

# Supplementary Information for Exploring Carbon Source related Localization and Phosphorylation in the Snf1/Mig1 Network using Population- and Single Cell-based Approaches

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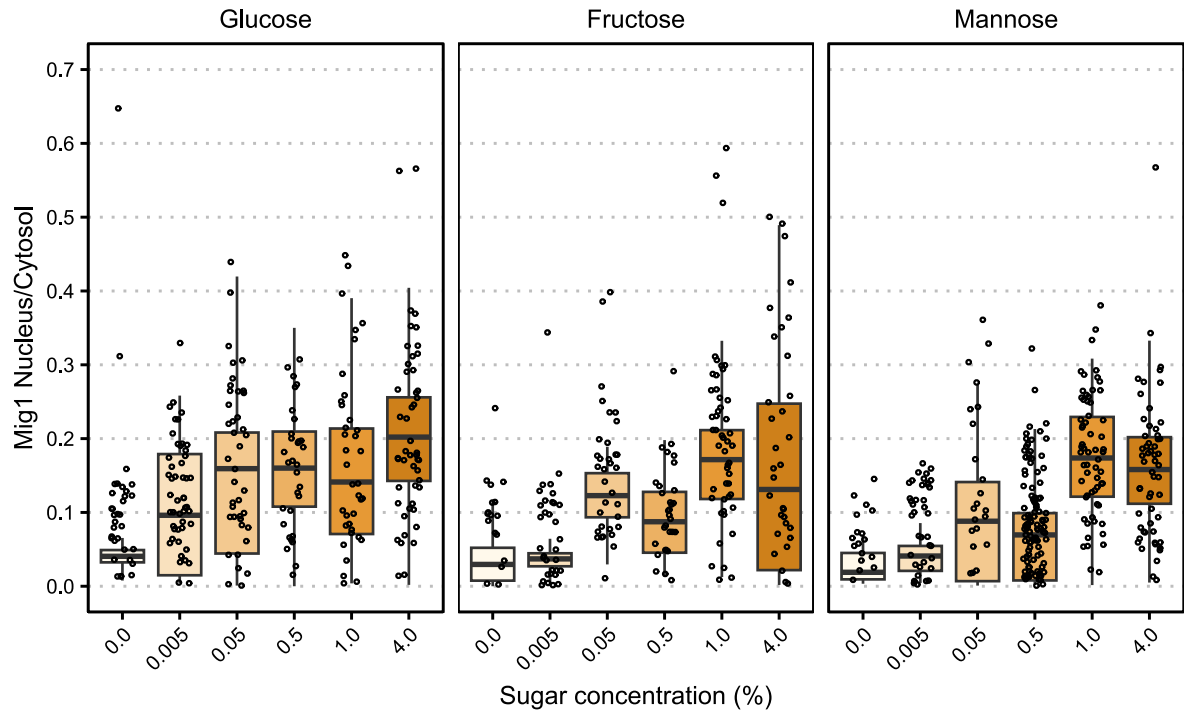
University of Milano-Bicocca

Piazza della Scienza 2, 20126 Milano

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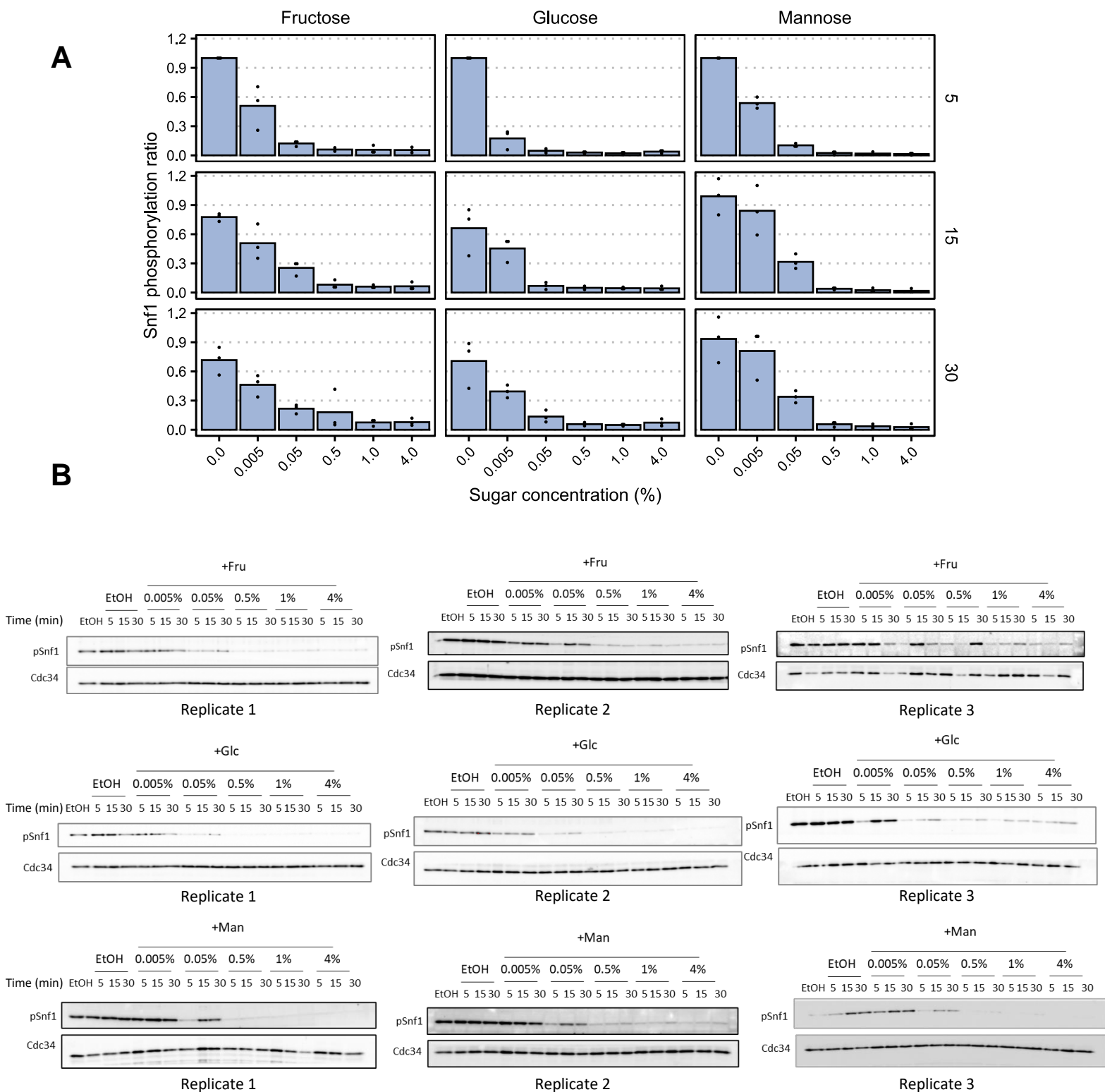
[farida.tripodi1@unimib.it](mailto:farida.tripodi1@unimib.it)

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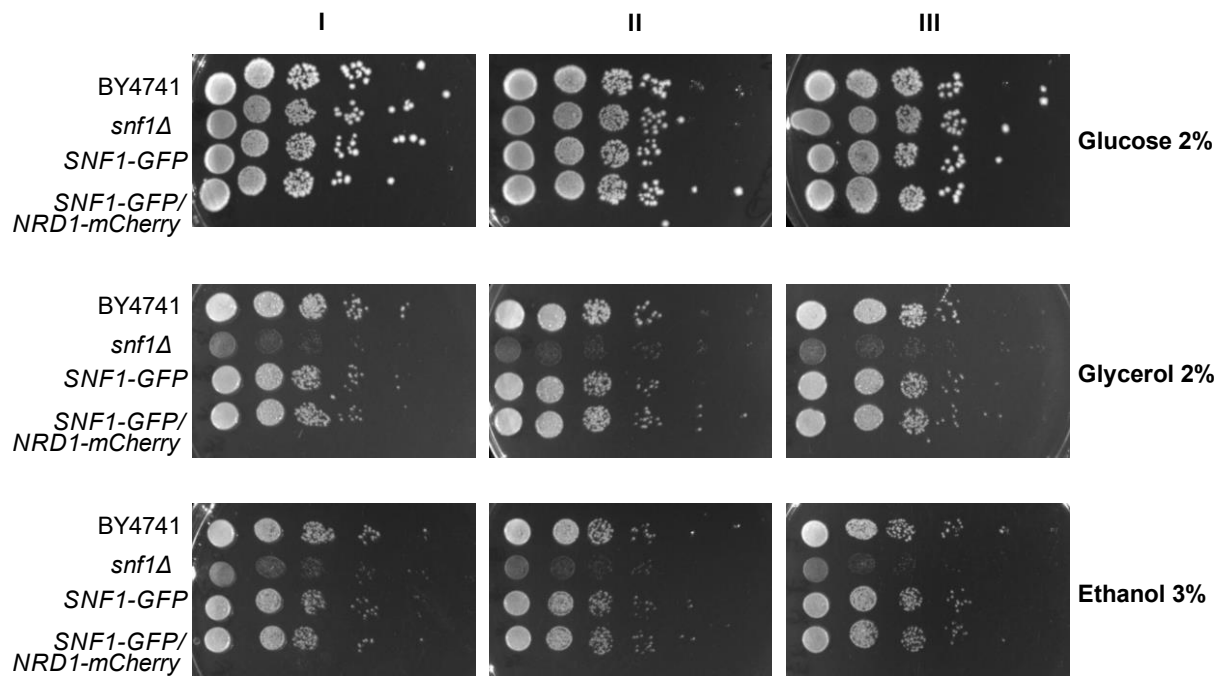
**Figure S1, Supplementary data:**

Mig1 nuclear localization ratio in cells 15 minutes after the shift from ethanol to the indicated concentration of glucose, fructose or mannose. Horizontal black lines indicate the median.



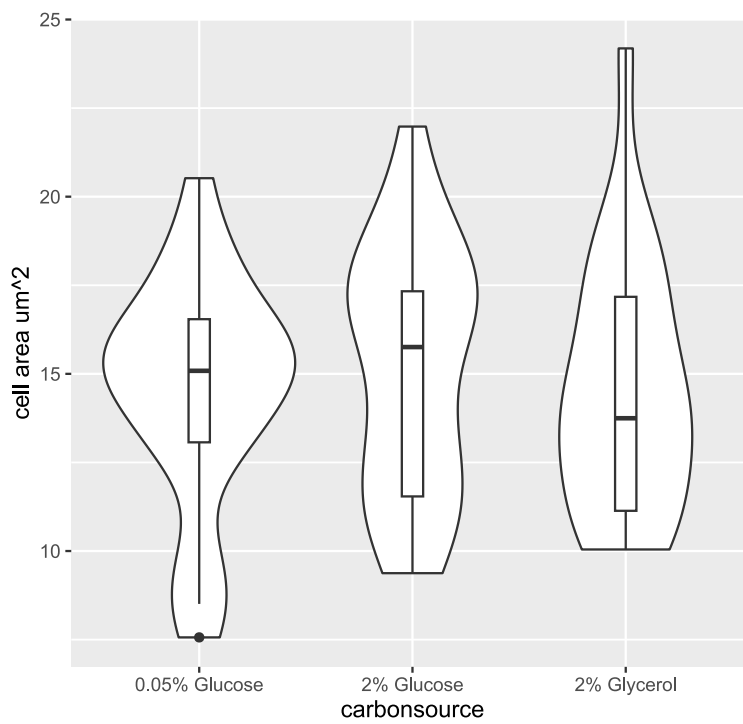
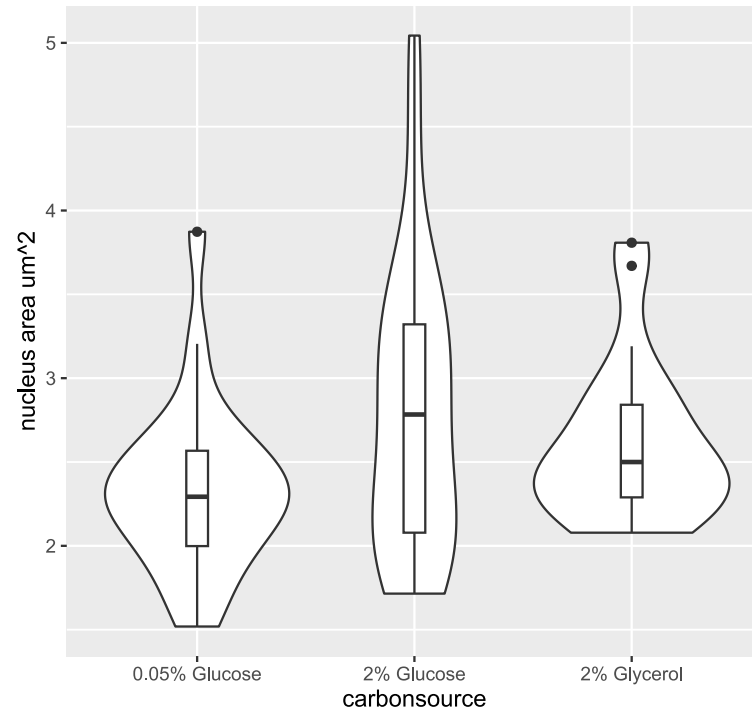
**Figure S2, Supplementary data:**

A) Mean of relative Snf1 phosphorylation by western blot quantification 5, 15 and 30 minutes after upshift from ethanol to glucose, fructose or mannose, dots represent biological replicates. B) Western blot images of all replicates tested for Snf1 phosphorylation quantification. Fru = fructose, Glc = glucose, Man = mannose Exemplary images also found in Figure 2C .



**Figure S3, Supplementary data:**

Three individual colonies of the indicated strains of the BY4741 background were grown over night in YPD supplemented with 2% glucose. The medium was removed, cells were washed once and diluted to an OD/ml of 0.1 in sterile water. Drops of 5  $\mu$ l of OD/ml 0.1 and ten fold dilutions up to  $10^{-5}$  were spotted onto YPD agar plates with respective carbon source and grown at 30°C for three days before imaging.



**Figure S4, Supplementary data:**

Measurements of cell- and nucleus area of cells subjected to FRAP.

Violin plots show the distribution as well as boxplot for the measured data. Horizontal lines indicate the mean, the boxplot has as lower and upper hinge respectively the 25<sup>th</sup> and 75<sup>th</sup> percentile and the whiskers denote the 95% confidence interval. Black dots denote outliers.

## S2: Monolix report: 0.05% glucose

Run: 240213\_glu005\_corr.mlxtran

Dataset: 240213\_FRAP\_complete\_norm\_one\_nominus\_glu005\_corr.csv

Date: 02-13-2024

### Tables

Table 1: Estimated population parameters

Parameter	Value	STOCH. APPROX.	
		S.E.	R.S.E.(%)
Fixed Effects			
I0_pop	0.152	0.0054	3.554
A1_pop	0.168	0.0103	6.136
tau_pop	0.0638	0.00839	13.146
Standard Deviation of the Random Effects			
	Value	C.V.(%)	
omega_I0	0.16	16.151	0.026 16.208
omega_A1	0.279	28.486	0.0466 16.68
omega_tau	0.566	61.425	0.1 17.684
Error Model Parameters			
b	0.135	0.00207	1.529

Table 2: Log-likelihood and Information criteria

CRITERIA	IMPORTANCE SAMPLING
-2 x log-likelihood (OFV)	-8675.2
Akaike Information Criteria (AIC)	-8661.2
Bayesian Information Criteria (BIC)	-8653
Corrected Bayesian Information Criteria (BICc)	-8634.8

### Plots

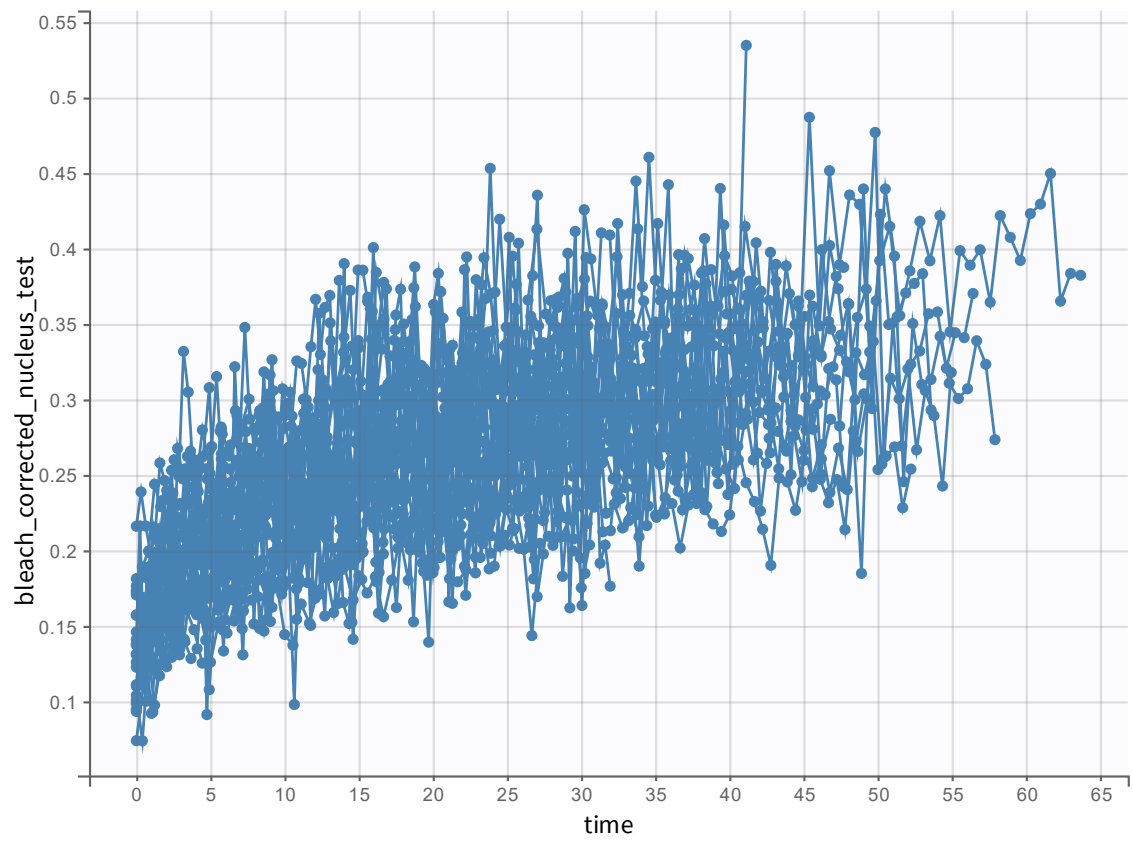


Figure 1: Observed data

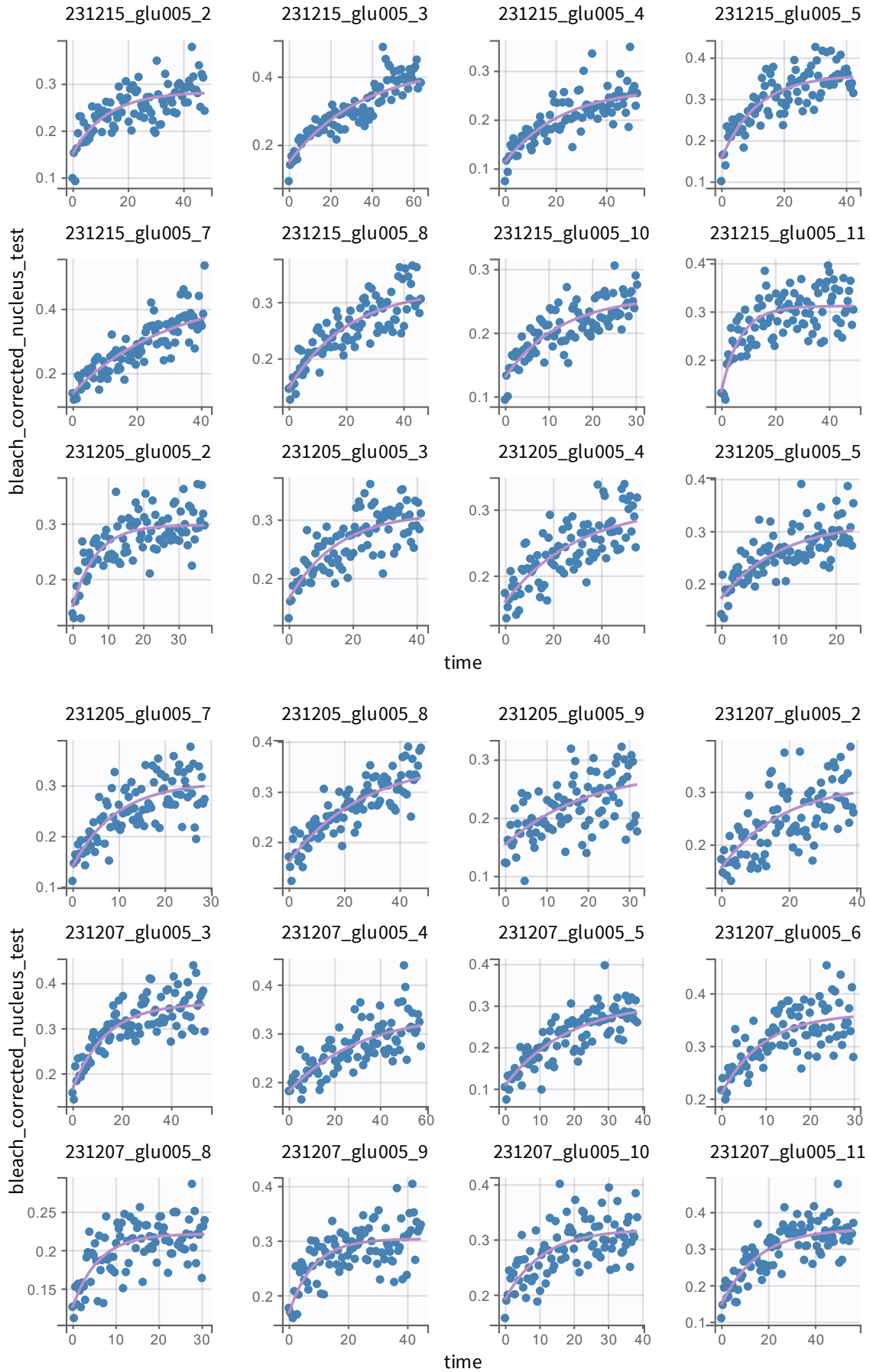




Figure 2: Individual fits

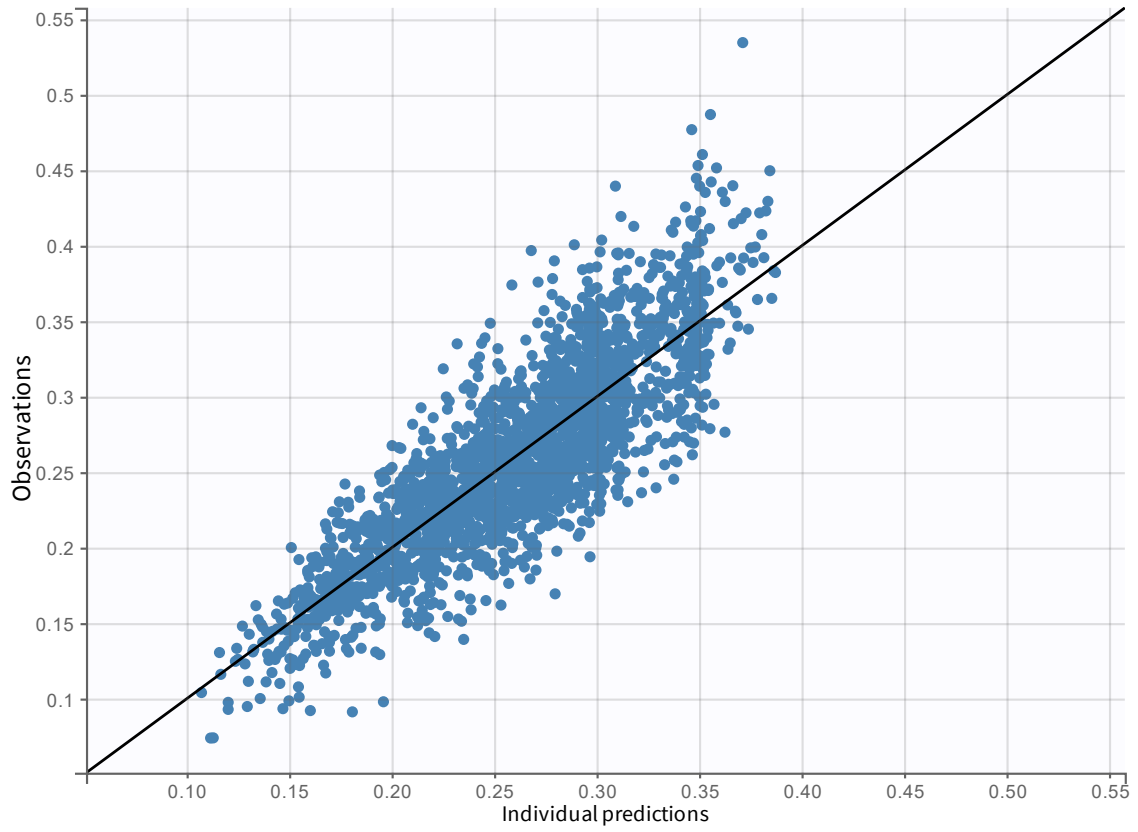


Figure 3: Observations vs predictions

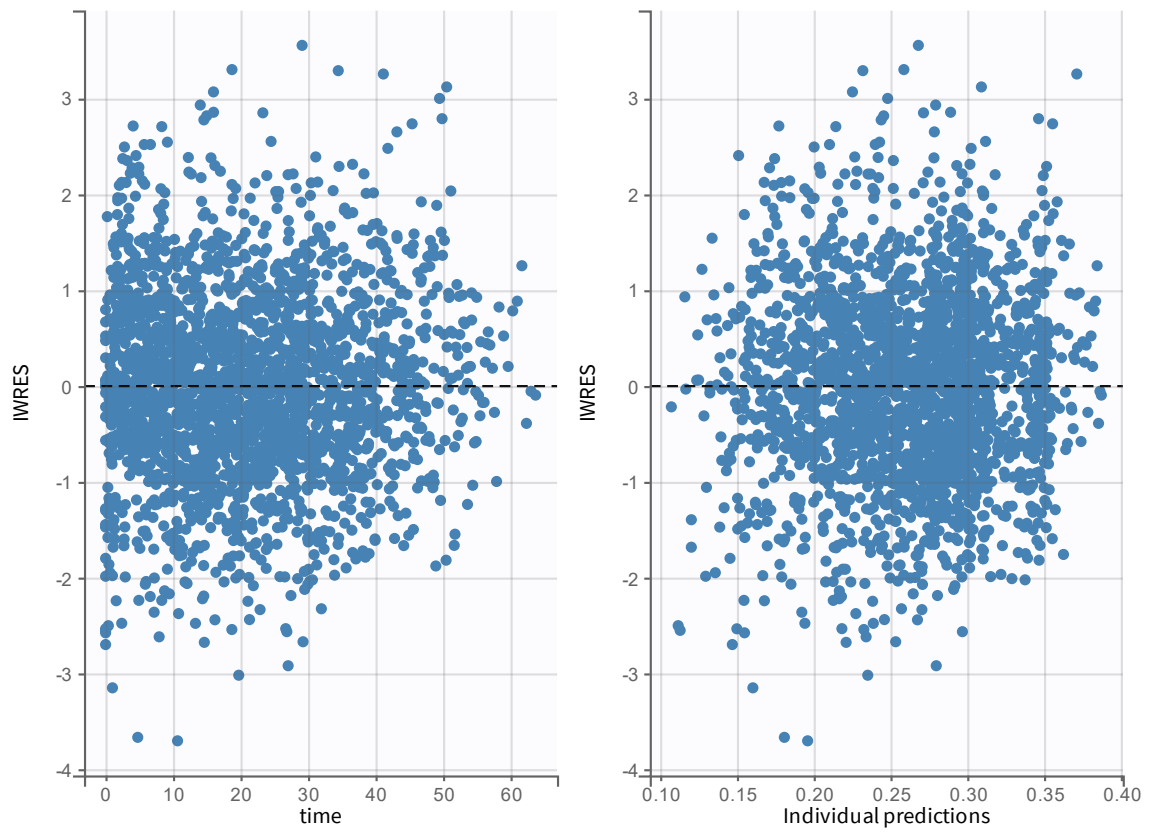


Figure 4: Scatter plot of the residuals

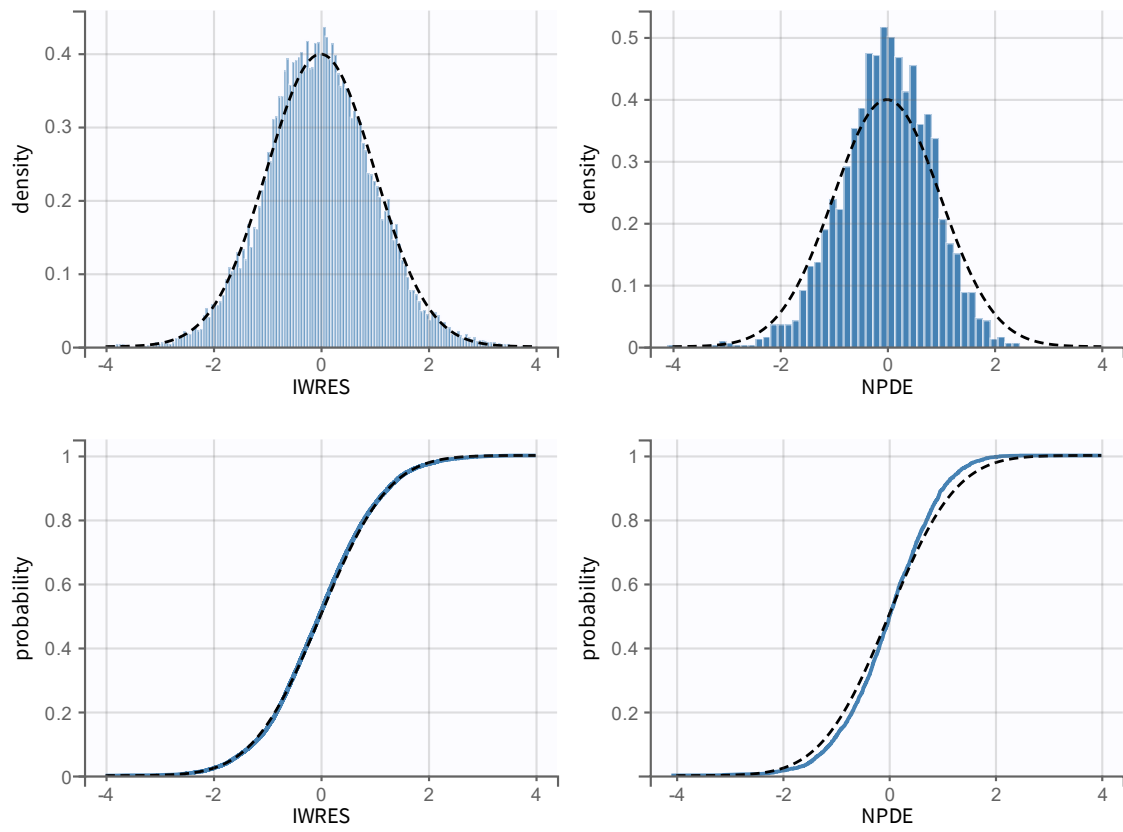


Figure 5: Distribution of the residuals

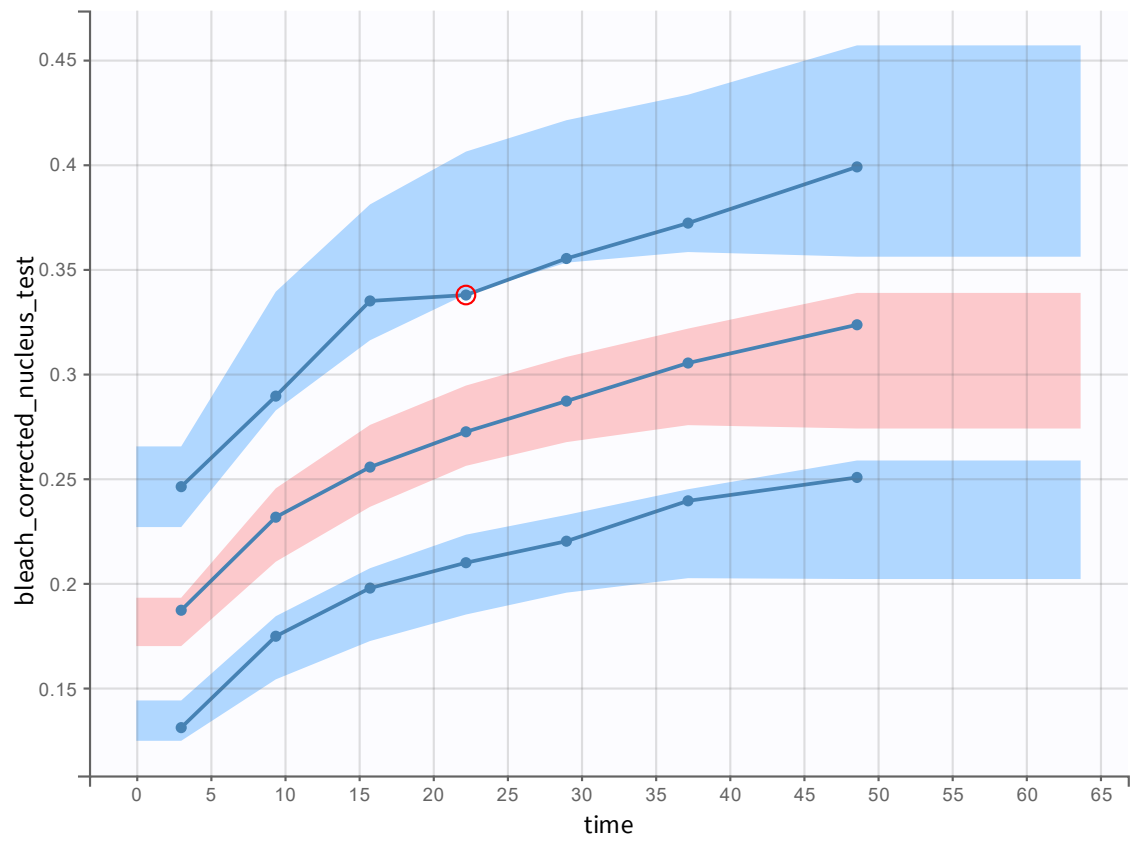


Figure 6: Visual predictive check

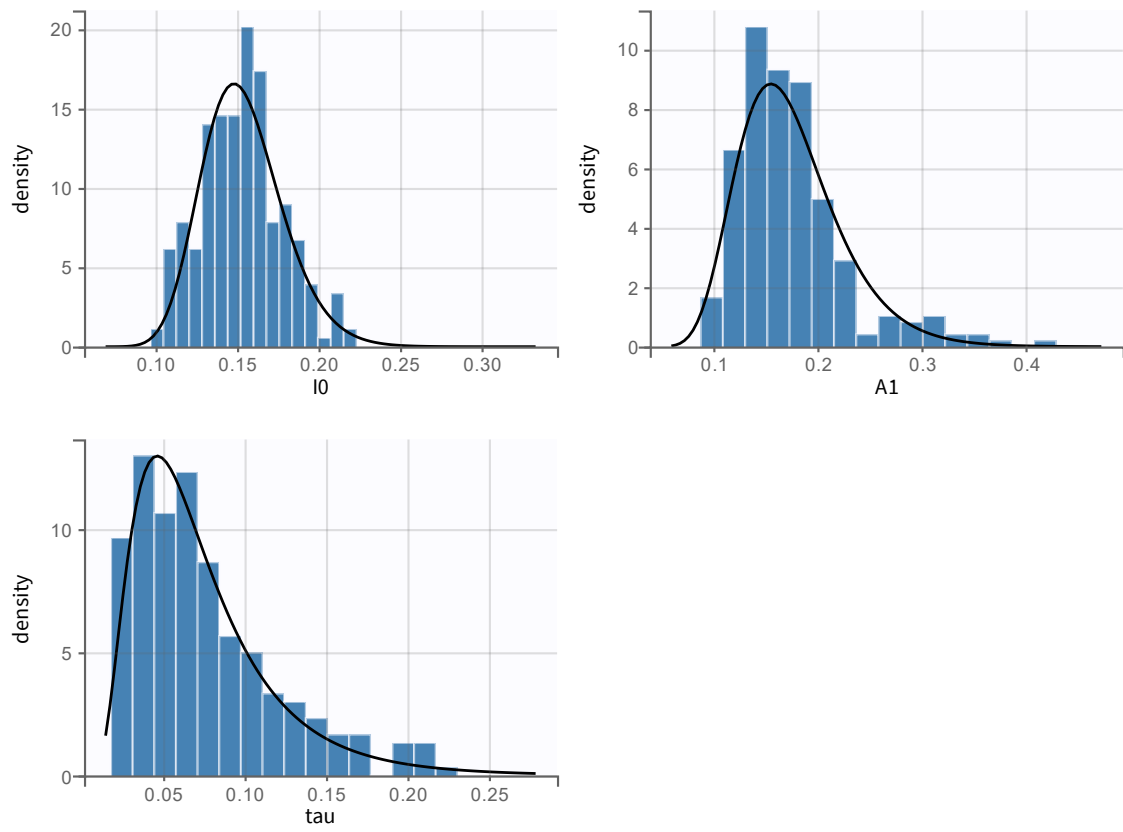


Figure 7: Distribution of the individual parameters

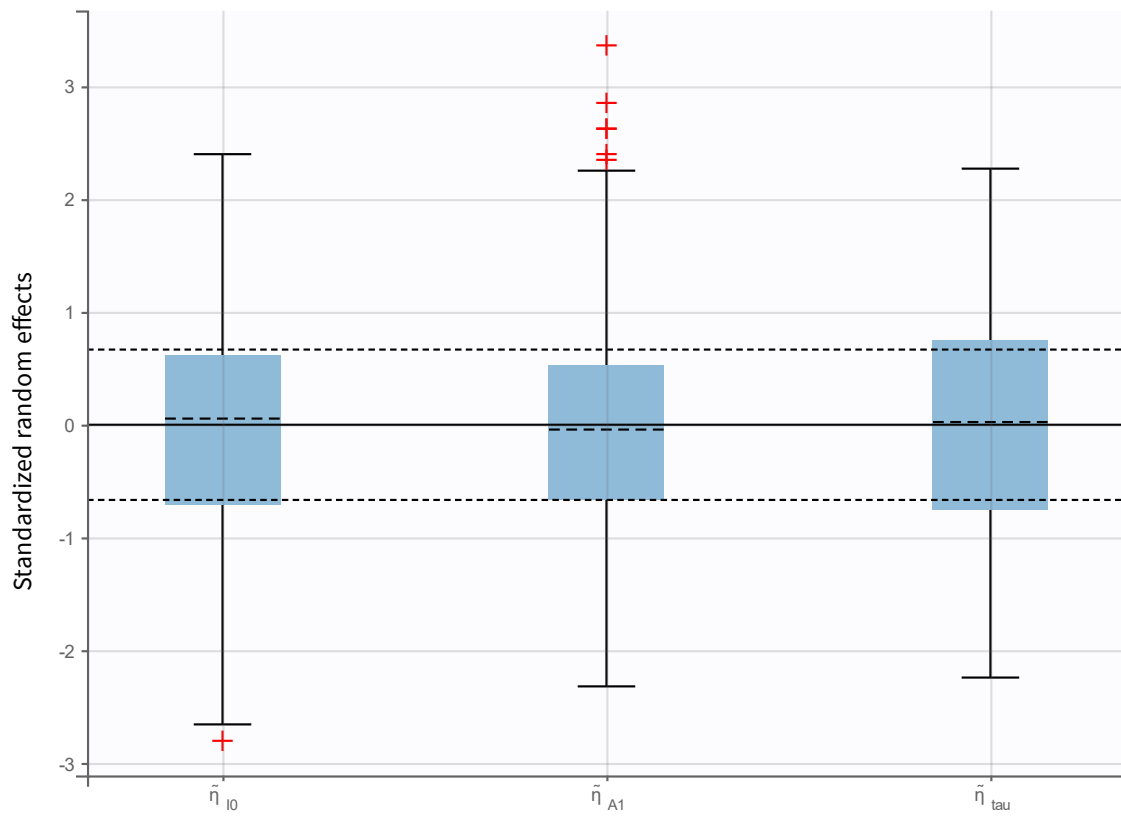


Figure 8: Distribution of the standardized random effects

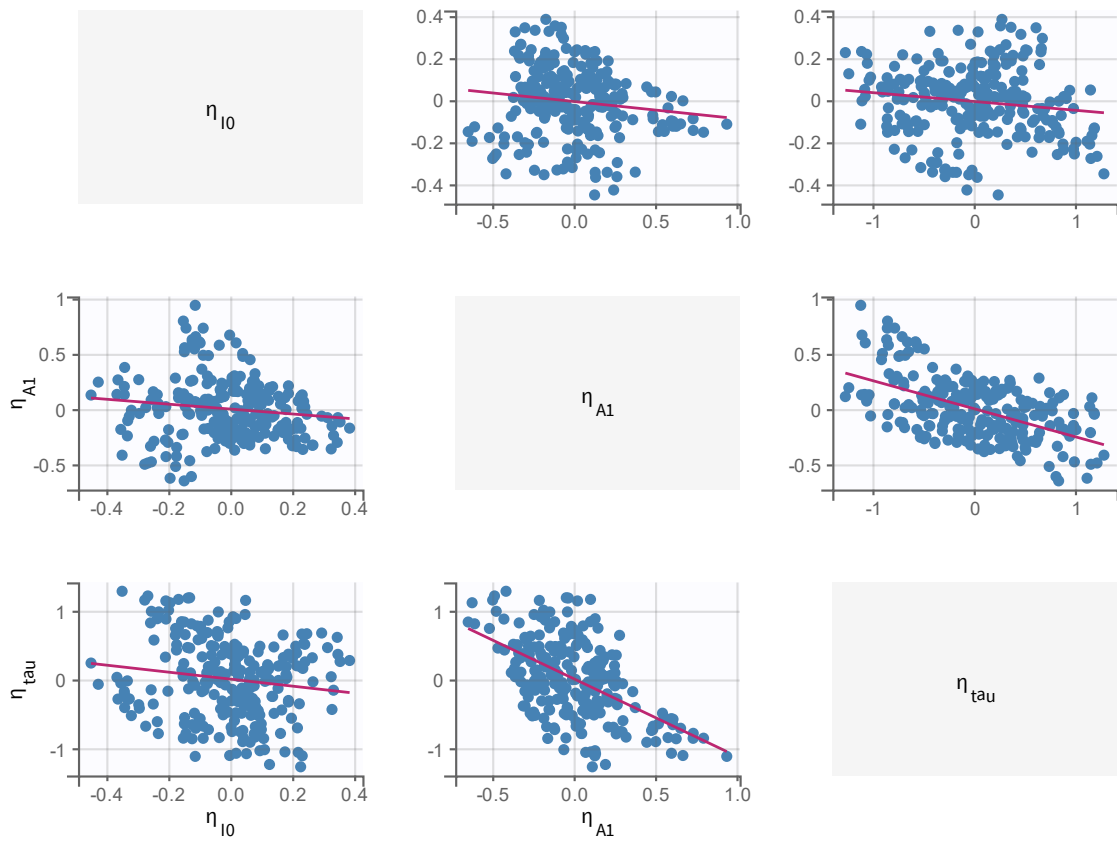


Figure 9: Correlation between random effects

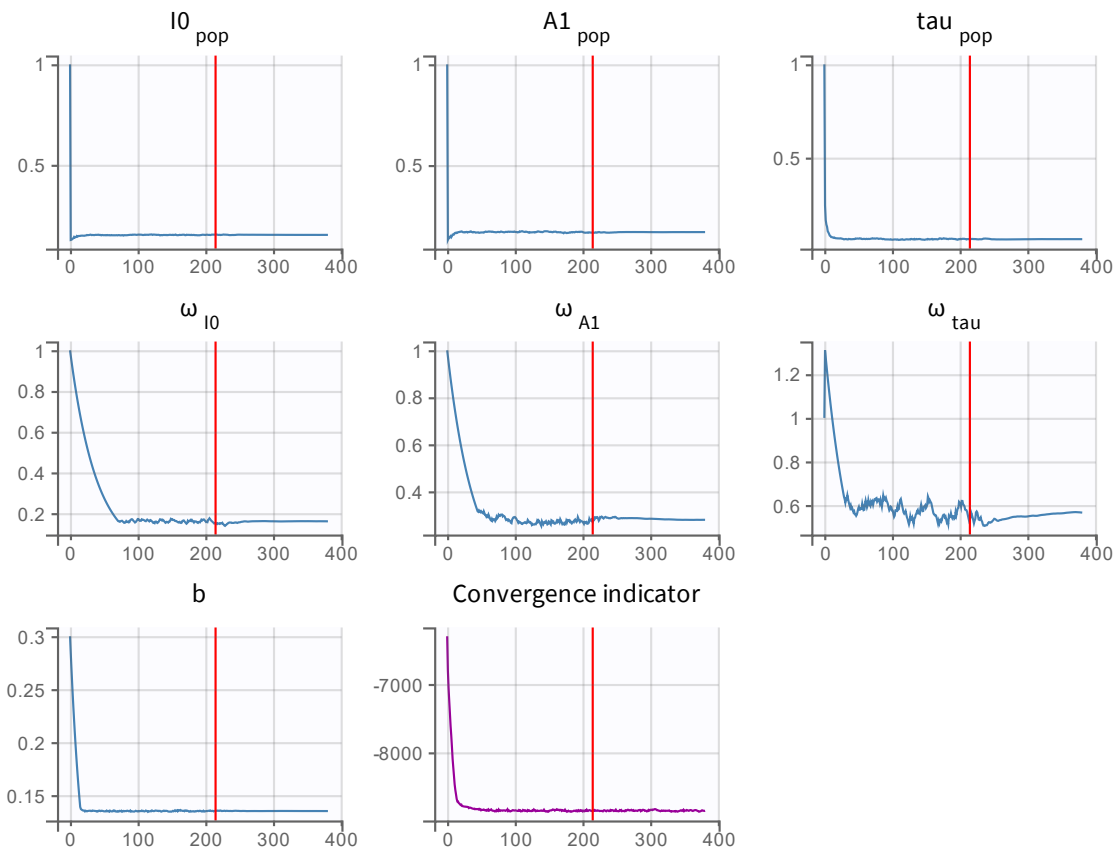


Figure 10: SAEM



## S2: Monolix report: 2% glucose

Run: 240213\_glu2\_corr.mlxtran

Dataset: 240213\_FRAP\_complete\_norm\_one\_nominus\_glu2\_corr.csv

Date: 02-13-2024

### Tables

Table 3: Estimated population parameters

Parameter	Value	STOCH. APPROX.	
		S.E.	R.S.E.(%)
Fixed Effects			
I0_pop	0.156	0.00607	3.888
A1_pop	0.172	0.011	6.38
tau_pop	0.0666	0.0074	11.123
Standard Deviation of the Random Effects			
	Value	C.V.(%)	
omega_I0	0.184	18.542	0.0286 15.529
omega_A1	0.302	30.925	0.0474 15.684
omega_tau	0.491	52.16	0.0827 16.868
Error Model Parameters			
b	0.128	0.00193	1.503

Table 4: Log-likelihood and Information criteria

CRITERIA	IMPORTANCE SAMPLING
-2 x log-likelihood (OFV)	-9120.5
Akaike Information Criteria (AIC)	-9106.5
Bayesian Information Criteria (BIC)	-9098
Corrected Bayesian Information Criteria (BICc)	-9079.8

### Plots

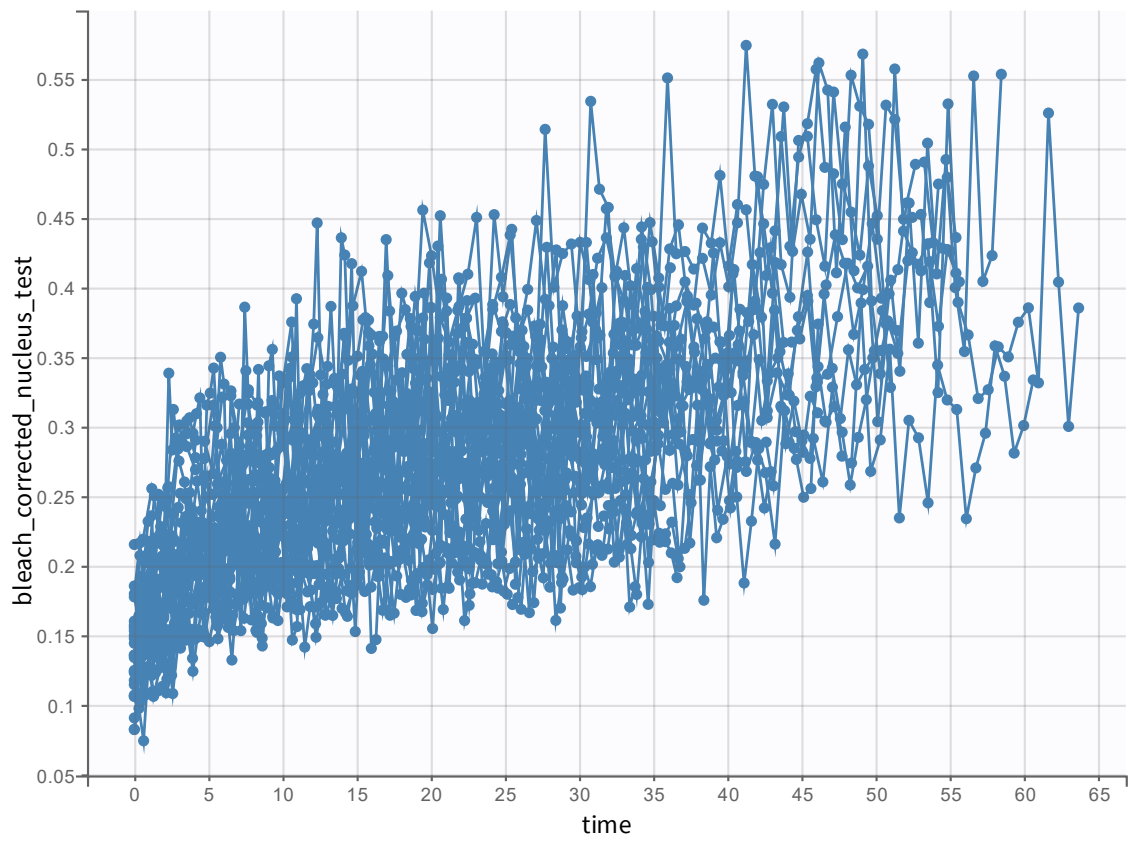
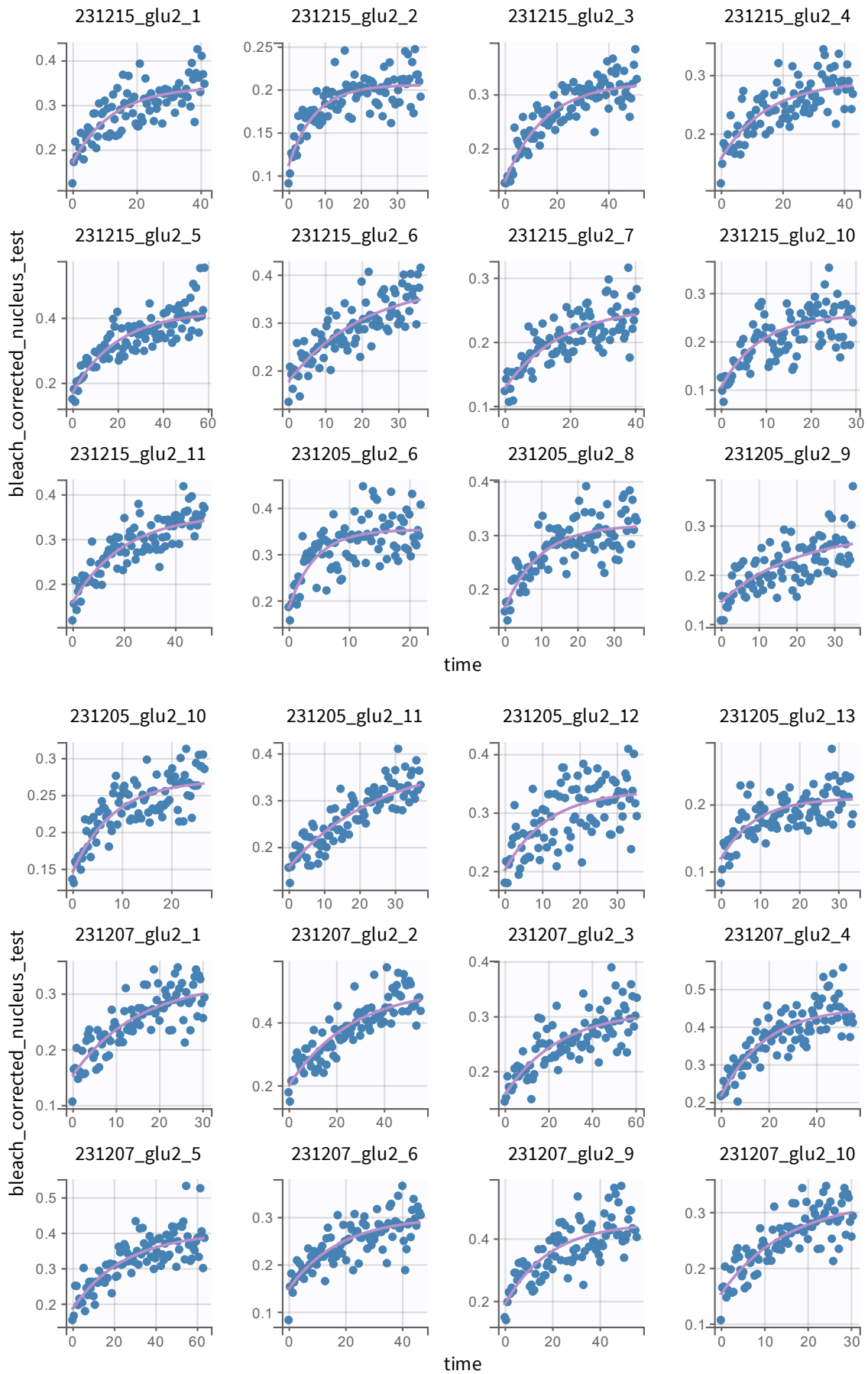


Figure 11: Observed data



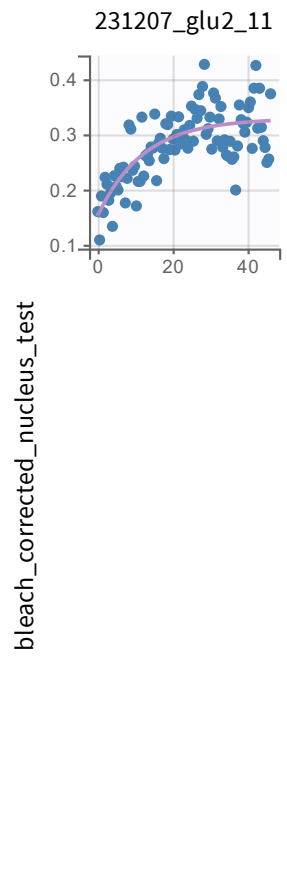


Figure 12: Individual fits

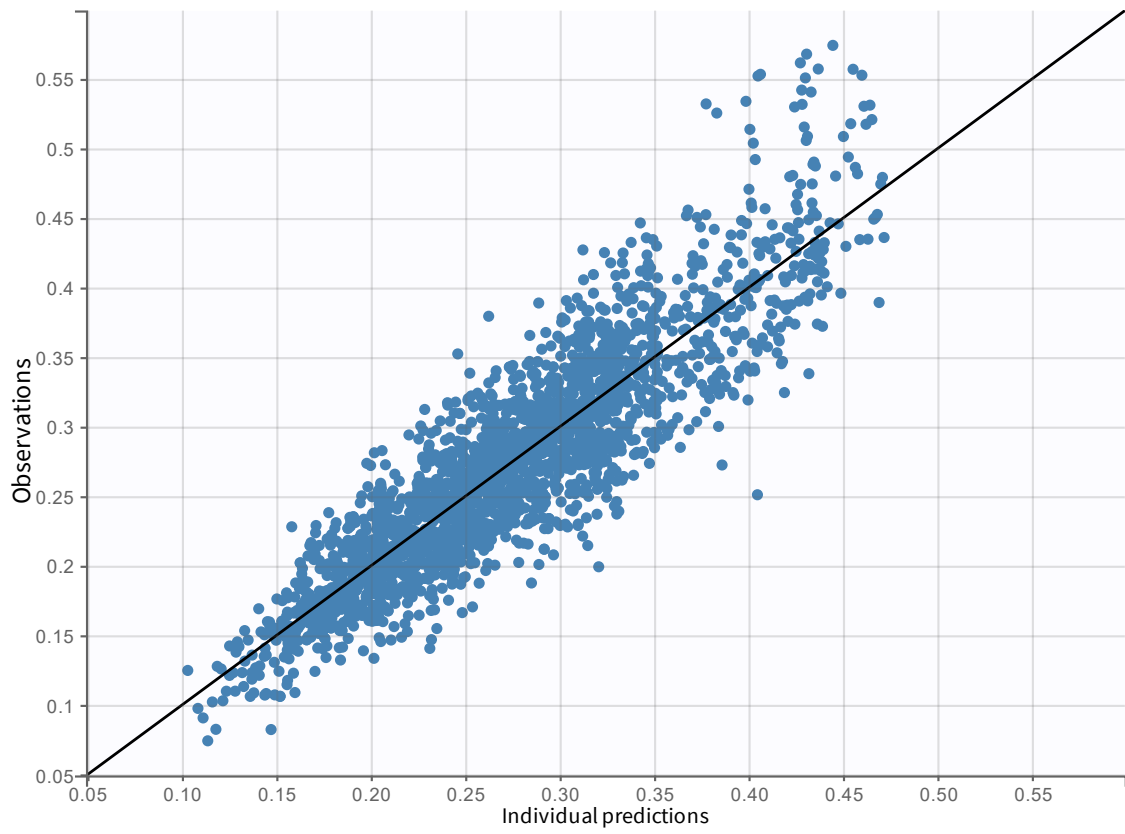


Figure 13: Observations vs predictions

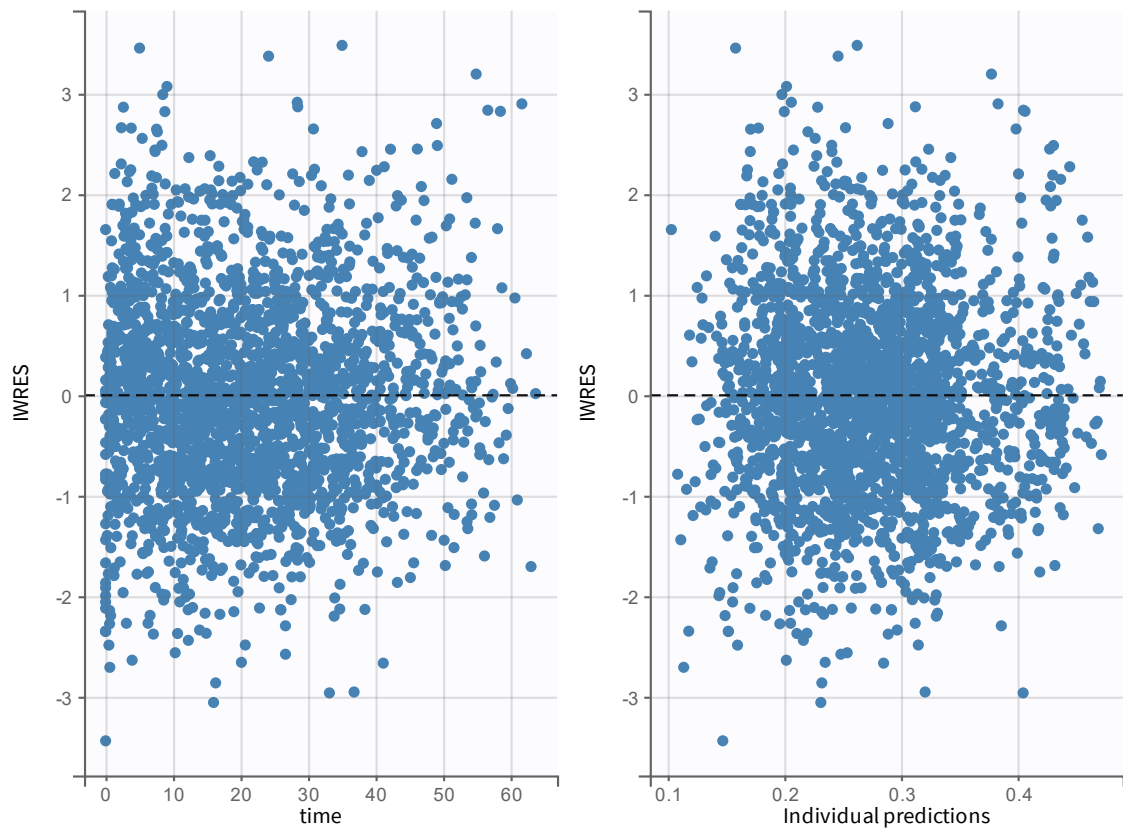


Figure 14: Scatter plot of the residuals

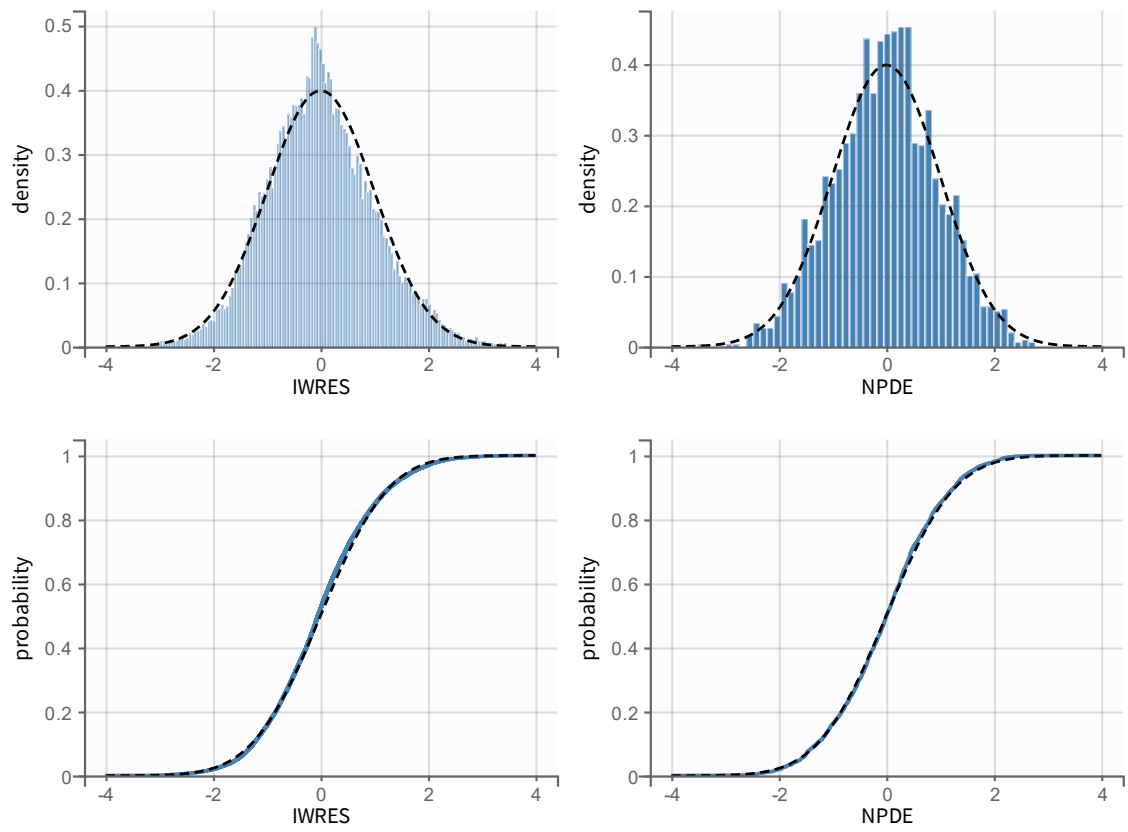


Figure 15: Distribution of the residuals

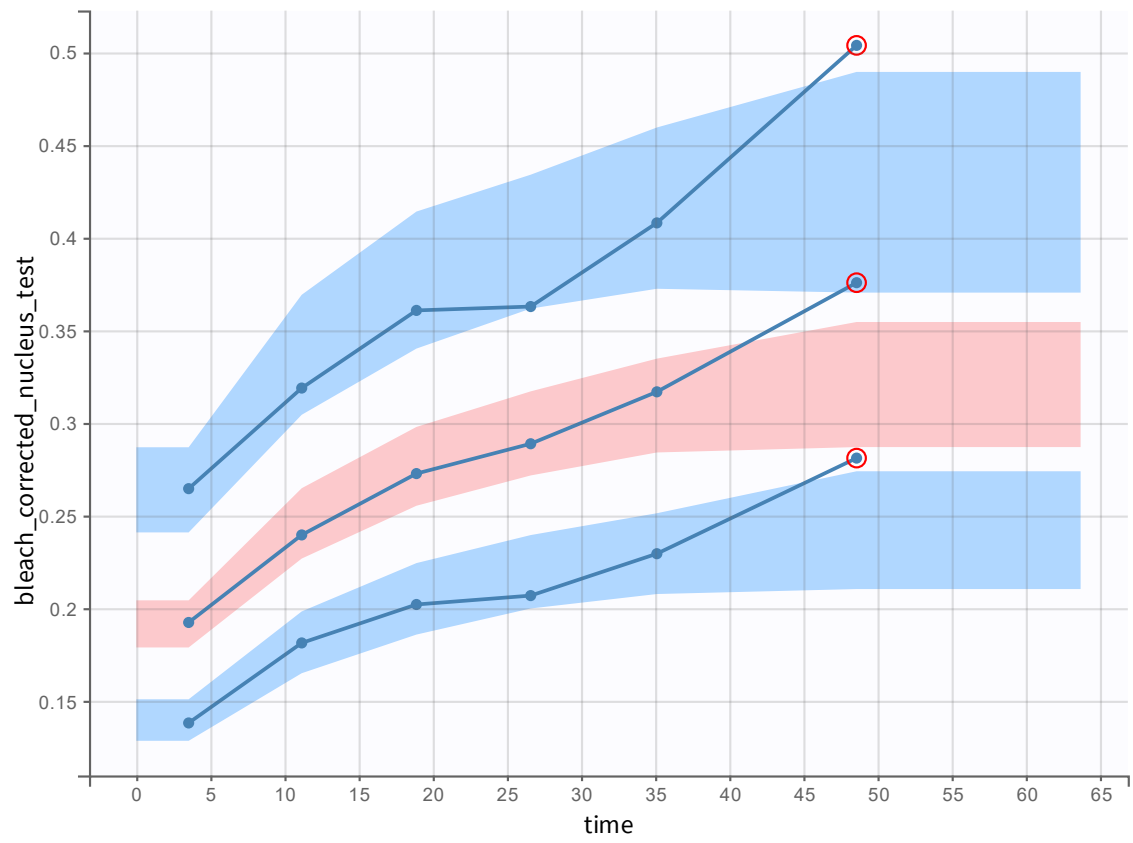


Figure 16: Visual predictive check



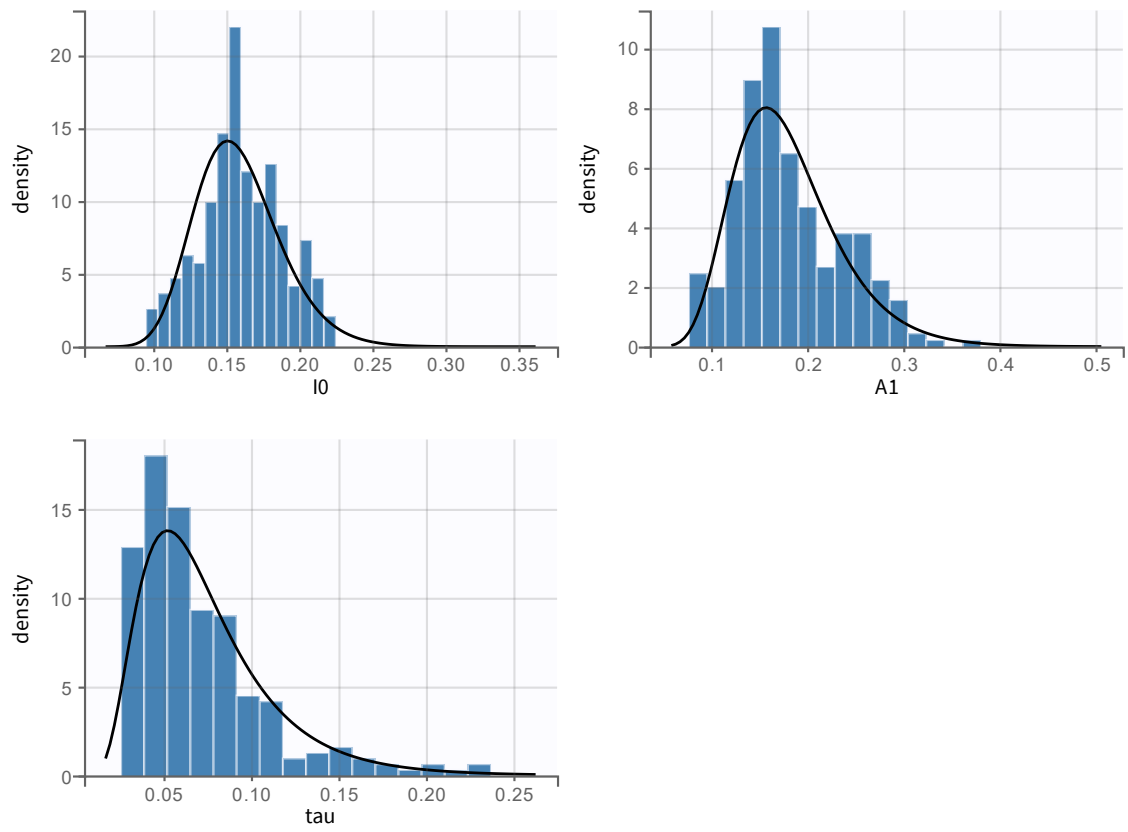


Figure 17: Distribution of the individual parameters

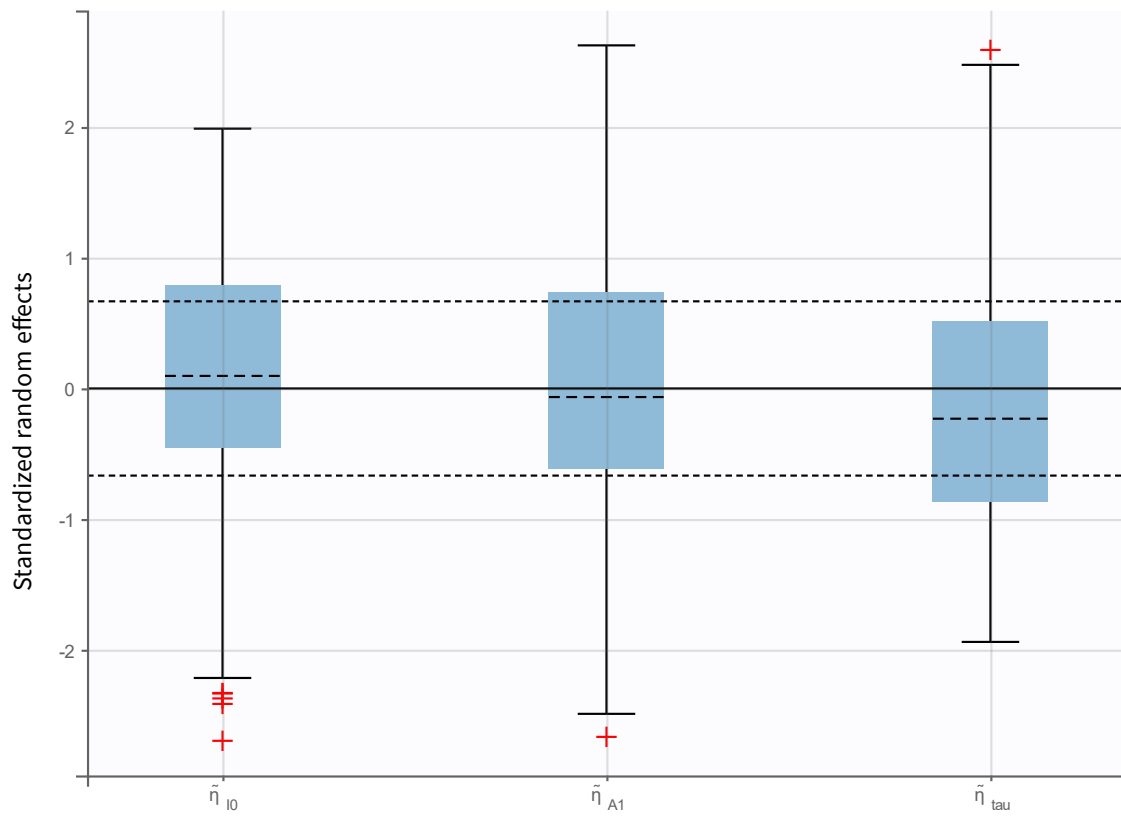


Figure 18: Distribution of the standardized random effects

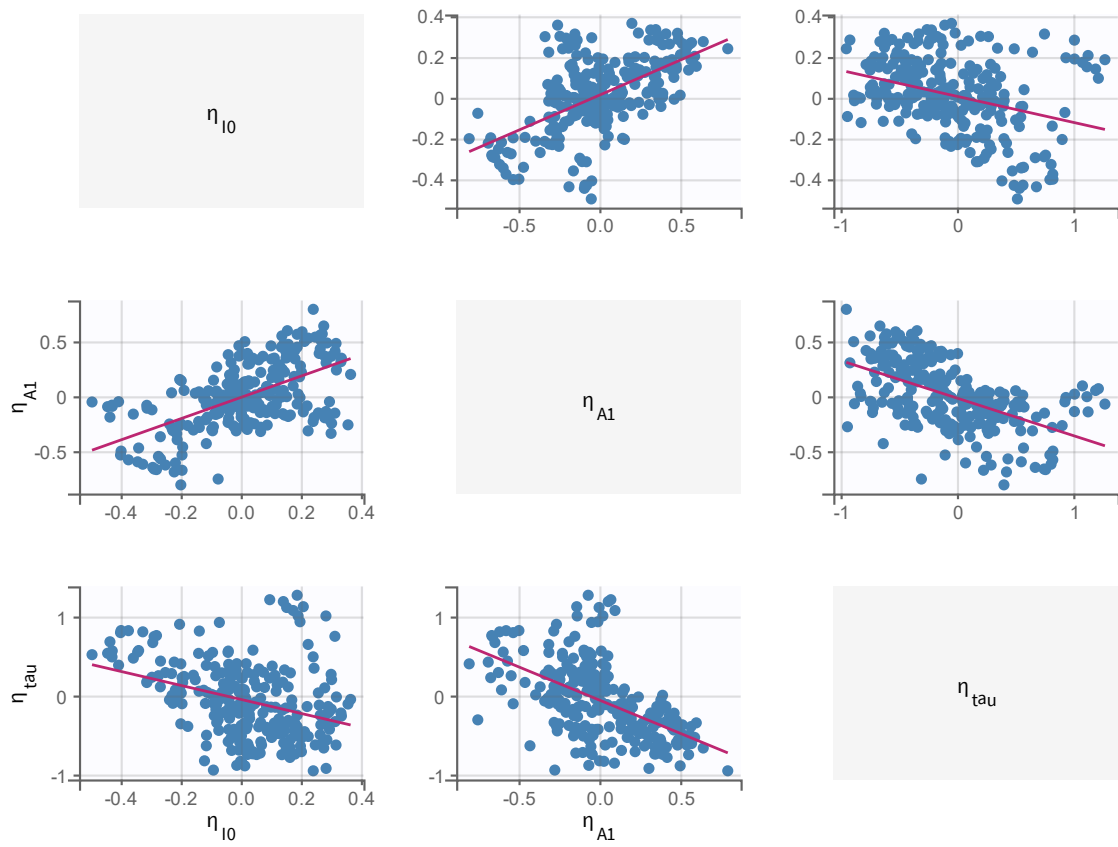


Figure 19: Correlation between random effects

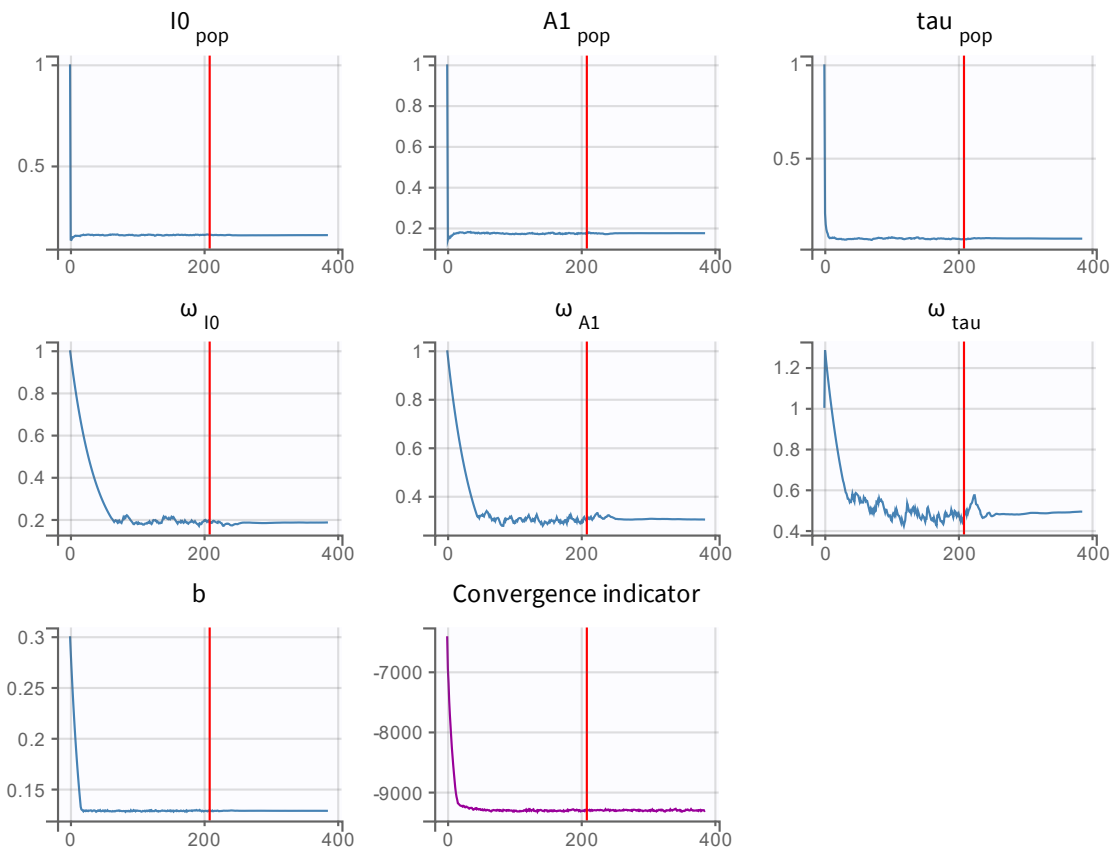


Figure 20: SAEM

## S2: Monolix report: 2%Glycerol

Run: 240213\_gly2\_corr.mlxtran

Dataset: 240219\_FRAP\_complete\_norm\_one\_nominus\_gly2\_corr.csv

Date: 02-19-2024

### Tables

Table 5: Estimated population parameters

Parameter	Value	STOCH. APPROX.	
		S.E.	R.S.E.(%)
Fixed Effects			
I0_pop	0.152	0.00646	4.239
A1_pop	0.157	0.00892	5.674
tau_pop	0.0774	0.0124	15.977
Standard Deviation of the Random Effects			
	Value	C.V.(%)	
omega_I0	0.185	18.621	0.0327 17.725
omega_A1	0.243	24.661	0.0411 16.929
omega_tau	0.685	77.393	0.122 17.8
Error Model Parameters			
b	0.124	0.00201	1.626

Table 6: Log-likelihood and Information criteria

CRITERIA	IMPORTANCE SAMPLING
-2 x log-likelihood (OFV)	-7940.2
Akaike Information Criteria (AIC)	-7926.2
Bayesian Information Criteria (BIC)	-7918.9
Corrected Bayesian Information Criteria (BICc)	-7900.7

### Plots

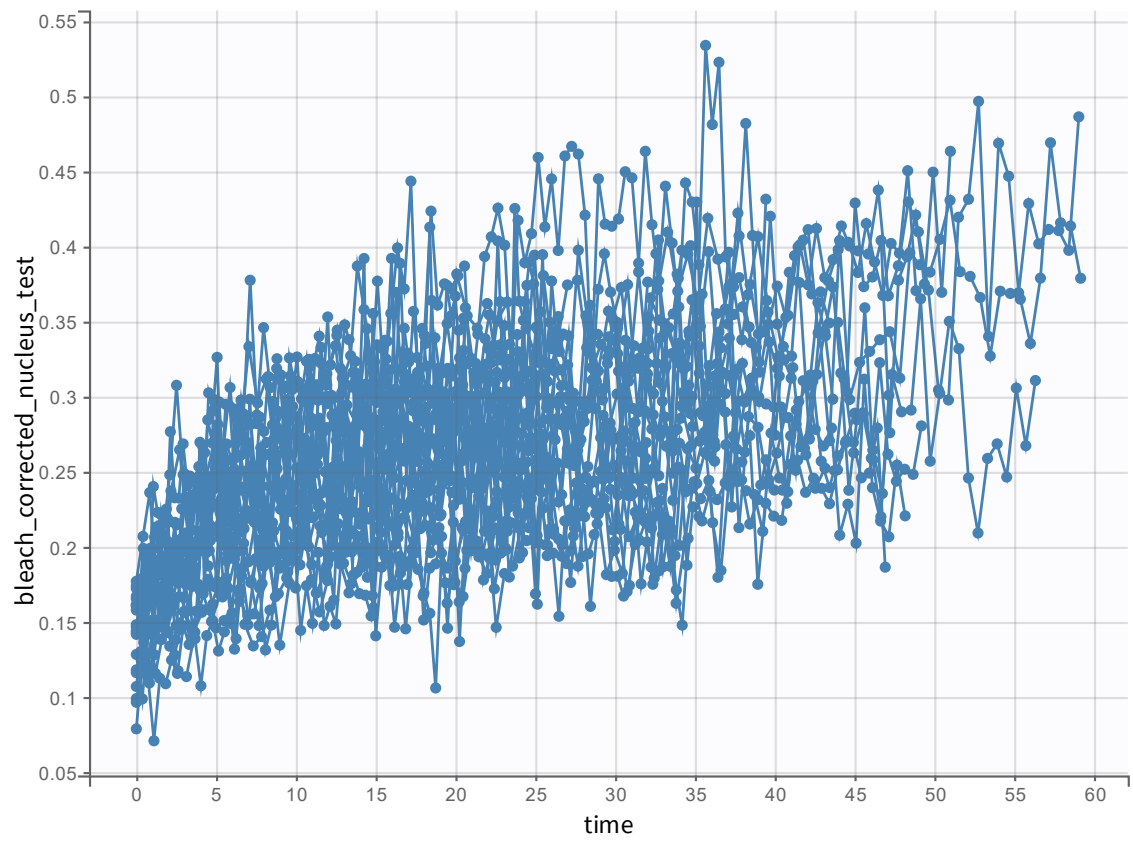


Figure 21: Observed data

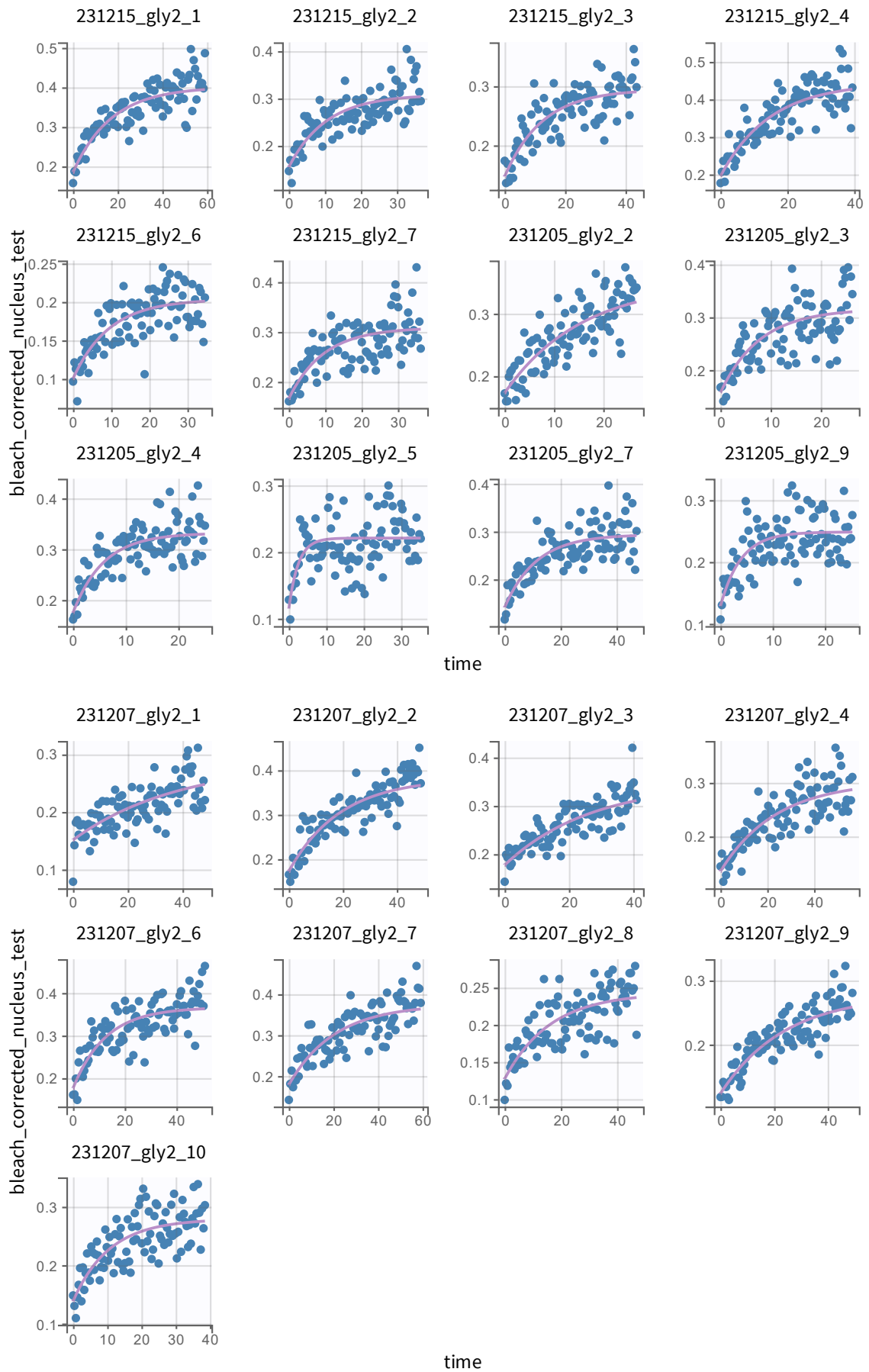


Figure 22: Individual fits

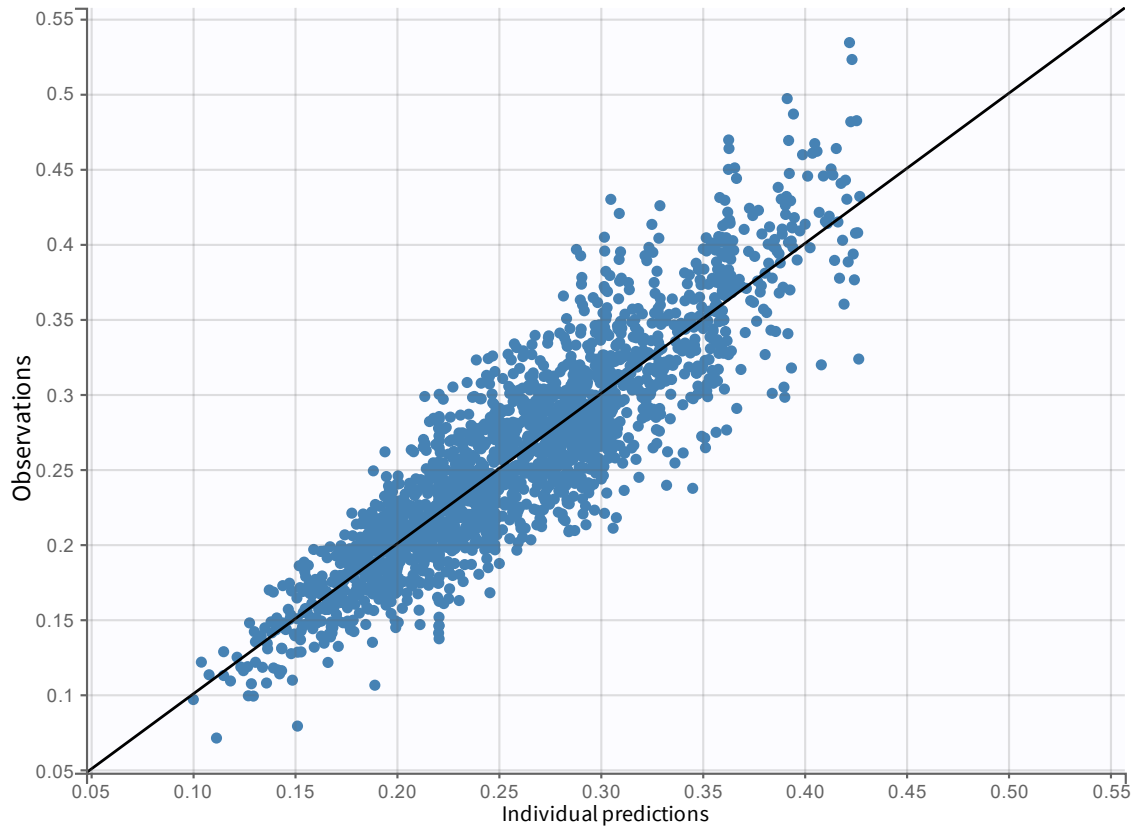


Figure 23: Observations vs predictions



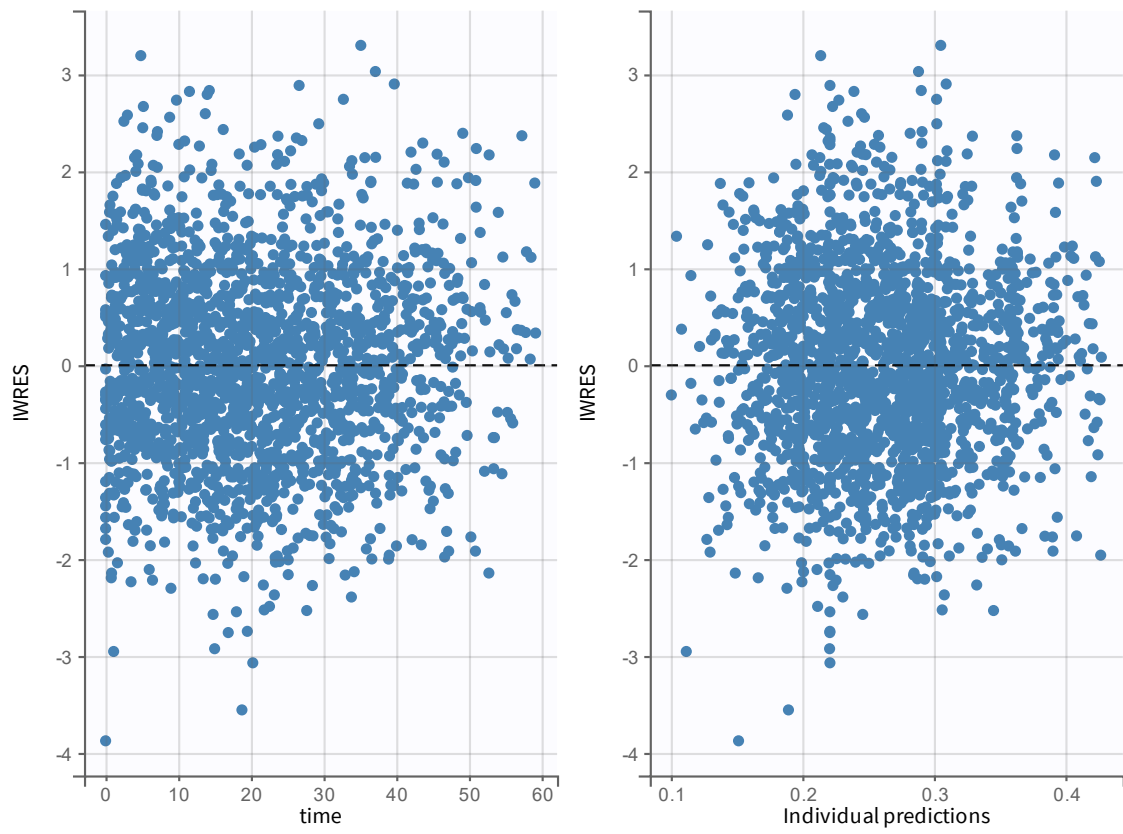


Figure 24: Scatter plot of the residuals

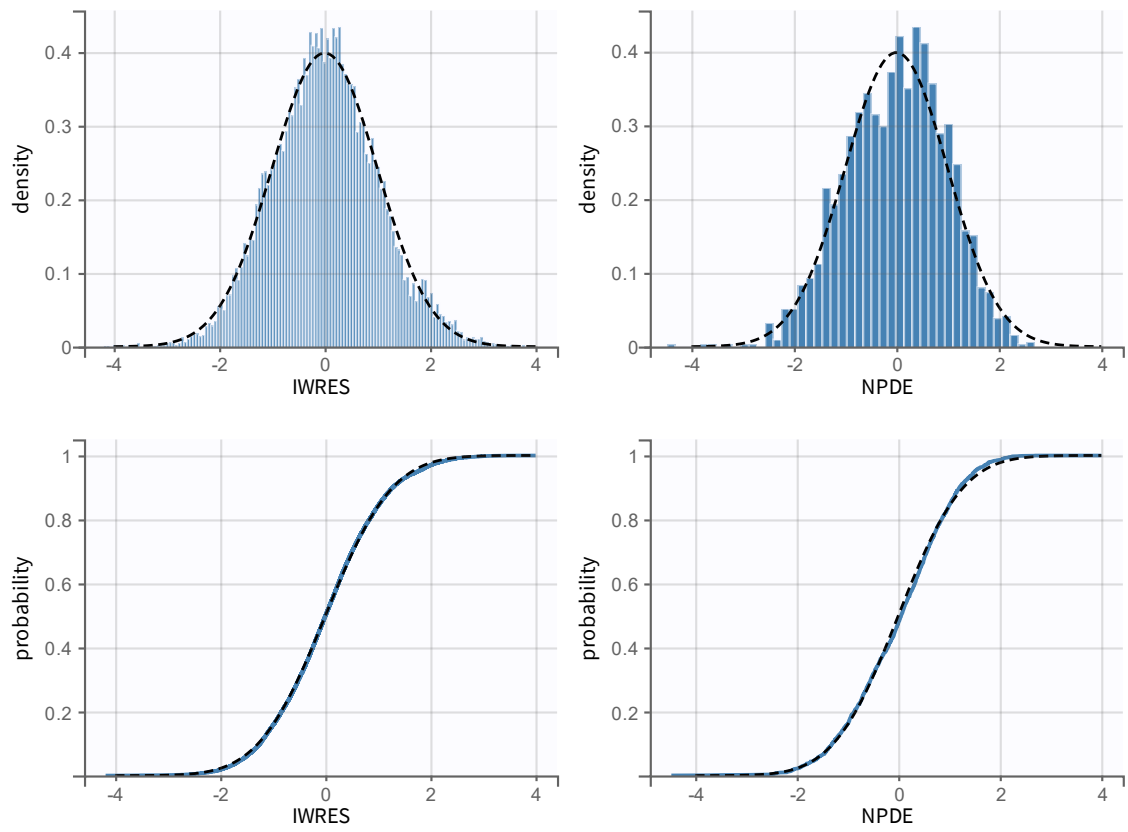


Figure 25: Distribution of the residuals

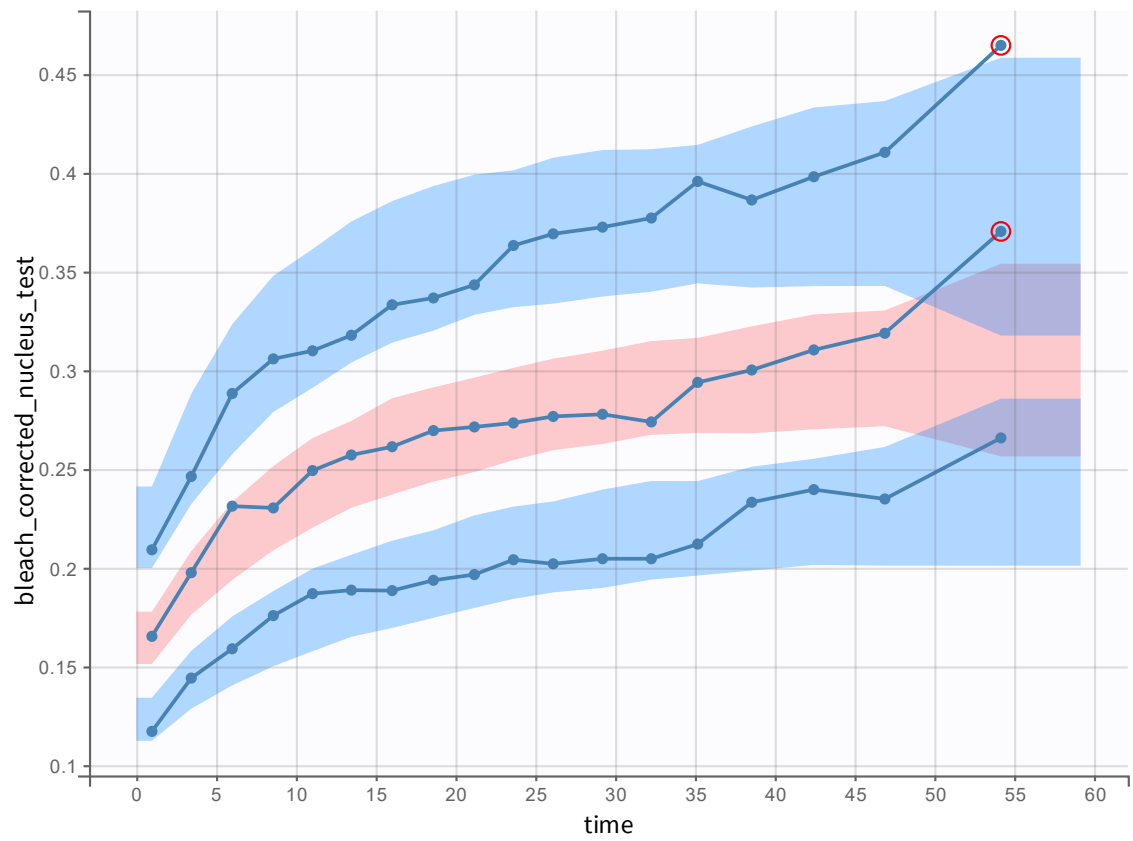


Figure 26: Visual predictive check

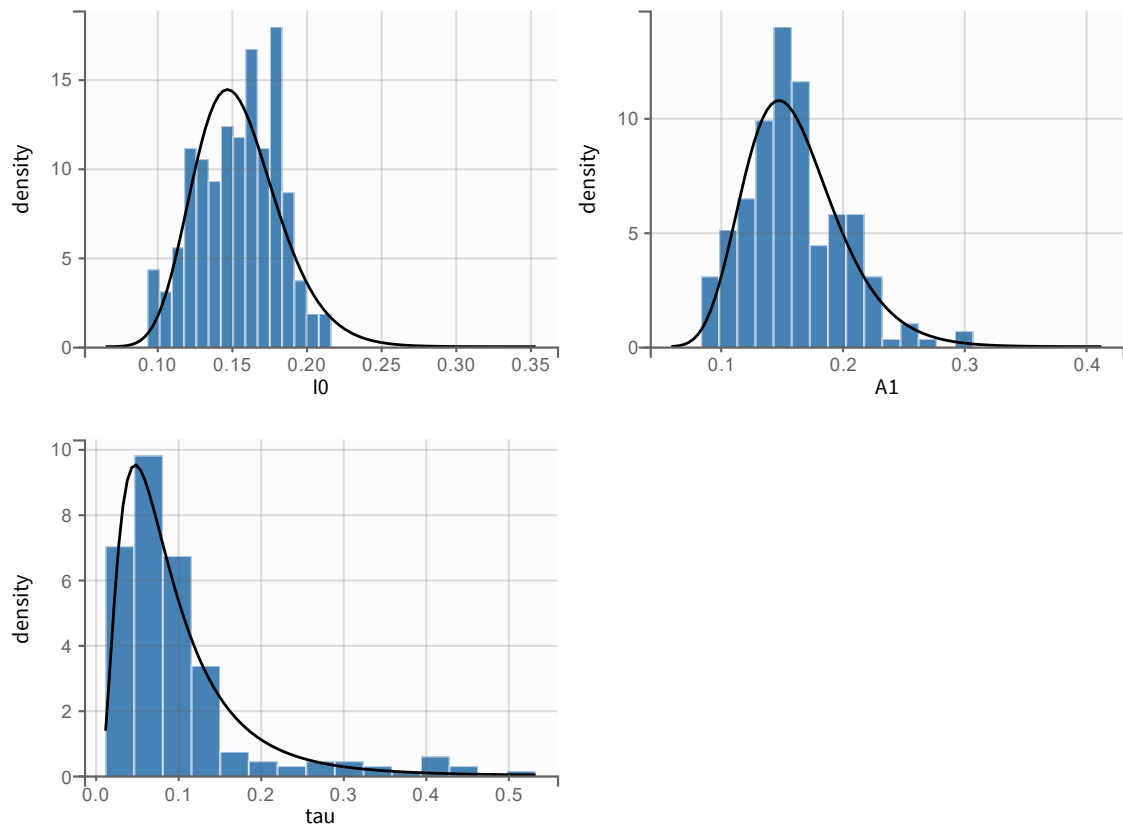


Figure 27: Distribution of the individual parameters

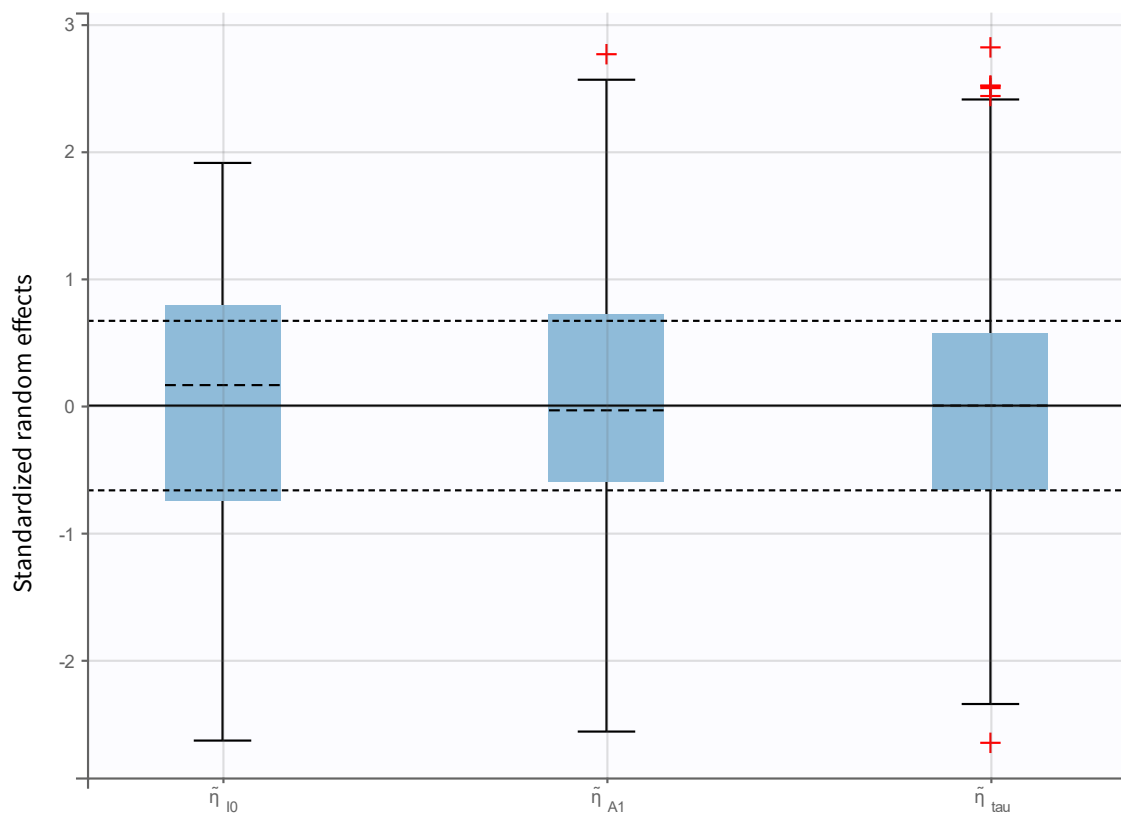


Figure 28: Distribution of the standardized random effects

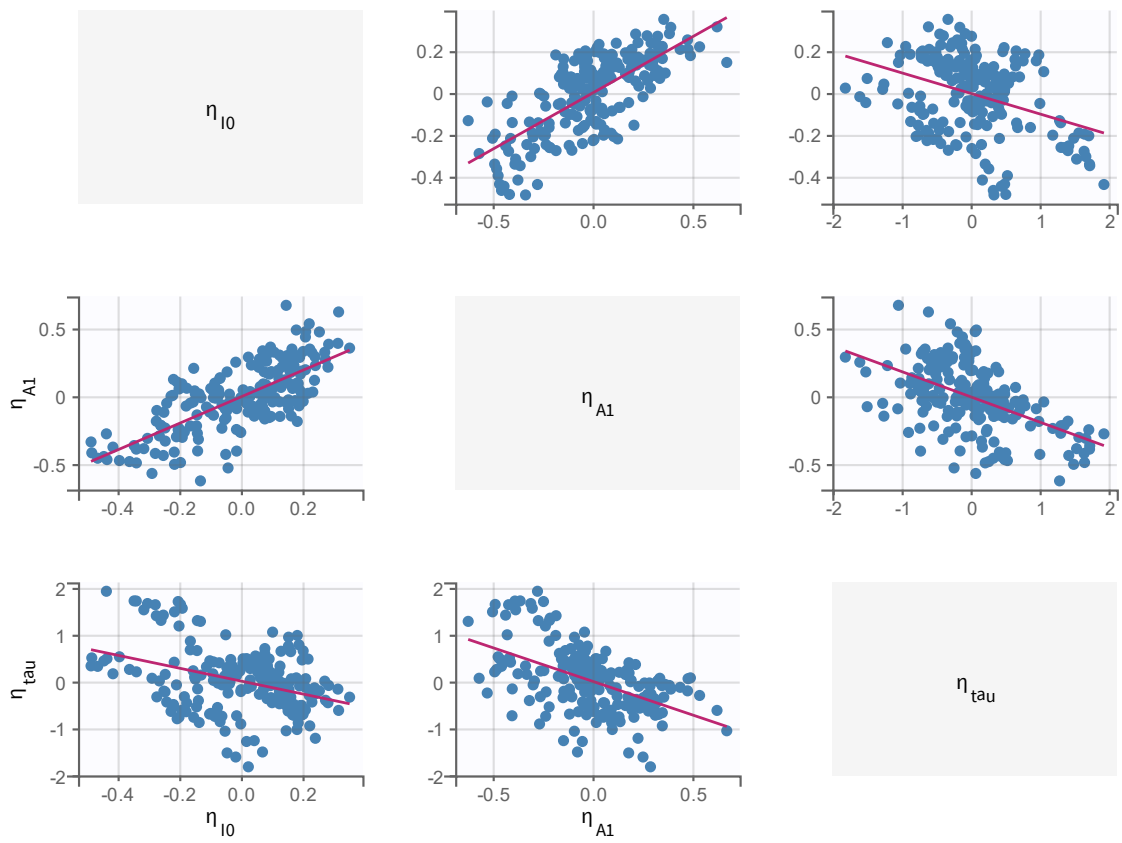


Figure 29: Correlation between random effects

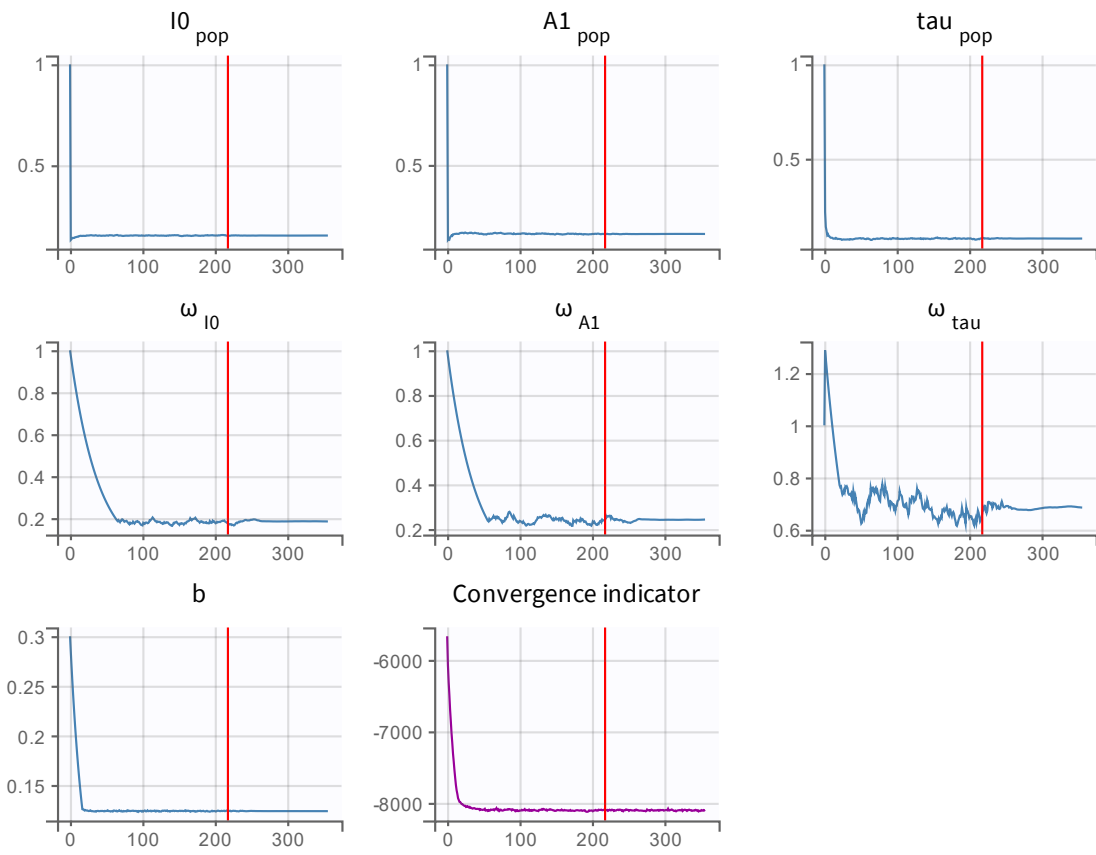


Figure 30: SAEM