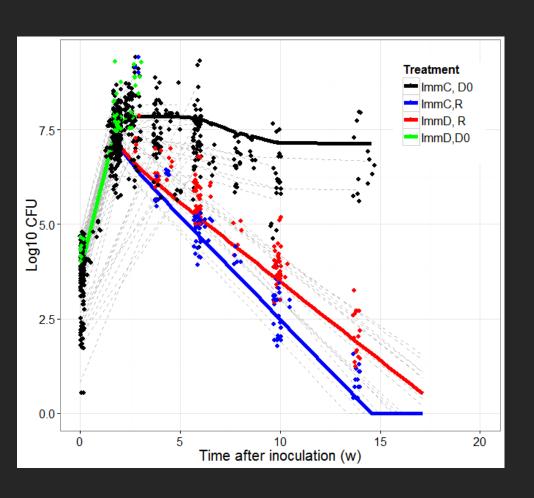


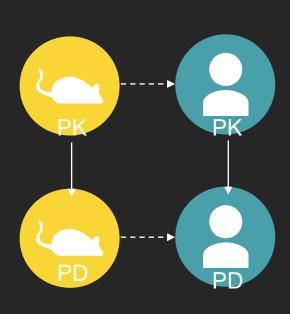


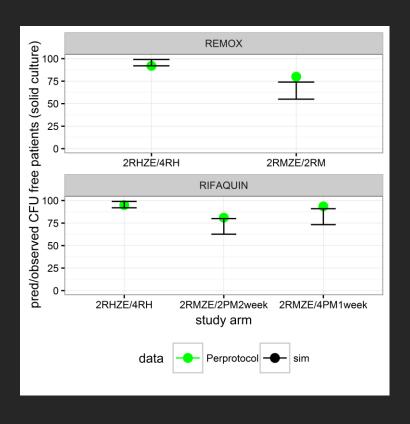
## Translating mouse data Input

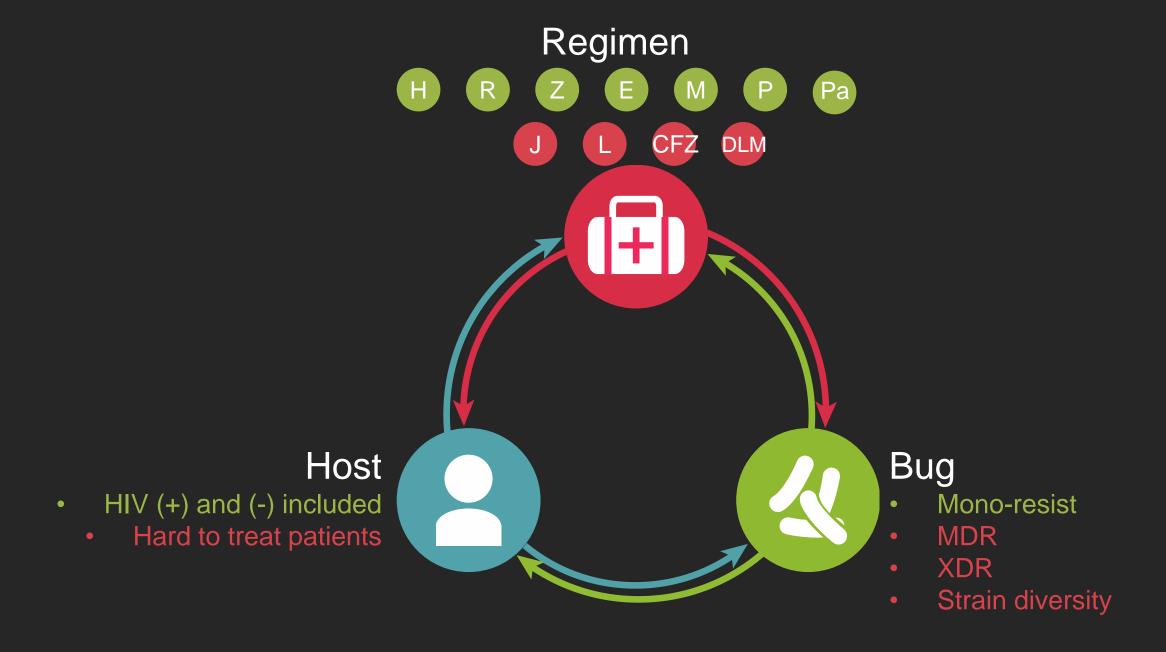


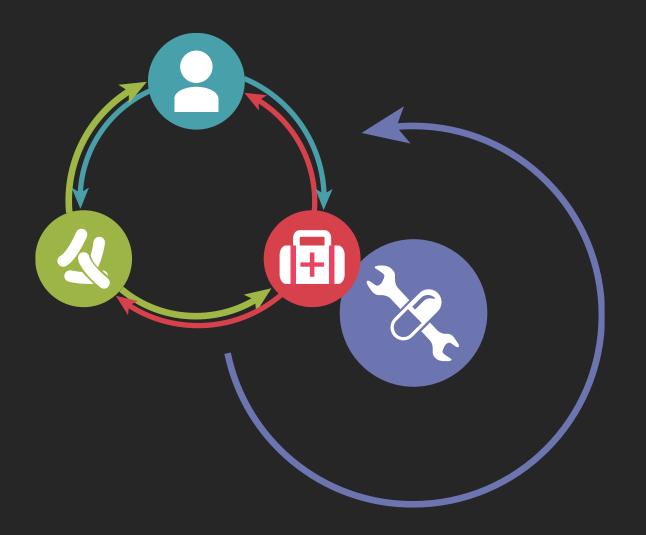


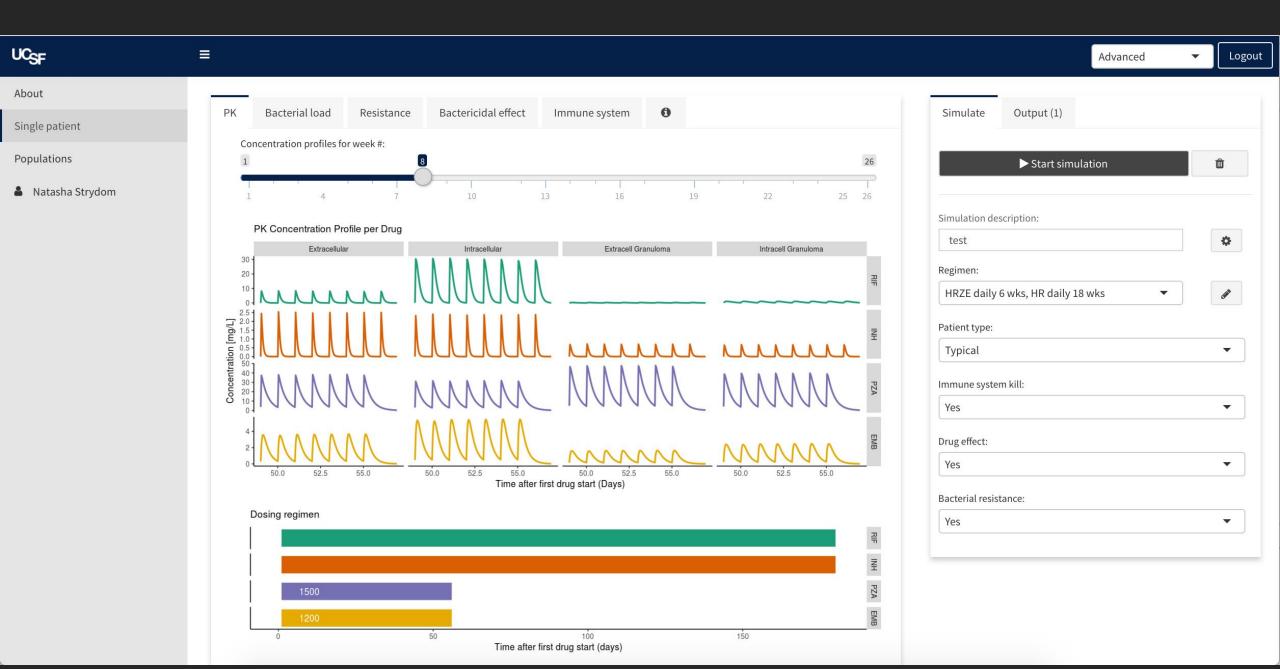


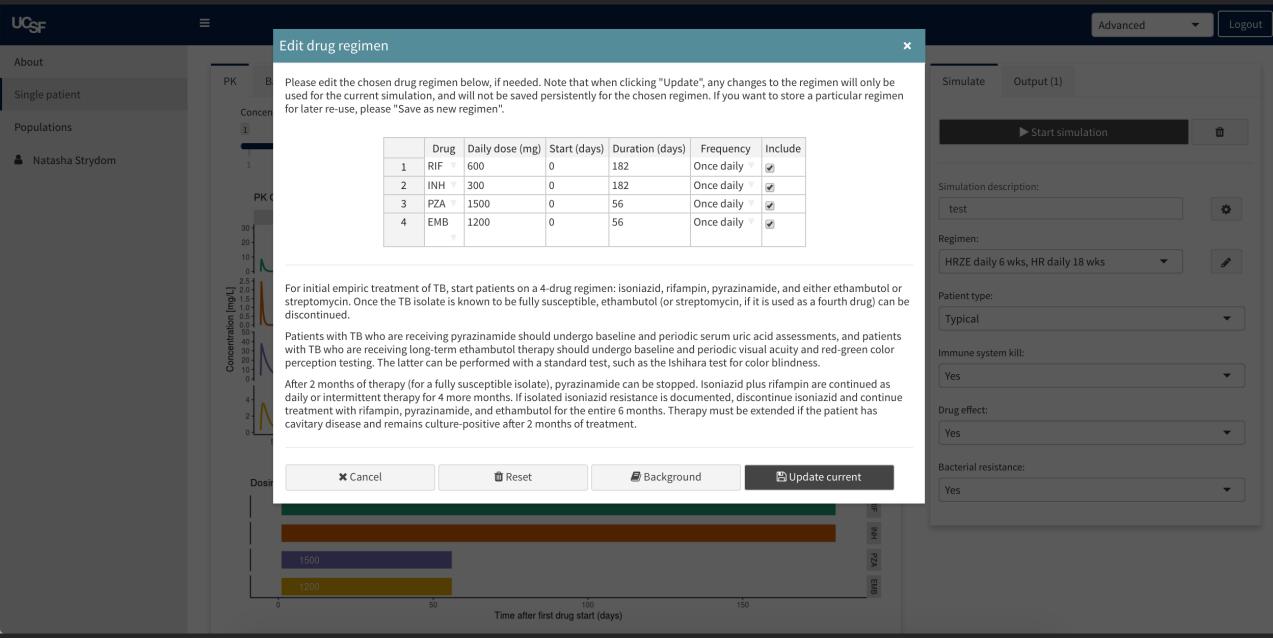












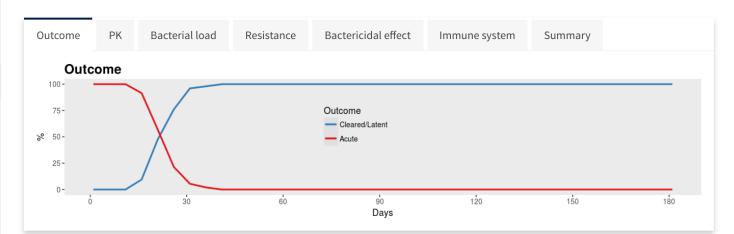


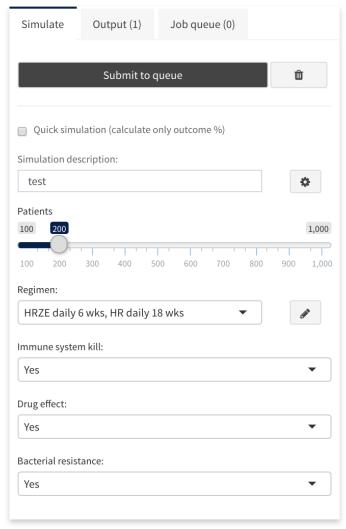
About

Single patient

Populations

Natasha Strydom





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