

# **nlmixr<sup>2</sup>: data specifications and exploration**

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On behalf of the nlmixr<sup>2</sup> development team:

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# Current nlmixr<sup>2</sup> team is composed of many companies collaborating for a common goal



Matthew Fidler, PhD



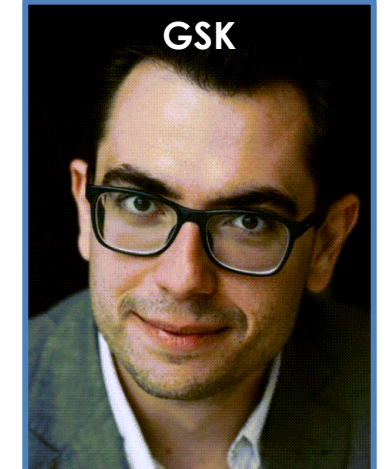
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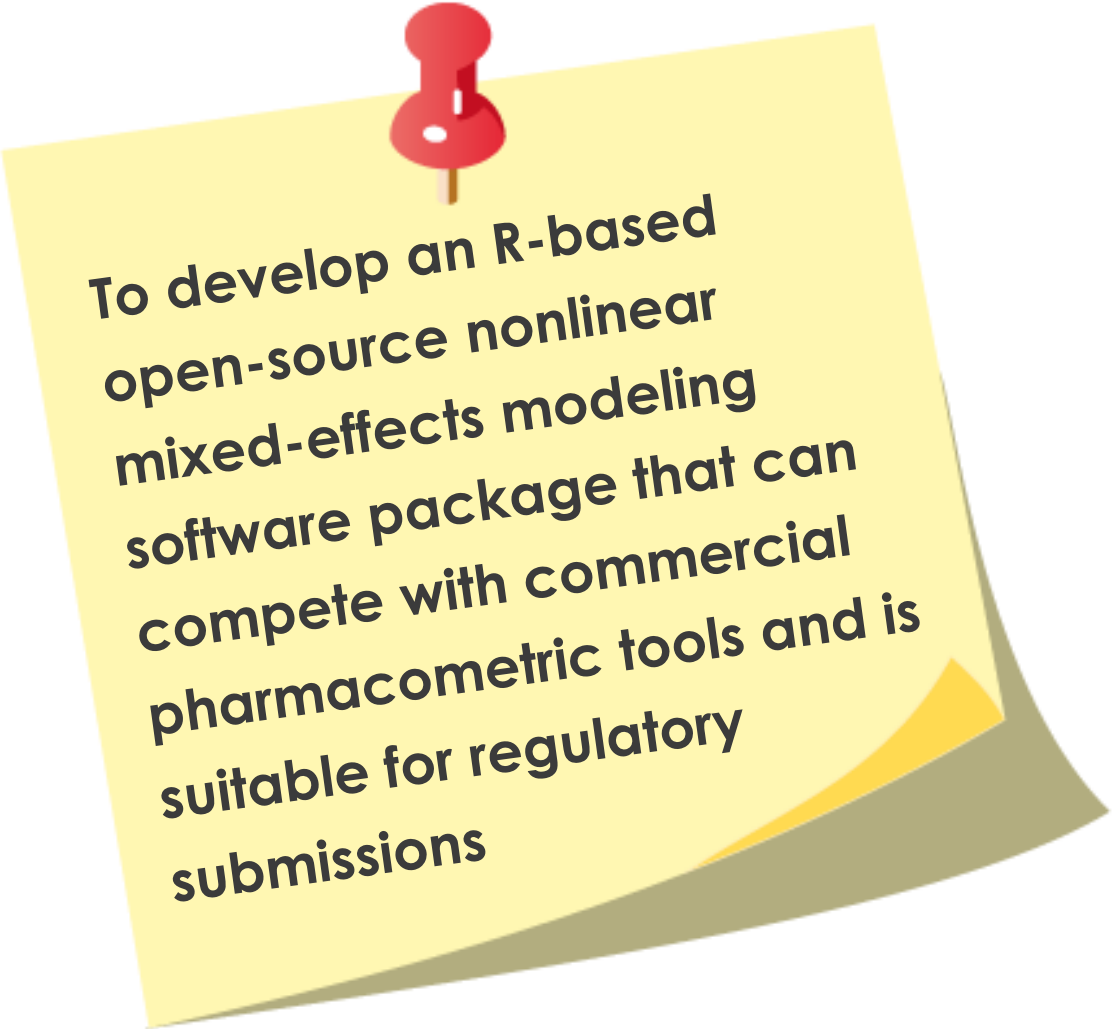


Justin Wilkins, PhD



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# Vision of **nlmixr<sup>2</sup>**



To develop an R-based  
open-source nonlinear  
mixed-effects modeling  
software package that can  
compete with commercial  
pharmacometric tools and is  
suitable for regulatory  
submissions

# **nlmixr<sup>2</sup> or rxode<sup>2</sup> model data define both the observations and dosing events; the basics are described below**

## **Observations**

### **TIME**

Independent Variable (sometimes called **x**), often TIME since pharmacometrics models describe drug concentrations and effects over time

### **DV**

Dependent Variable (sometimes called **y**), which often describes the observed drug response or concentration

### **CMT**

Compartment/Effect Location. The parsed nlmixr2 model describes this for a specific model

### **EVID**

The event id, in this case EVID=0 for observations

### **DVID**

Dependent Variable ID. The parsed nlmixr2 model describes this for a specific model

## **Dosing Events**

### **AMT**

Amount of Drug or Amount of Event at the time.

### **CMT**

ODE compartment name or number where dosing occurs

### **EVID**

Nlmixr2 event type (0: Observation, 1: Dose, 2: Other, 3: Reset, 4: Reset+Dose, 5: Replace; 6: Multiply; 7: Phantom/Transit compartment)

### **RATE or DUR**

Rate (RATE) or Duration (DUR) of an infusion

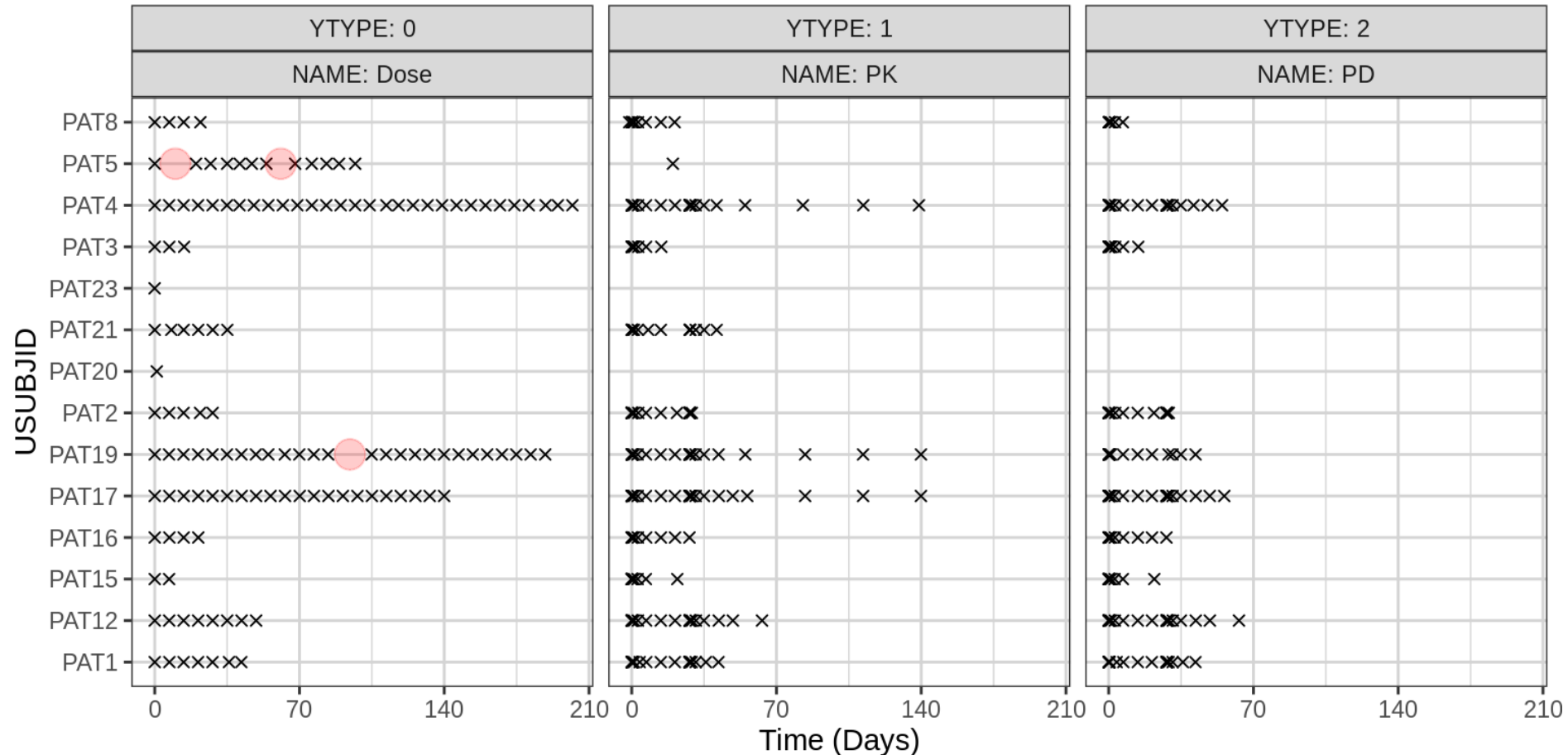
## **Subject Identifier (ID) text/numeric**

# First step in any analysis is to make sure your data are correct (from xgx)

Some common checks are:

- Patient Information
  - Number of Patients per Treatment Arm? More or less than expected?
  - Number of Observations/Doses per Treatment Arm? More or less than expected?
- Dosing:
  - Patients that received a dose of 0?
  - Patients that never received a dose?
- Observations:
  - Duplicate, or missing times or observations?
  - Summary statistics of observations per time point?
- Demographics
  - Summary of key demographic covariates (Number in category or mean/sd/range median)

# This includes graphical exploration of subject dosing/observation history (and perhaps missing values too)



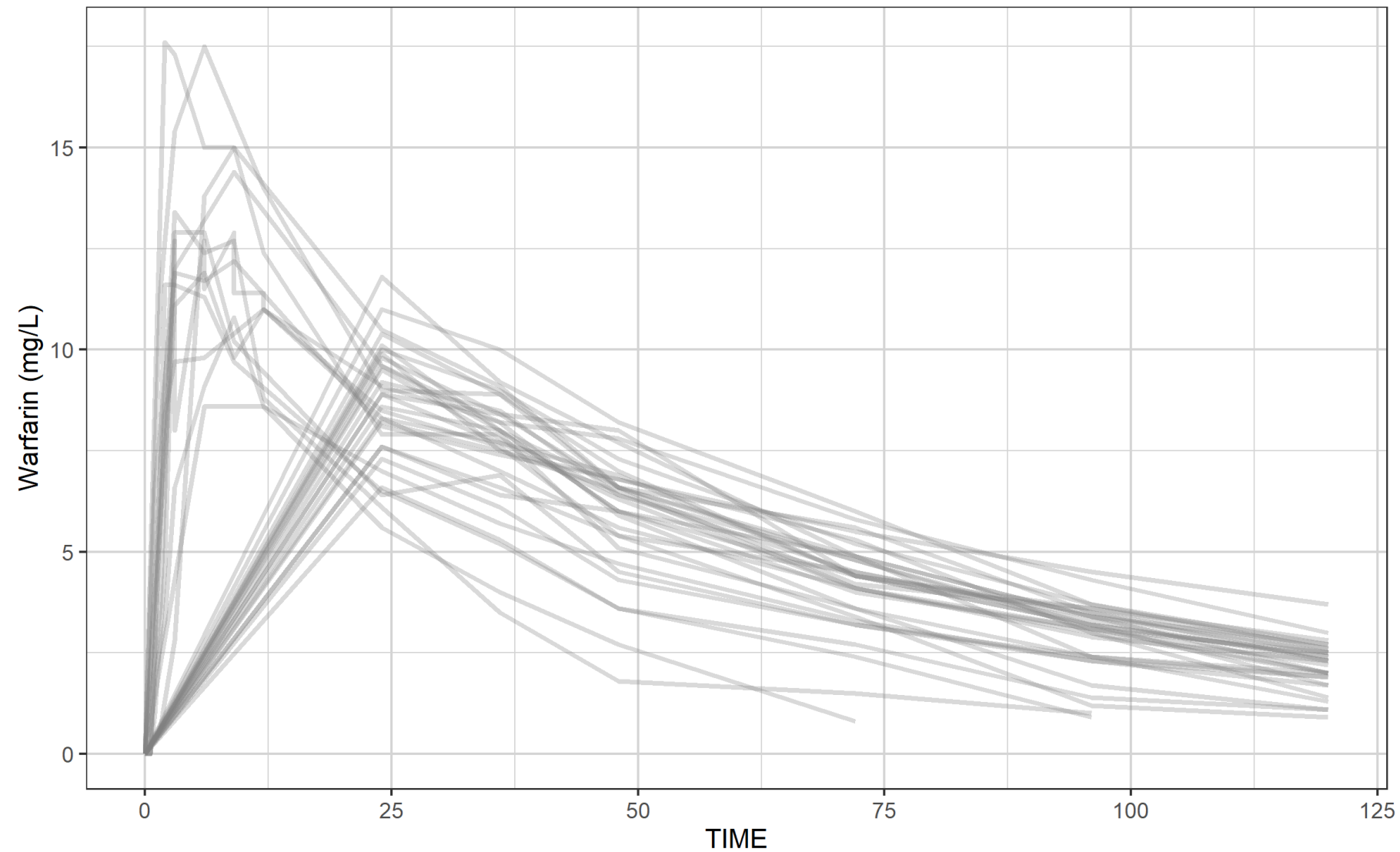
Code available at [http://opensource.nibr.com/xgx/Data\\_Checking.html](http://opensource.nibr.com/xgx/Data_Checking.html)

## Assess the data before you start analysis (from PopSim Course)

- Classic data sets used by Nick Holford in his courses:
  - O'Reilly RA, Aggeler PM. Studies on coumarin anticoagulant drugs initiation of warfarin therapy without a loading dose. Circulation 1968;38:169-177
  - O'Reilly RA, Aggeler PM, Leong LS. Studies of the coumarin anticoagulant drugs: The pharmacodynamics of warfarin in man. Journal of Clinical Investigation 1963;42(10):1542-1551
- Some simple plots to get a feel of the data
- Additional xgxr functionality to improve and summarize the profiles

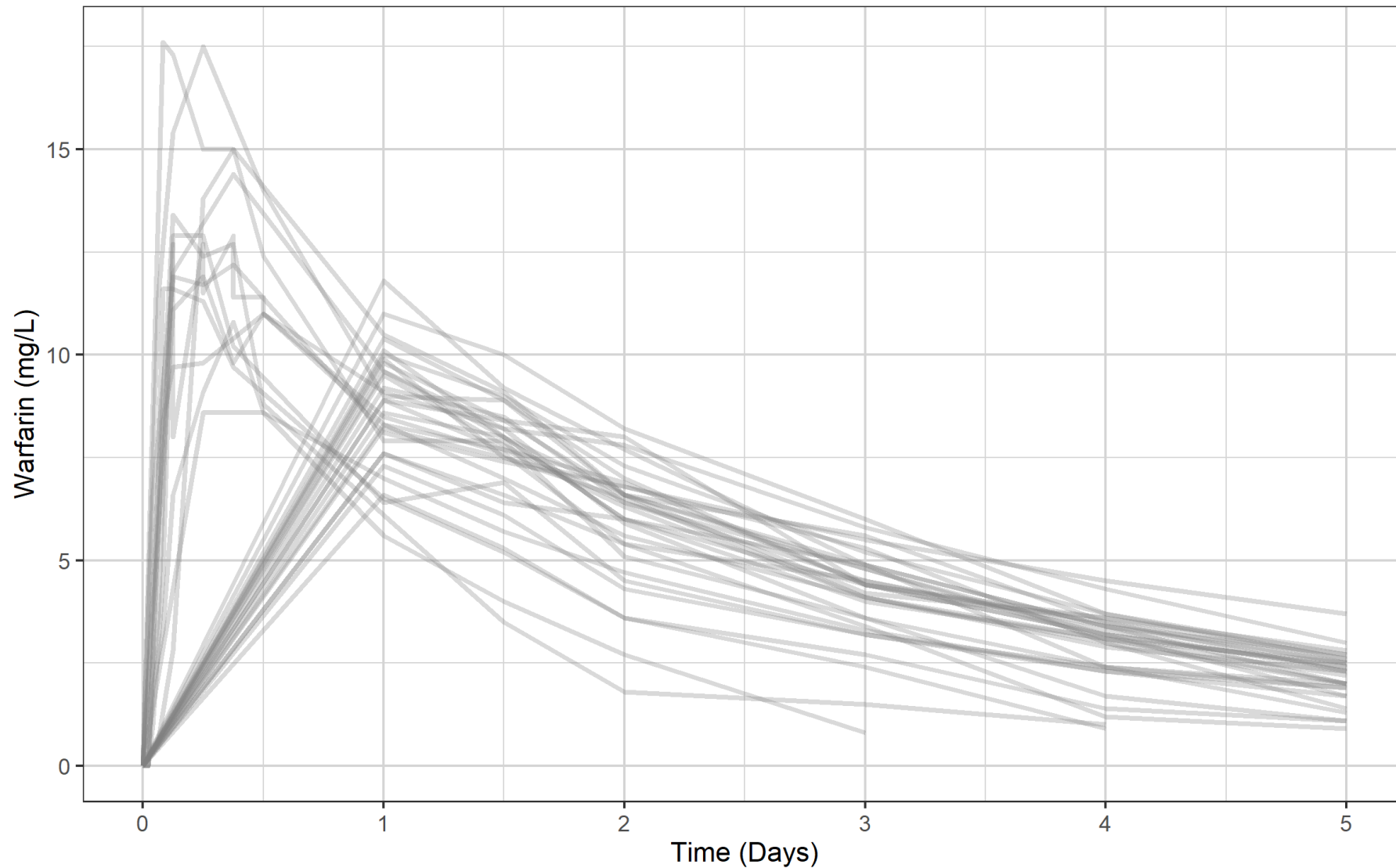


## Our warfarin data file: a simple ggplot to provide an impression

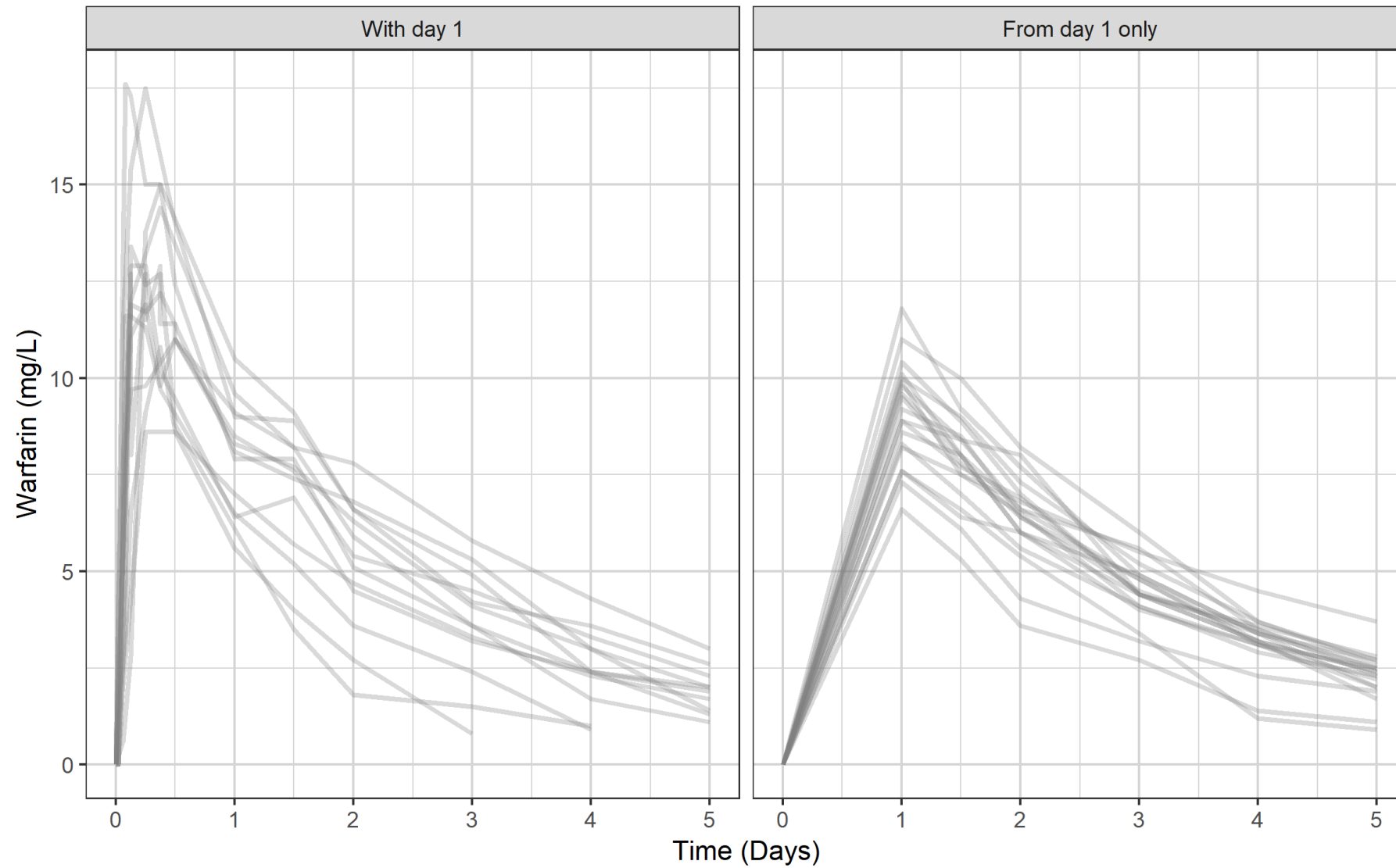




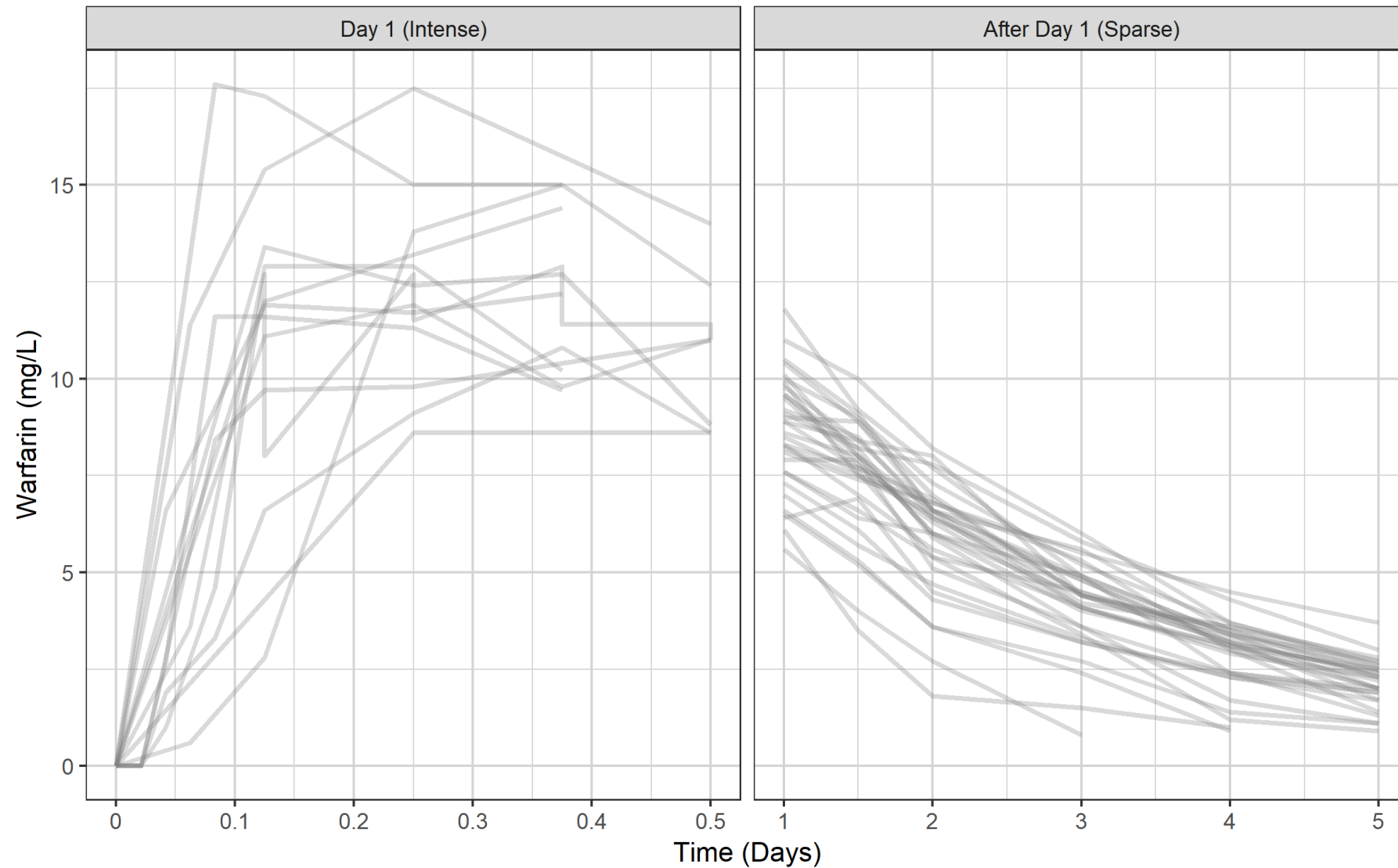
Change the x-axis from hours to days and add a proper label using the `xgx` helper `xgx_scale_x_time_units(units_dataset = "hours", units_plot = "days")`



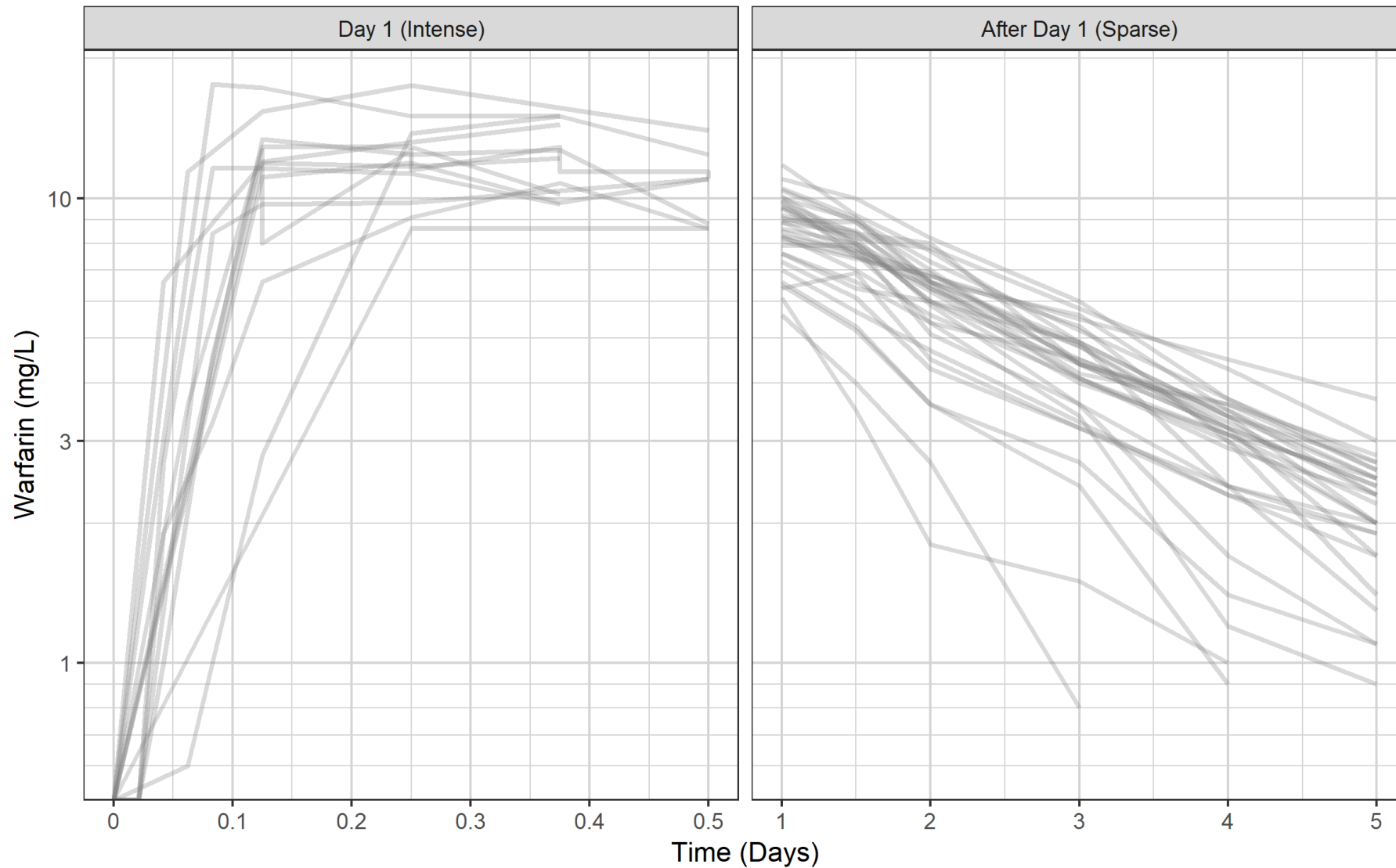
## The data set has two types of profiles...



...but you can also group by rich day 1 and sparse later days...

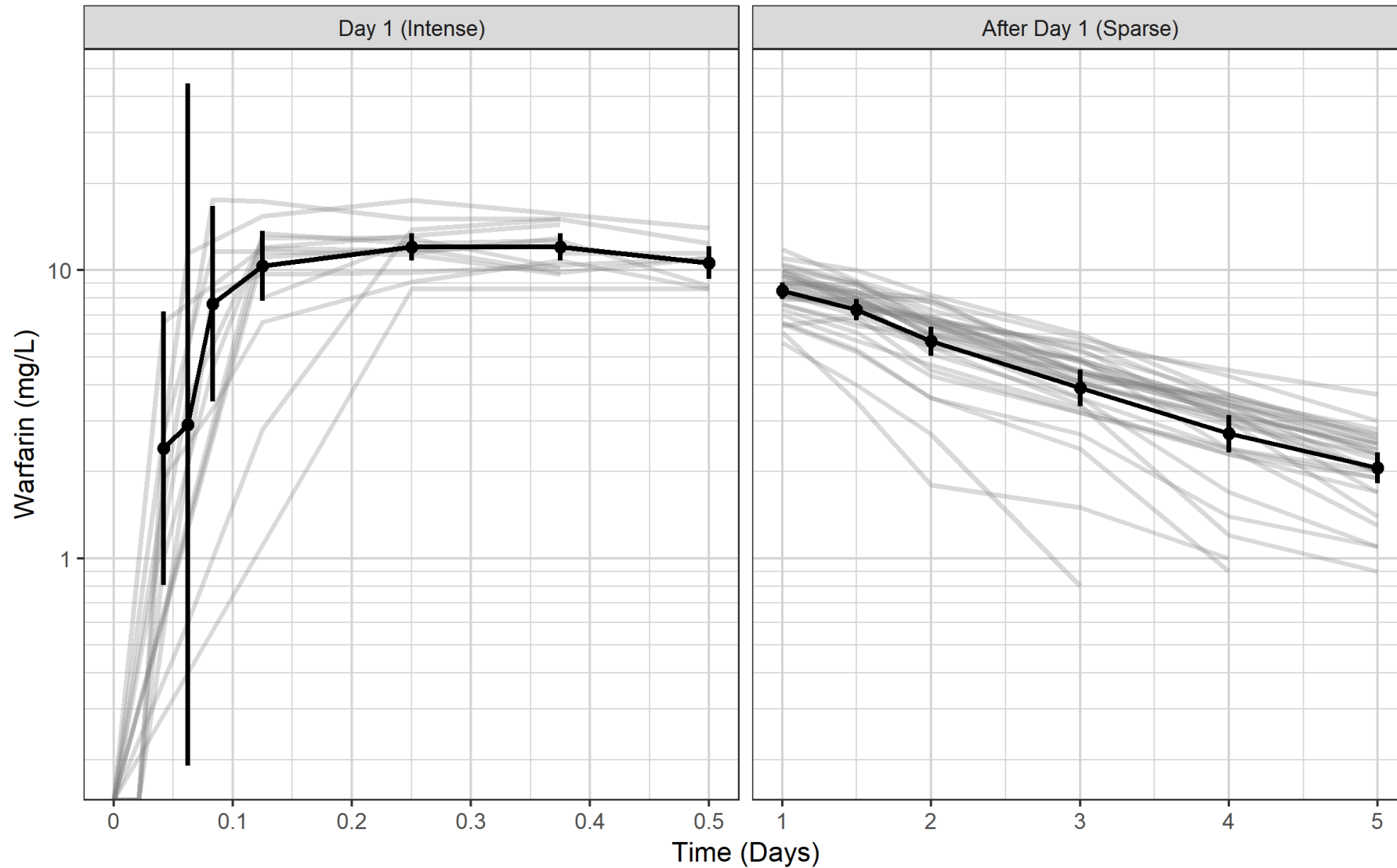


Switch to semi-log scale using xgx helper `xgx_scale_y_log10()`  
Any clues to what model we should use?

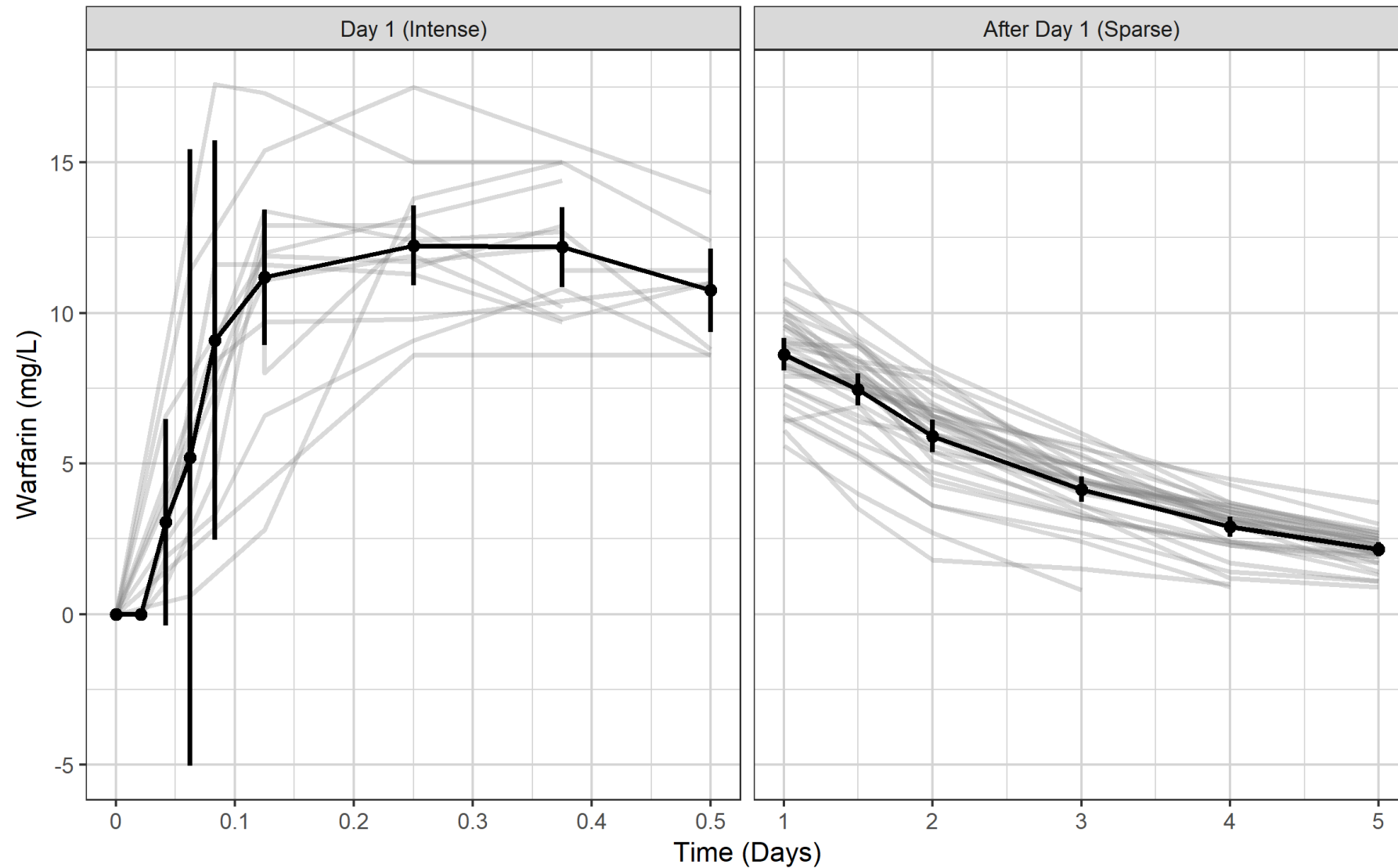


## xgx can also add nice summary information if data has nominal times: summaries of mean plus 95% CI

```
xgx_geom_ci(aes(x = TIME, color = NULL, group = NULL, shape = NULL), conf level = 0.95)
```

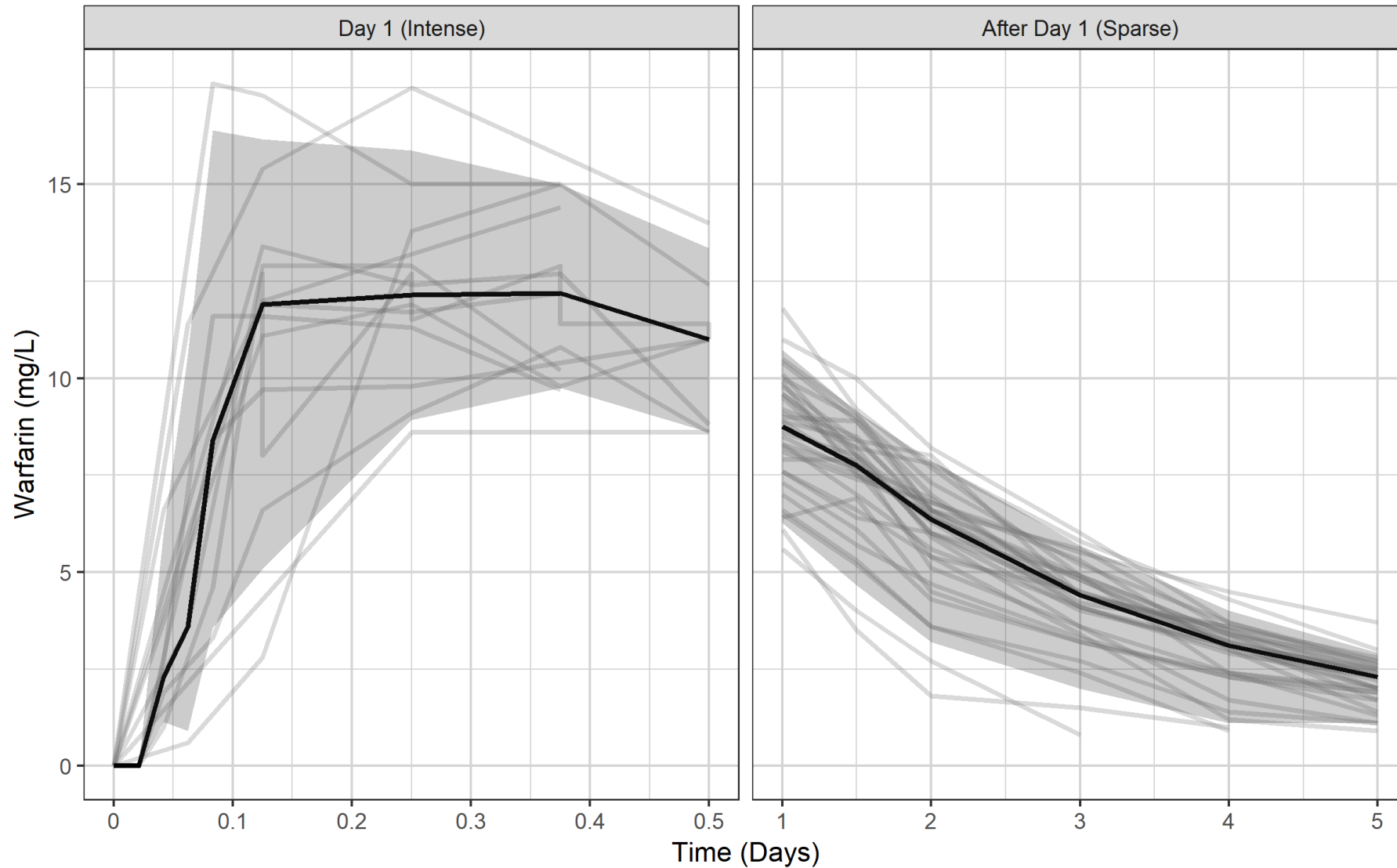


On linear scale this would result in a CI crossing zero because CIs are assumed symmetrical



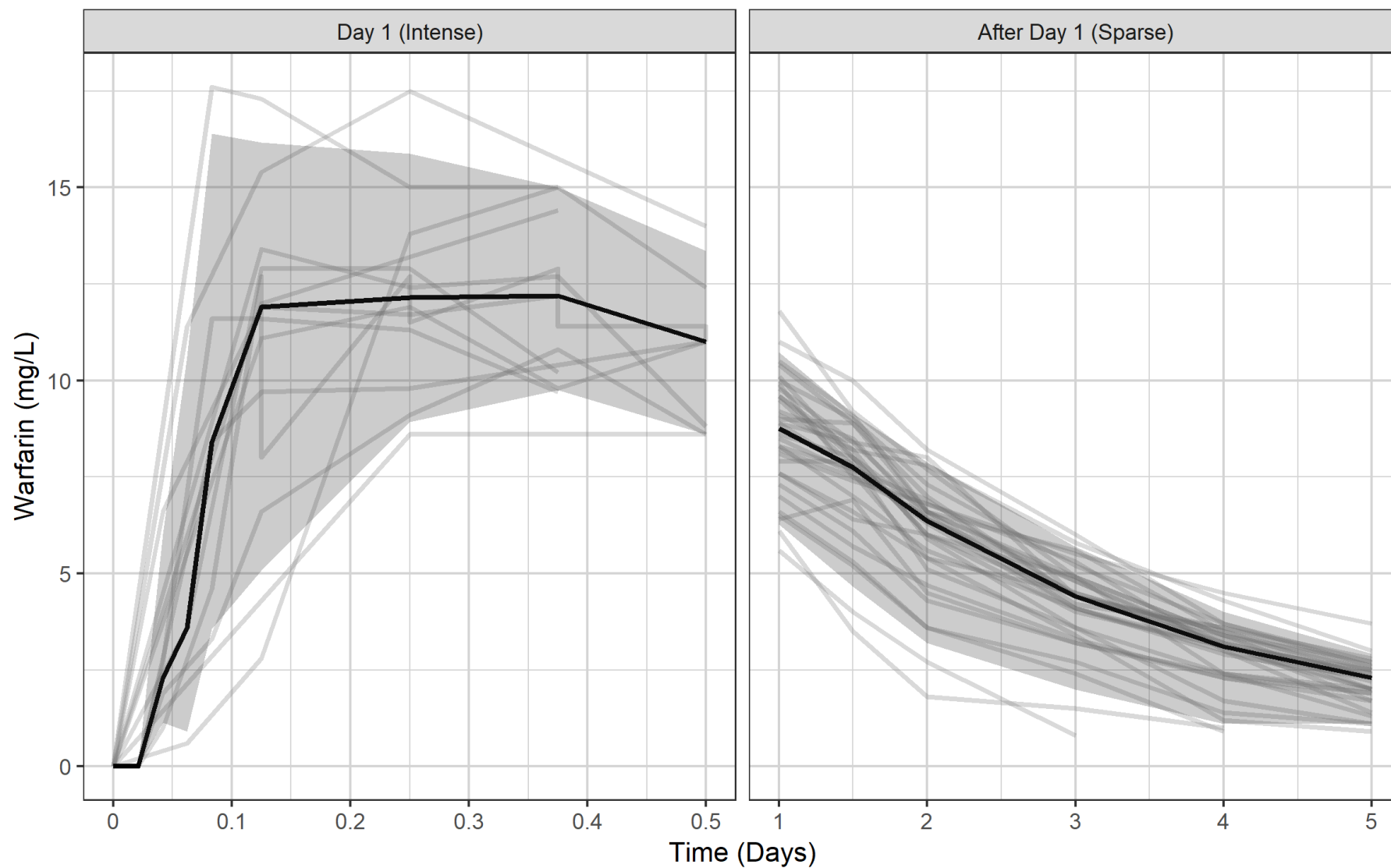
...so perhaps a median and 95% of the data would be more suitable

```
xgx_geom_pi(aes(x = TIME, color = NULL, group = NULL, shape = NULL))
```

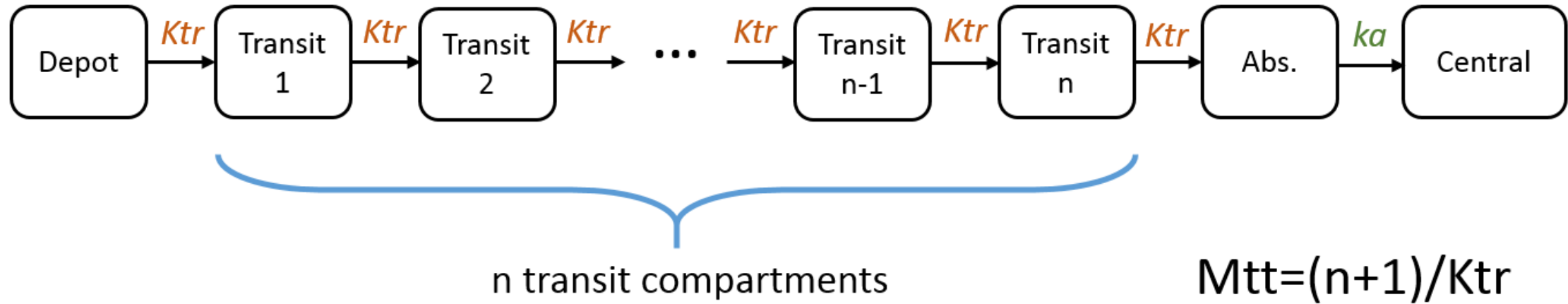




There appears to be a delay in absorption...



## One way to model delayed absorption is through ODE compartments that must be crossed first (transit compartment)



- Transit compartments take more time to enter the system because they have to go through n transit compartments before entering the blood
- Transit compartments and any arbitrary ODE can be fit with nlmixr2
- (Image from <https://mlxtran.lixoft.com/examples/transit-compartments-weibull-absorption/>)