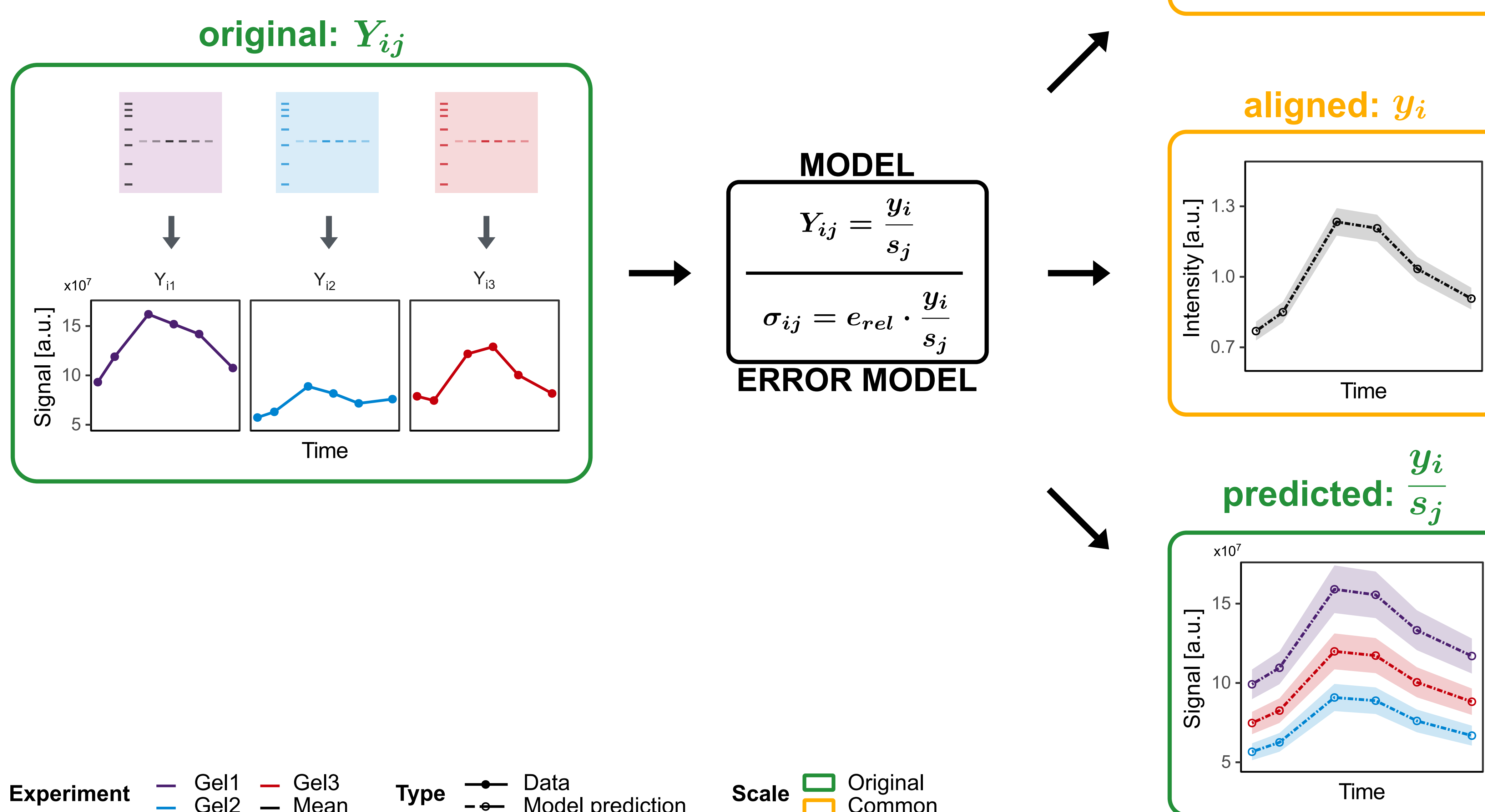


WITH blotIt YOU CAN DETERMINE A COMMON SCALE FOR BIOANALYTICAL REPLICATE DATA

Severin Bang^{1,2}, Svenja Kemmer^{1,2}, Marcus Rosenblatt^{1,2}, Jens Timmer^{1,2,3}, Daniel Kaschek^{1,2,4}

Idea

- Extend the amount of comparable measurements
- Calculate mean values with higher precision
- Disentangle treatment effect and experimental scaling



Problem

- Measurements of different experiments are **not comparable**
- Analysis of time series with many measurements is **impossible**
- Treatment effect can be **obscured** by experiment-dependent scaling
- Existing scaling methods rely on **overall reference** treatments

Solution

- Determine a **common scale** by fitting a **scaling model** to the full data set
- **Determine errors** by a simultaneously fitted **error model**
- **Pairwise overlap** between experiments is sufficient
- Model and error model can be **freely chosen**

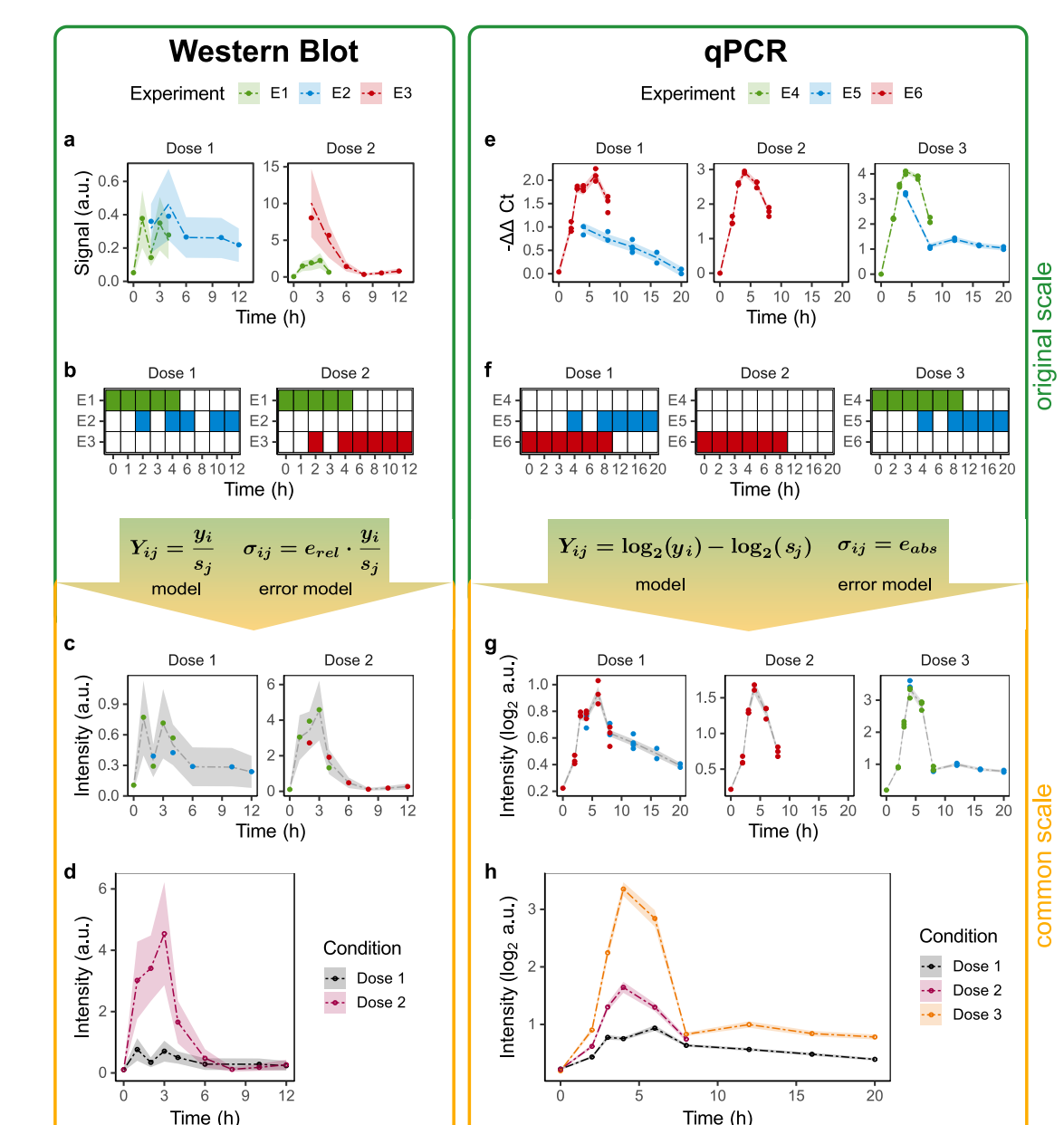
Implementation

- Method implemented as R package **blotIt** available on GitHub
- **Scaled:** original data scaled to a common scale
- **Aligned:** estimated true values, quantifying the mean values
- **Predicted:** model evaluation for estimated parameters

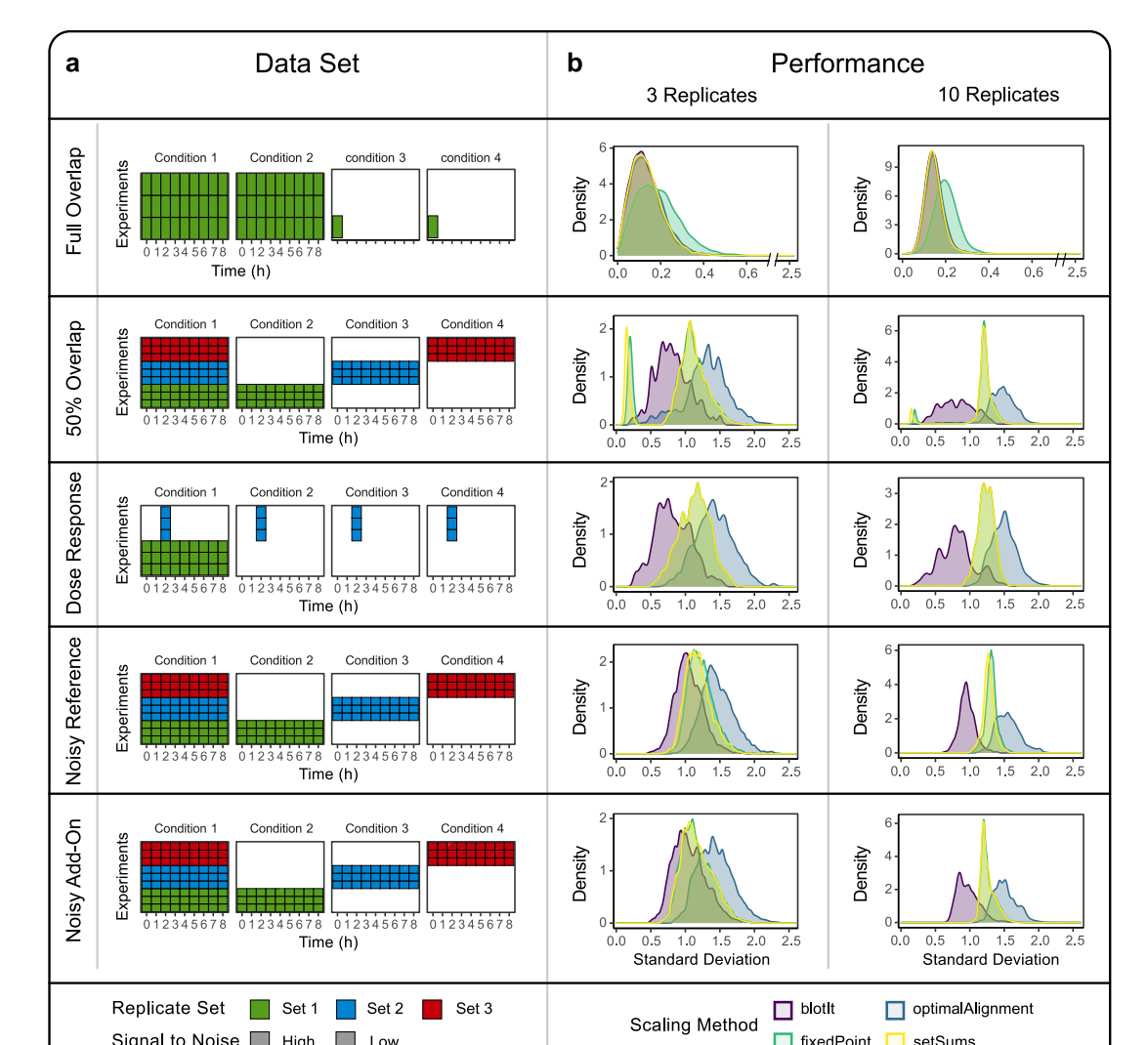
Details

- Scaling is **data driven**
- Parameters estimated by **maximum likelihood estimation**:

$$-2 \log L(\theta) = \sum_{ij} \left(\frac{f(y, s) - Y_{ij}}{h(y, s, e)} \right)^2 + \sum_{ij} \log(h(y, s, e)^2) + \log(\pi) + \left(\frac{1 - \bar{y}}{10^{-3}} \right)^2$$
- Custom **models and error models**
- Input on **linear and log scale** possible
- Applicable to **all relative data**
- Pairwise linking is enough:



- **Aligned** data composed from **maximum likelihood estimates** of true values
- Error of aligned set from **Fisher information** quantifying the **goodness of fit**
- Scaling of data is **more robust** than in other methods, especially for **low overlap between experiments**:



More questions?

severin.bang@physik.uni-freiburg.de

www.jeti.uni-freiburg.de

Preprint: 10.1101/2022.02.09.479689

in Severin Bang

JetiLab/blotIt



¹Institute of Physics, University of Freiburg, Freiburg, Germany

²FDM - Freiburg Center for Data Analysis and Modeling, University of Freiburg, Freiburg, Germany

³Signalling Research Centers BIOS and CIBSS, University of Freiburg, Freiburg, Germany

⁴IntiQuan GmbH, Basel, Switzerland

