

BLOQ

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1 Introduction

Censoring occurs when the value of a measurement or observation is only partially known.

- The lower limit of detection **LLOD** is the lowest quantity of a substance that can be distinguished from its absence.
- A measuring device can also have an upper limit of quantification **ULOQ** such that any value above this limit cannot be measured and reported.

We usually distinguish between three types of censoring:

- left
- right
- interval.

1.1 MONOLIX Censored observations

To define that a measurement is censored, the observation data set should include a CENSORING column (default to CENS) and put :

- **1** for lower limit.
- **-1** for upper limit

Optionally, data set can contain have a limit column (default to LIMIT) column to set the other limit.

1.2 pmx_bloq

Whithin ggPMX, to define a bloq we use `pmx_bloq` function.

```
str(pmx_bloq(),1)
```

```
## List of 6
## $ cens : chr "CENS"
## $ limit: chr "LIMIT"
## $ show : logi TRUE
## $ color: chr "pink"
## $ size : num 2
## $ alpha: num 0.9
## - attr(*, "class")= chr "pmxBLOQClass"
```

This will create a `pmxBLOQ` object that defines the censoring and column definition and some graphical parameters. In the following ,we will show the use of it through some examples.

2 PK data below a lower limit of quantification

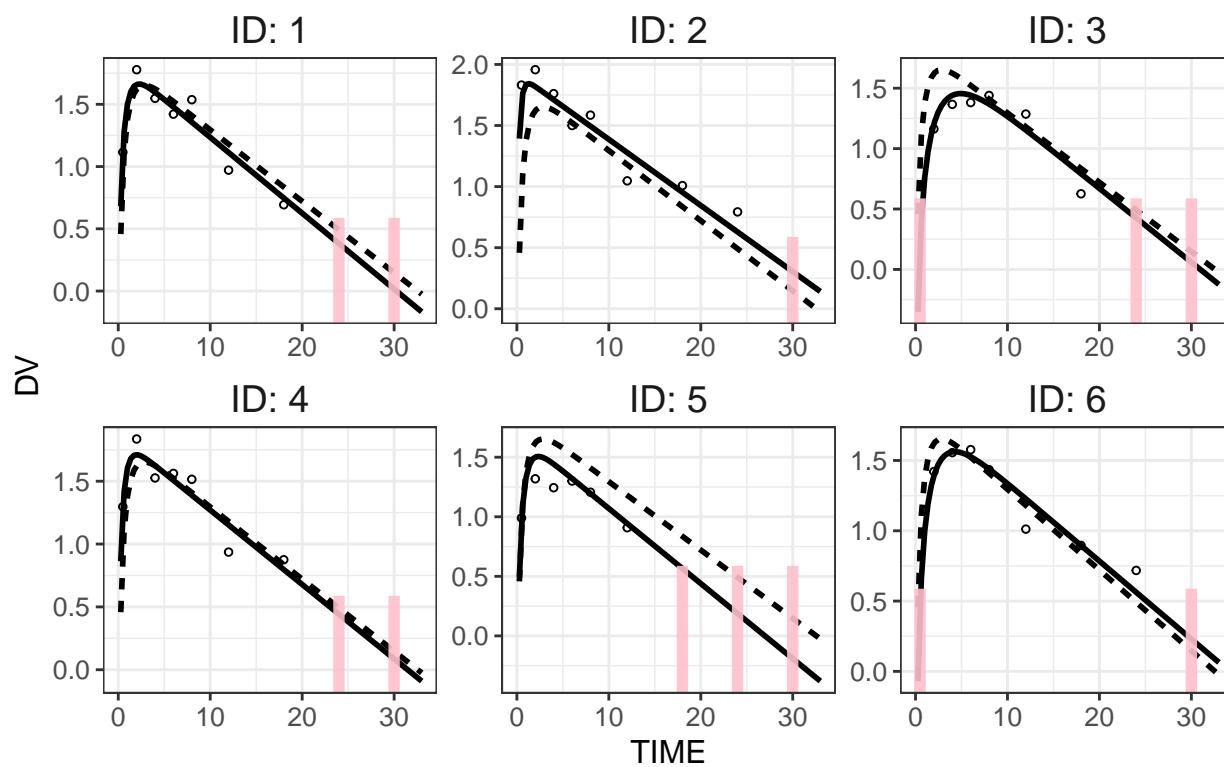
2.1 Left censored data

```
mlx_file <- "/home/agstudy/Downloads/2.2.censored_data/censoring1log_project.mlxtran"
ctr <- pmx_mlxtran(file_name=mlx_file)
```

```
ctr %>% pmx_plot_individual(
  is.draft = FALSE,
  facets=list(ncol=3,nrow=2),
  bloq=pmx_bloq()
)
```

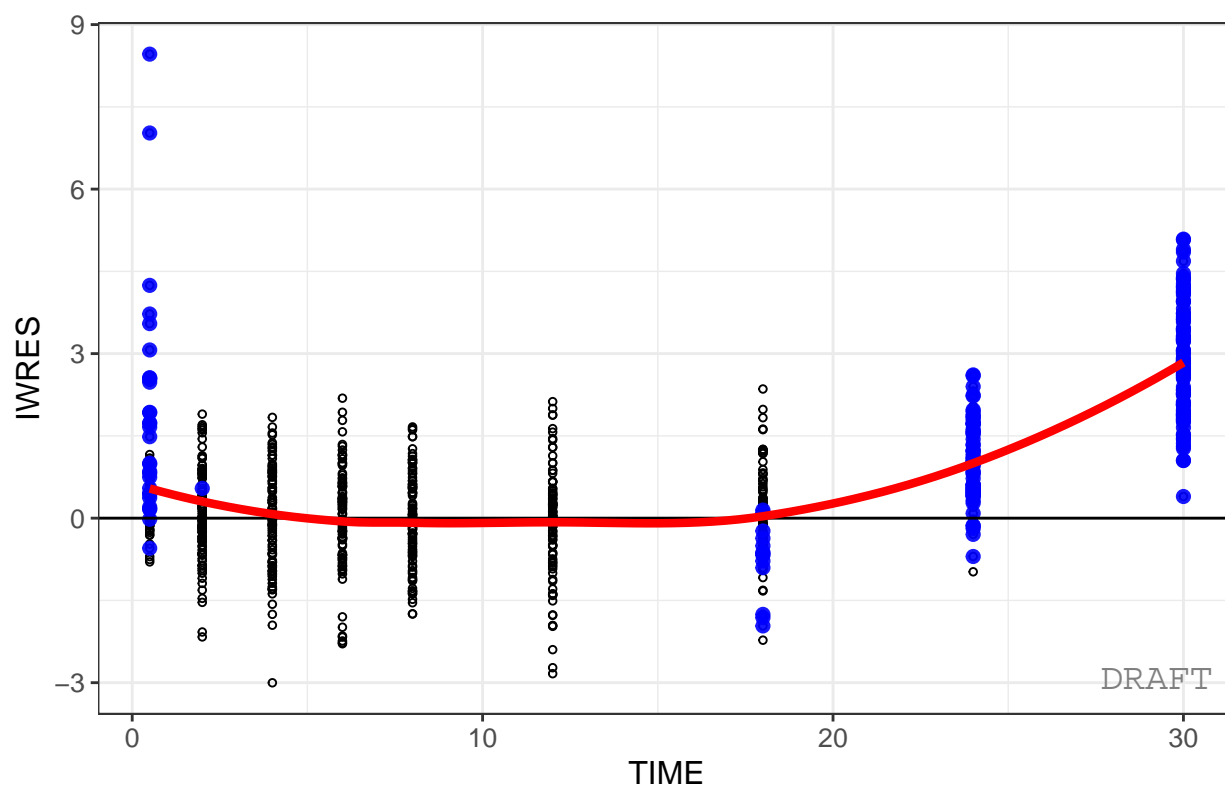
```
## Warning: Removed 100 rows containing missing values (geom_point).
```

Individual fits



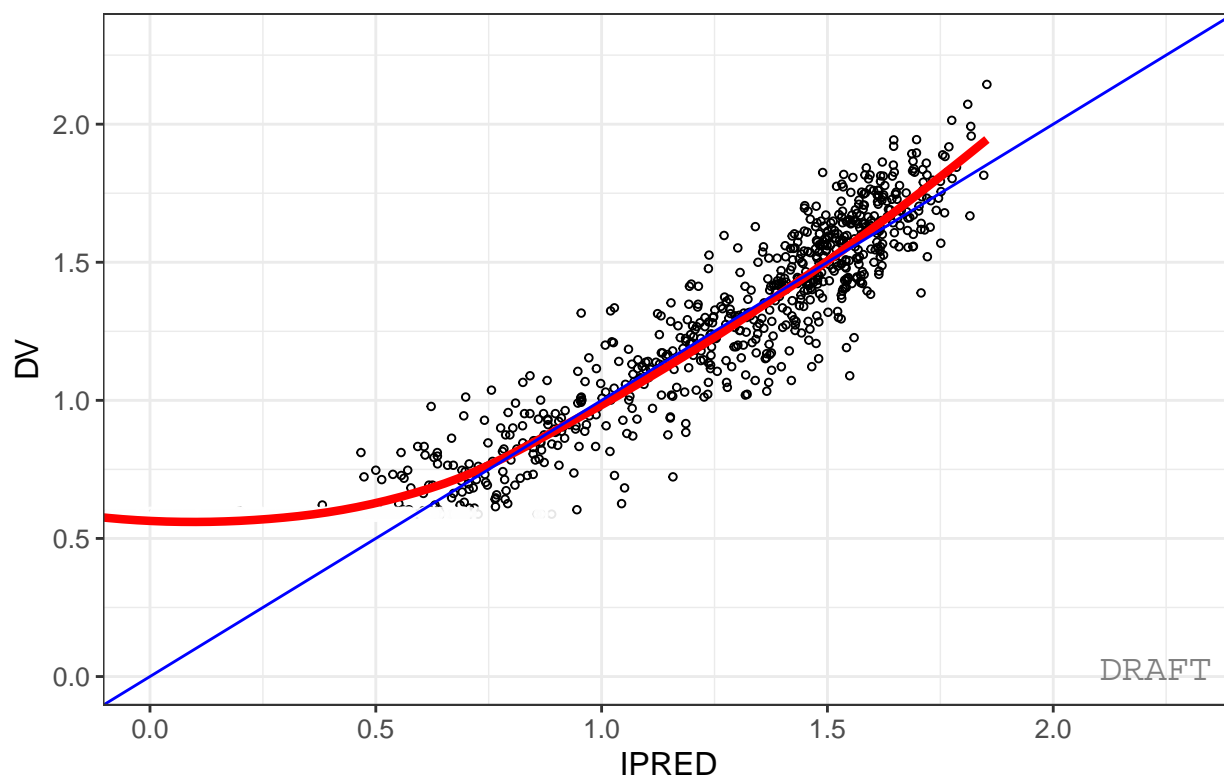
```
ctr %>% pmx_plot_iwres_time(bloq=pmx_bloq(color="blue"))
```

IWRES vs TIME



```
ctr %>% pmx_plot_dv_ipred(bloq=pmx_bloq(color="white"))
```

DV vs IPRED

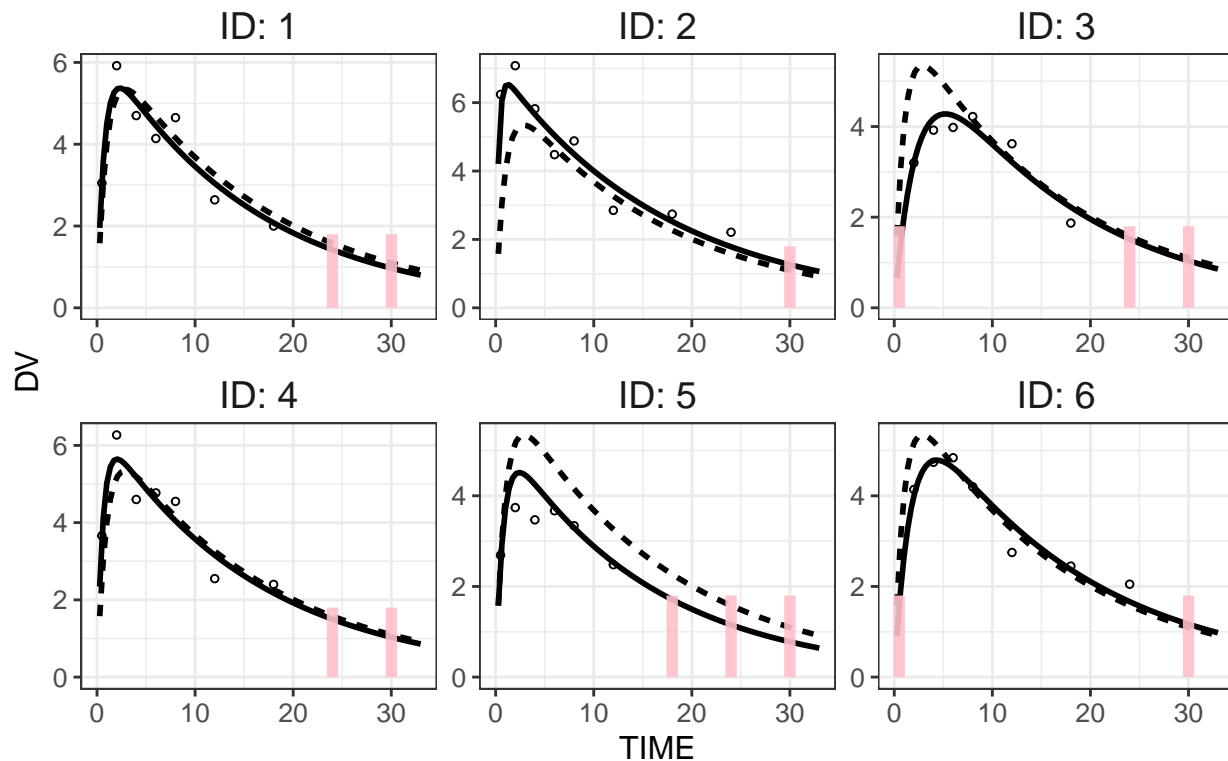


2.2 Interval censored data

```
mlx_file <- "/home/agstudy/Downloads/2.2.censored_data/censoring1_project.mlxtran"  
ctr <- pmx_mlxtran(file_name=mlx_file)
```

```
## Warning: Removed 100 rows containing missing values (geom_point).
```

Individual fits



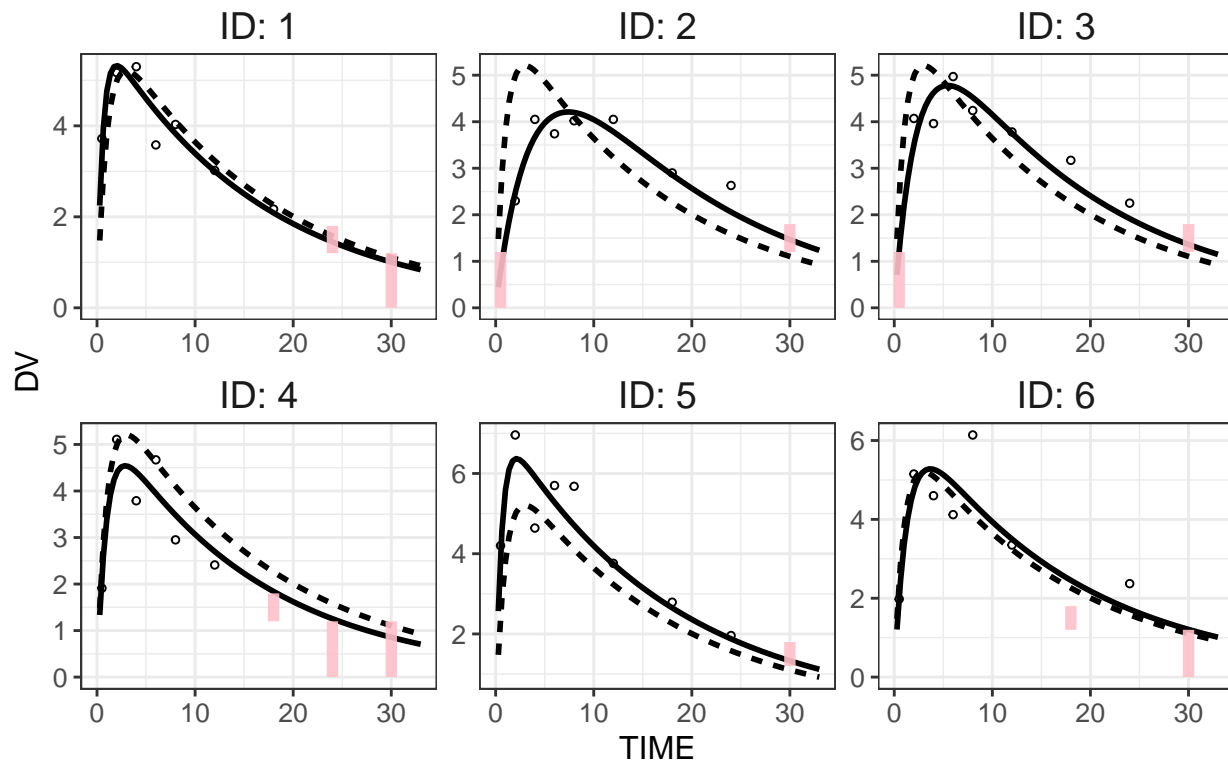
3 PK data below a lower limit of quantification or below a limit of detection

```
mlx_file <- "/home/agstudy/Downloads/2.2.censored_data/censoring2_project.mlxtran"
ctr <- pmx_mlxtran(file_name=mlx_file)
```

```
ctr %>% pmx_plot_individual(
  is.draft = FALSE,
  facets=list(ncol=3,nrow=2),
  bloq=pmx_bloq()
)
```

```
## Warning: Removed 100 rows containing missing values (geom_point).
```

Individual fits

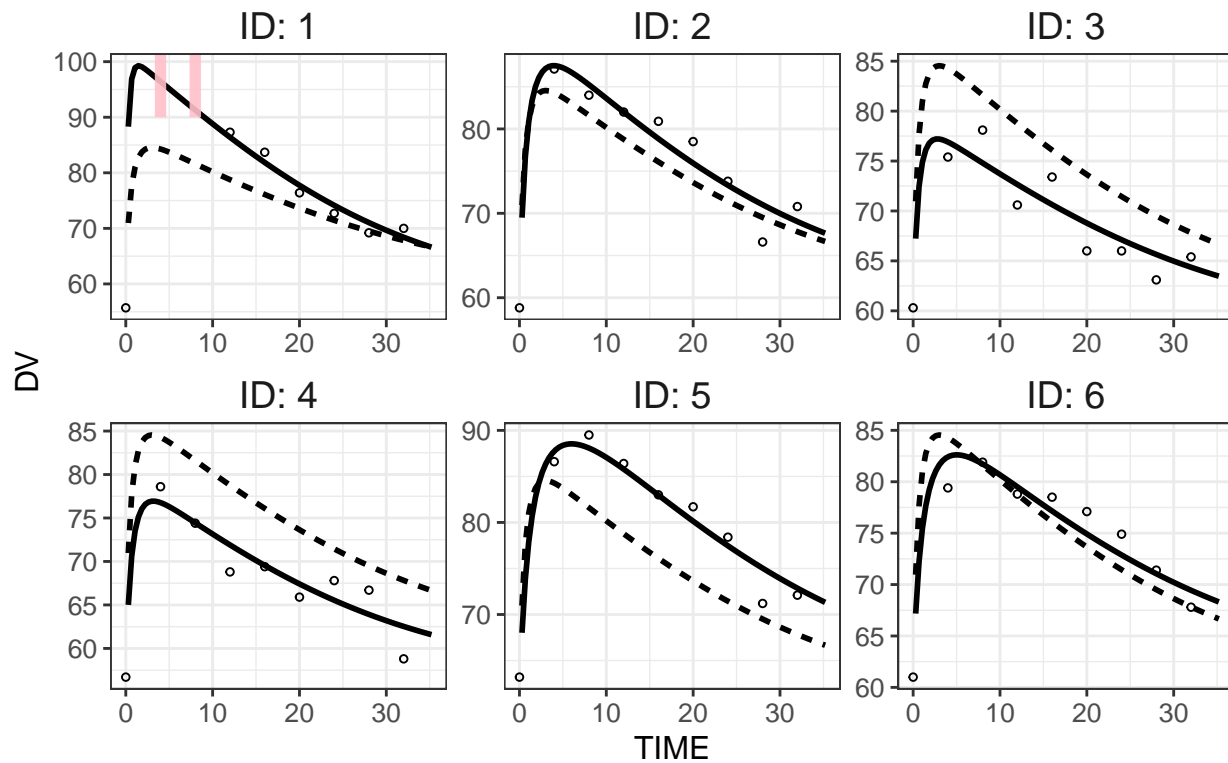


4 PK data below a lower limit of quantification and PD data above an upper limit of quantification

```
mlx_file <- "/home/agstudy/Downloads/2.2.censored_data/censoring3_project.mlxtran"  
ctr <- pmx_mlxtran(file_name=mlx_file,endpoint="2")
```

```
ctr %>% pmx_plot_individual(  
  is.draft = FALSE,  
  facets=list(ncol=3,nrow=2),  
  bloq=pmx_bloq()  
)
```

Individual fits



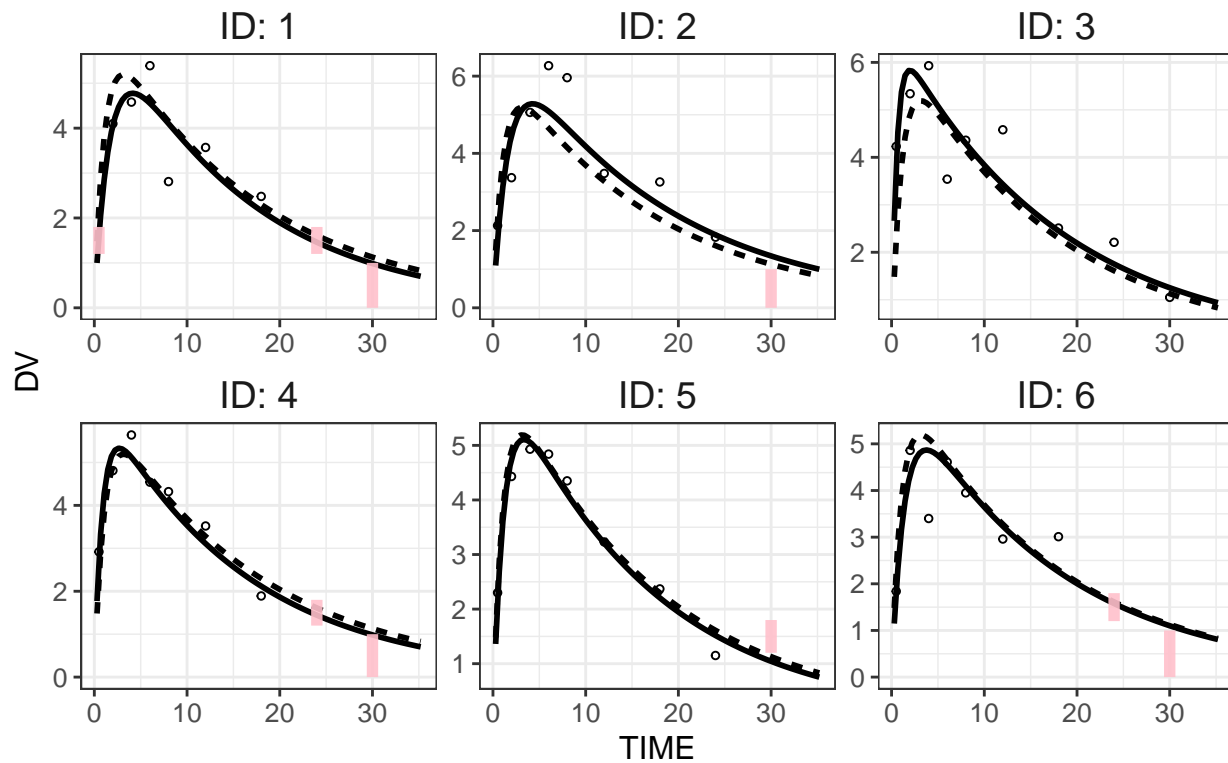
5 Combination of interval censored PK and PD data

5.1 Pk data

```
mlx_file <- "/home/agstudy/Downloads/2.2.censored_data/censoring4_project.mlxtran"
ctr <- pmx_mlxtran(file_name=mlx_file,endpoint="1")
```

```
ctr %>% pmx_plot_individual(
  is.draft = FALSE,
  facets=list(ncol=3,nrow=2),
  bloq=pmx_bloq()
)
```


Individual fits



5.2 PD data

```
mlx_file <- "/home/agstudy/Downloads/2.2.censored_data/censoring4_project.mlxtran"
ctr <- pmx_mlxtran(file_name=mlx_file,endpoint="2")
```

```
ctr %>% pmx_plot_individual(
  is.draft = FALSE,
  facets=list(ncol=3,nrow=2),
  bloq=pmx_bloq()
)
```

Individual fits

