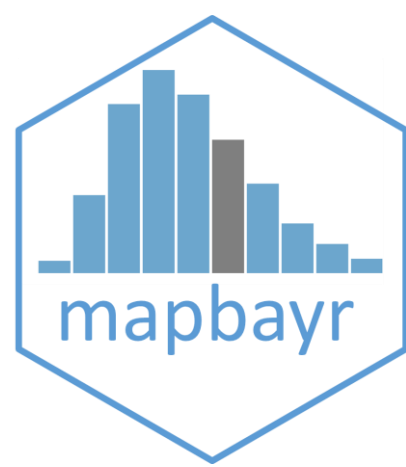




mapbayr: Maximum A Posteriori (MAP) Bayesian Estimation of PK parameters in R

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What is mapbayr?

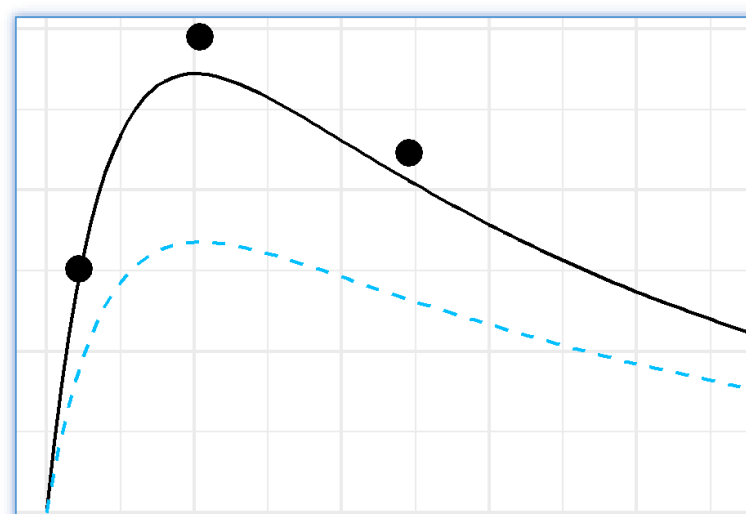
A free open-source R package to perform maximum *a posteriori* (MAP) Bayesian estimation of PK parameters. Code a population PK model (that you developed, or from the literature) and pass concentration data relative to your patient in order to estimate individual PK parameters. You can use these to derive an AUC, to predict concentrations at relevant times or to simulate other dosing regimens.

```
> print(my_data)
  ID TIME EVID AMT CMT  DV
1  1  0.0   1  500   1  0.0
2  1  1.1   0    0   2 15.1
3  1  5.2   0    0   2 29.5
4  1 12.3   0    0   2 22.3

> see(my_model)
Model file: my_model.cpp
$PARAM ETA1 = 0, ETA2 = 0,
KA = 0.5, TVCL = 1.1, TVV = 23.3
$OMEGA 0.41 0.32
$SIGMA 0.04 0
$CMT DEPOT CENT
$PK
double CL=TVCL*exp(ETA1+ETA(1));
double V=TVV*exp(ETA2+ETA(2));
$ERROR
double DV=CENT/V*(1+EPS(1))+EPS(2);
$PKMODEL ncmt = 1, depot = TRUE
$CAPTURE DV CL
```

Data passed with
NM-TRAN format

Population
PK model
defined in:



```
> mapbayest(my_model, my_data)
Estimates:
```

```
  ID  ETA1  ETA2
1  1 -0.3826972 -0.5050322
```

Output (4 lines):

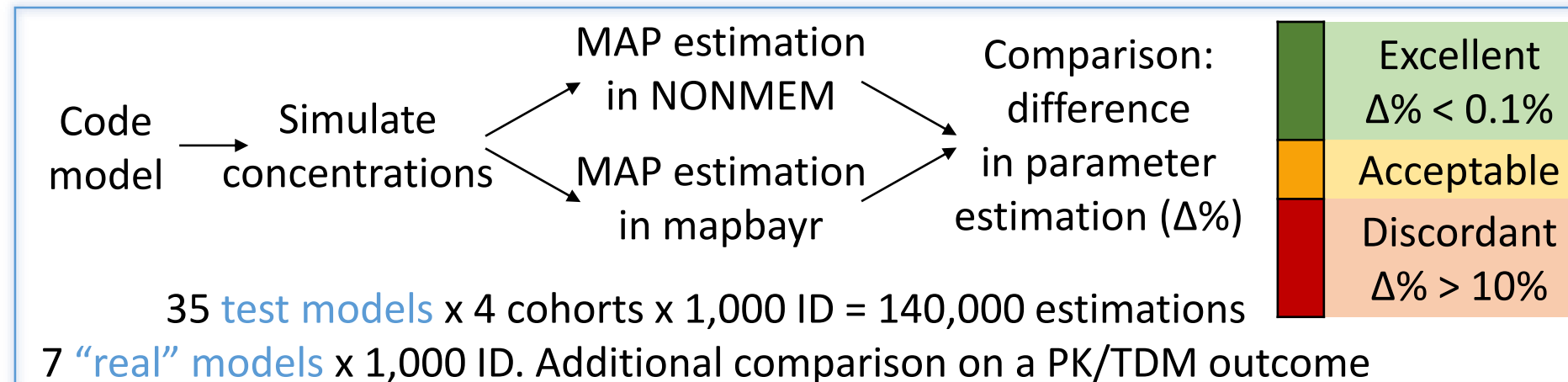
```
  ID time evid amt cmt  DV IPRED  PRED  CL  ETA1  ETA2
1  1  0.0   1  500   1  0.0  0.00  0.00  0.75 -0.383 -0.505
2  1  1.1   0    0   2 15.1 14.57  8.83  0.75 -0.383 -0.505
3  1  5.2   0    0   2 29.5 27.21 16.78  0.75 -0.383 -0.505
4  1 12.3   0    0   2 22.3 20.57 13.21  0.75 -0.383 -0.505
```

Code / Documentation: <http://github.com/FelicienLL/mapbayr>
<https://CRAN.R-project.org/package=mapbayr>

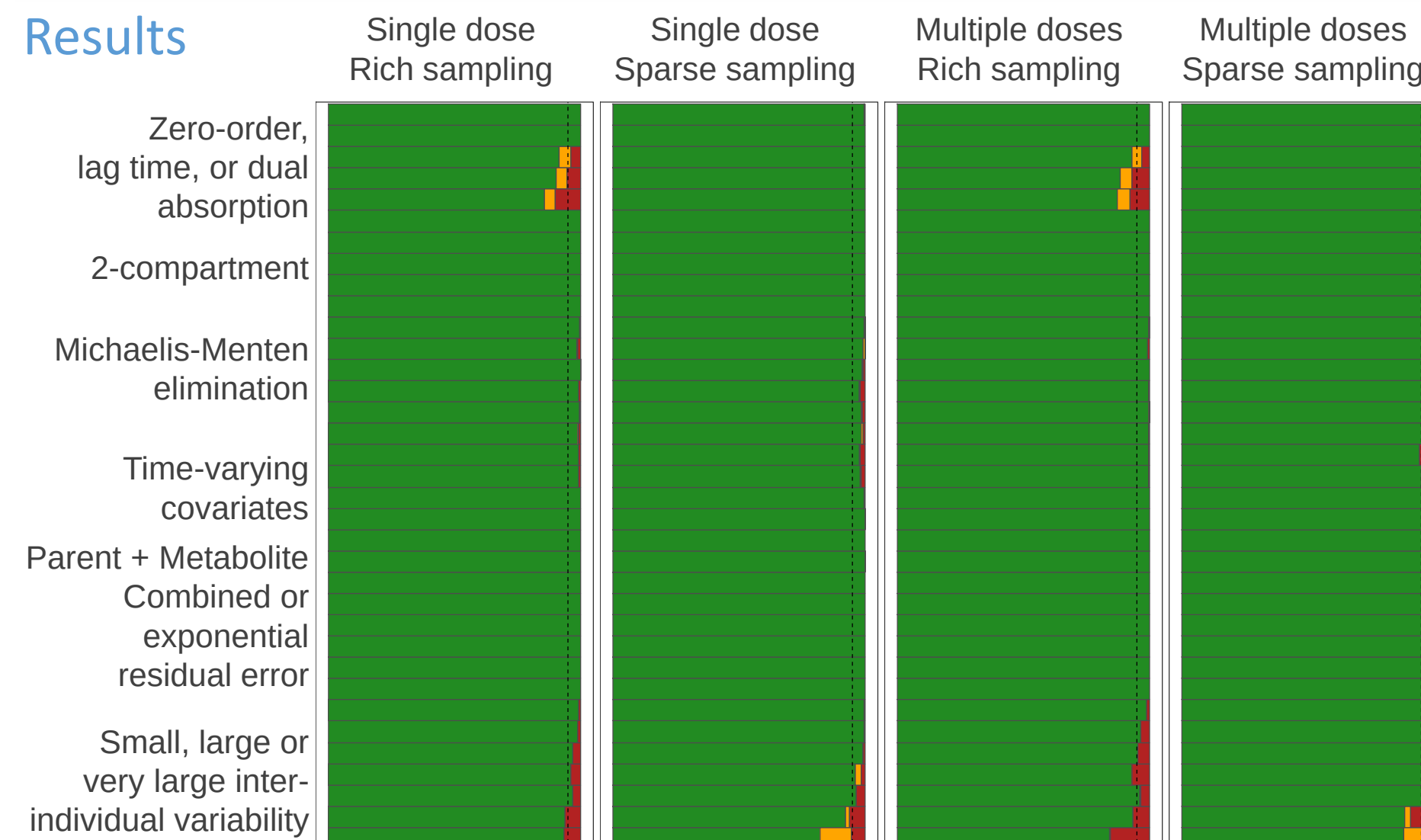
Is it reliable?

Yes! A validation study was conducted vs. NONMEM

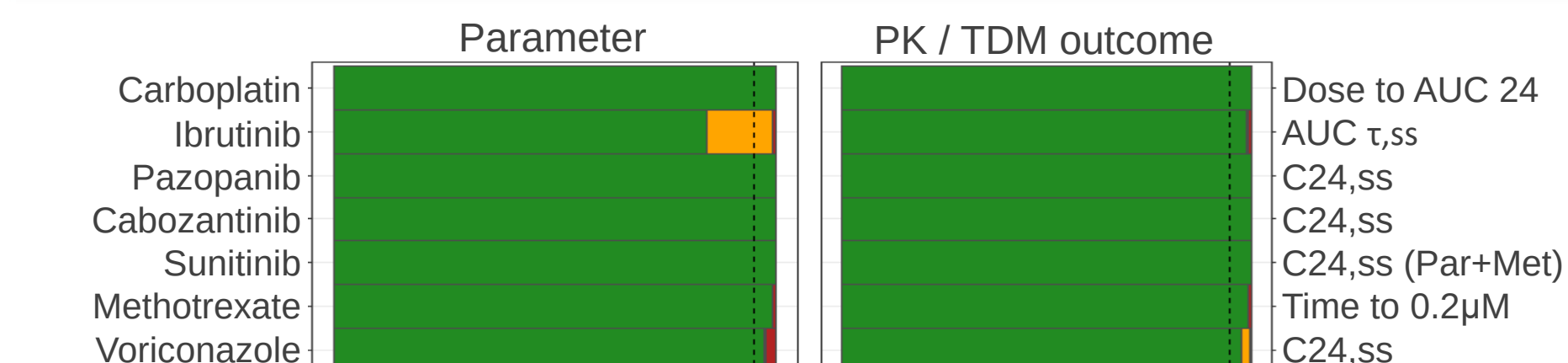
Methods



Results



Test models: 98% of excellent estimations, 0.5% acceptable, 1.5% discordant



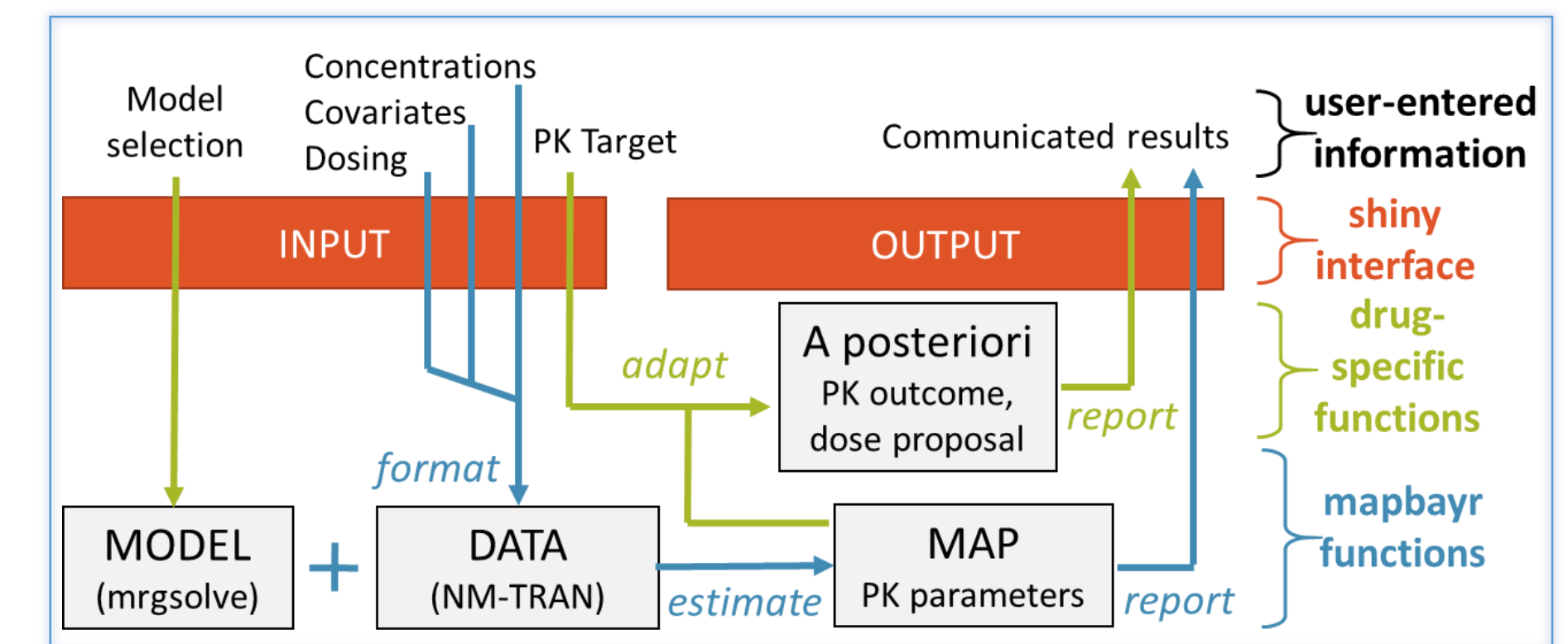
"Real" models: nearly 100% concordance on PK / TDM outcome

Full article available at: <https://doi.org/10.1002/psp4.12689>
Le Louedec *et al*, CPT: Pharmacometrics & System Pharmacology, 2021

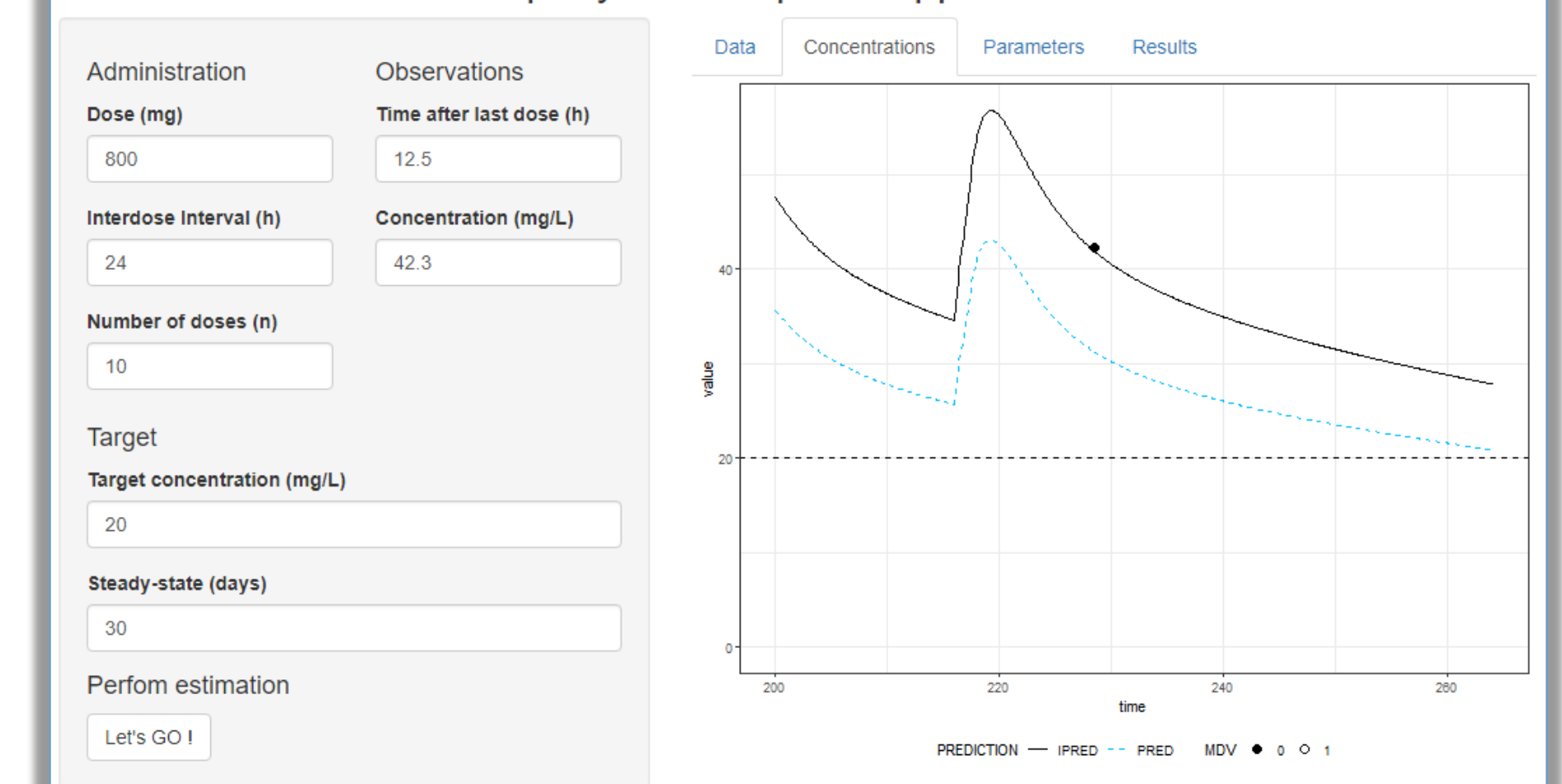
What's the point?

Integration into any R framework. Suitable approach for standalone Shiny Applications dedicated to Therapeutic Drug Monitoring with Bayesian dose individualization :

- any PK model
- any clinical / TDM protocol
- without additional software other than R



Oral kinase inhibitor - mapbayr - Example of application



Browse examples at:

<http://github.com/FelicienLL/mapbayr-shiny>