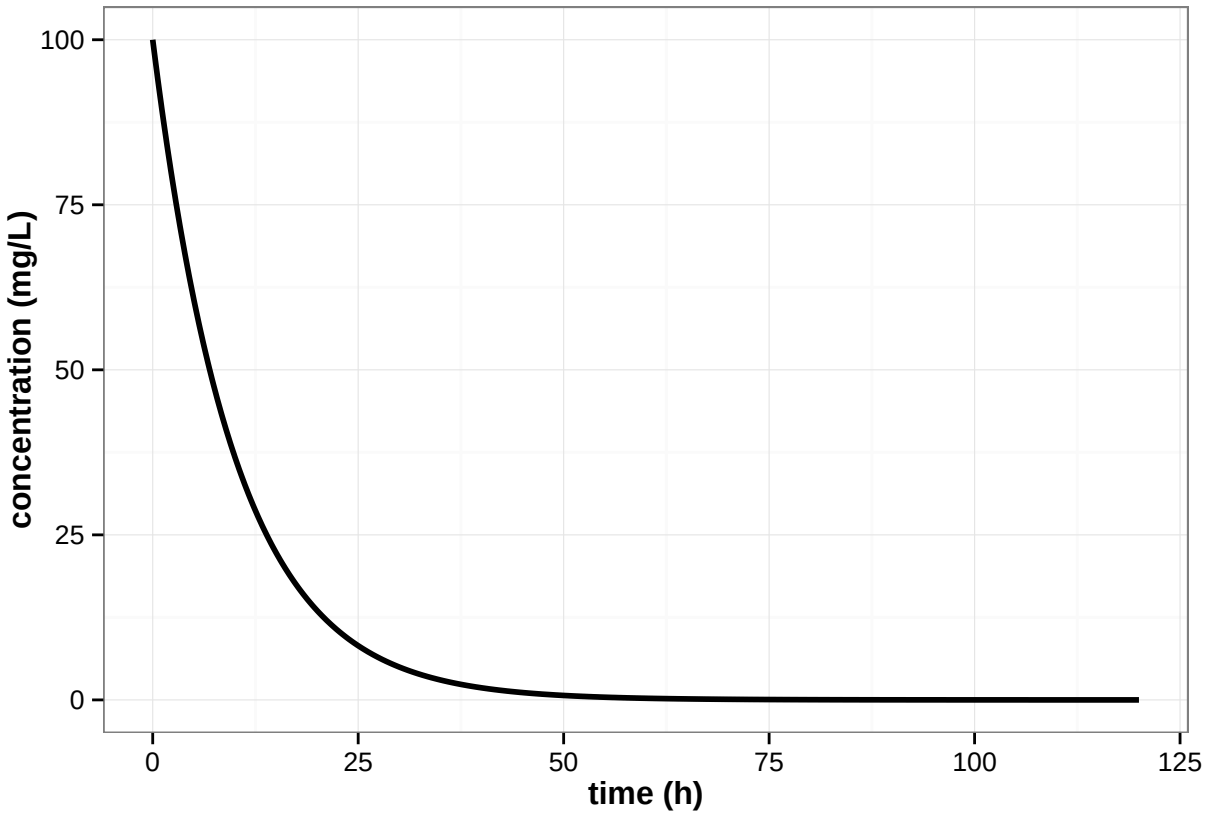
```r
# required libraries
library("PKPDmisc")
library("ggplot2")
library("mlxR")
library("reshape2")
library("knitr")
library("dplyr")
```

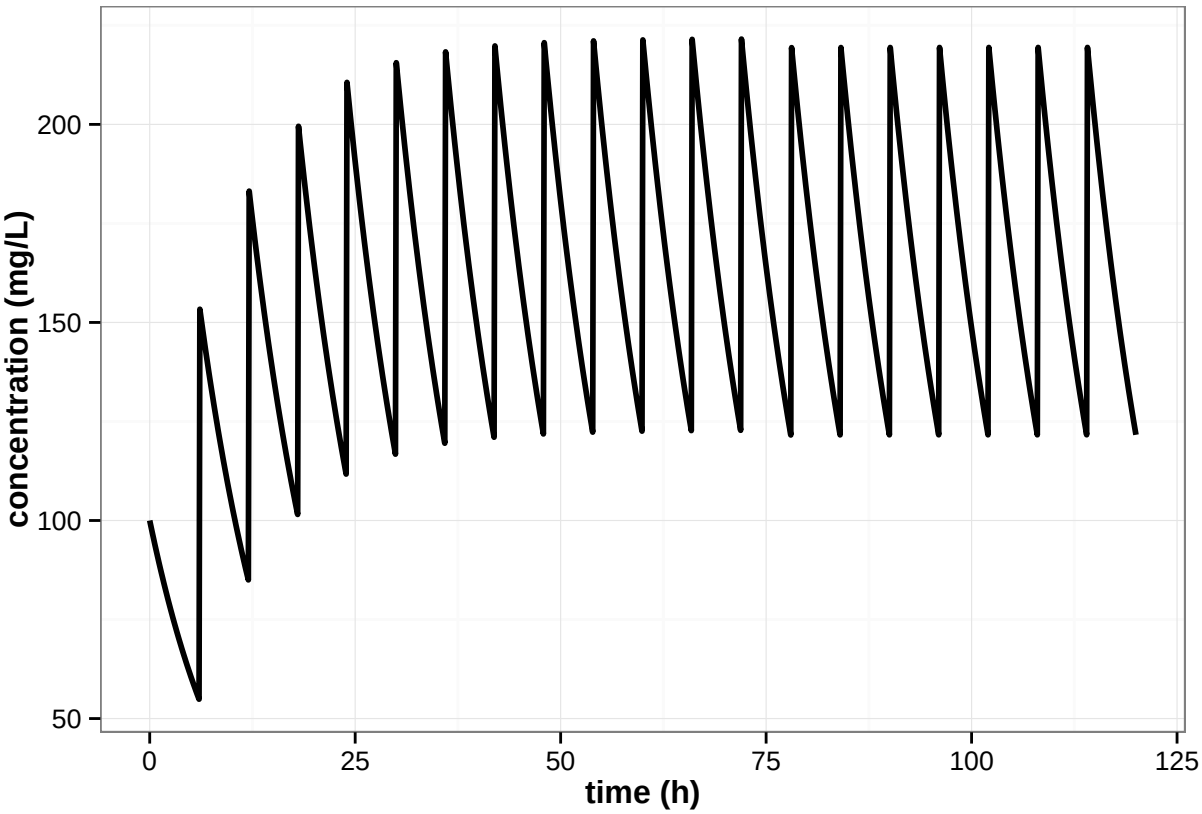
```
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
##     filter, lag
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
knitr::opts_chunk$set(echo=FALSE)
```

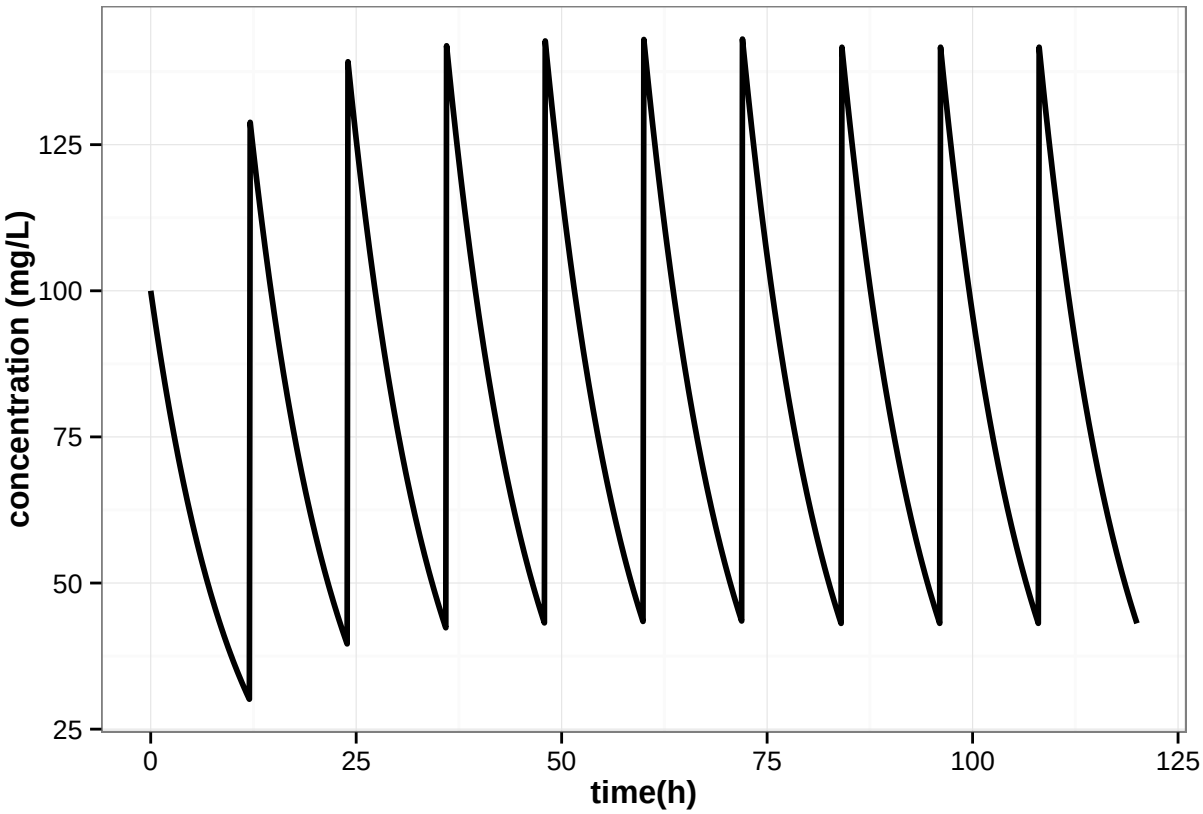
1. pk profile of 100 mg iv bolus (sd), CL = 0.1 L/hr, V = 1 L



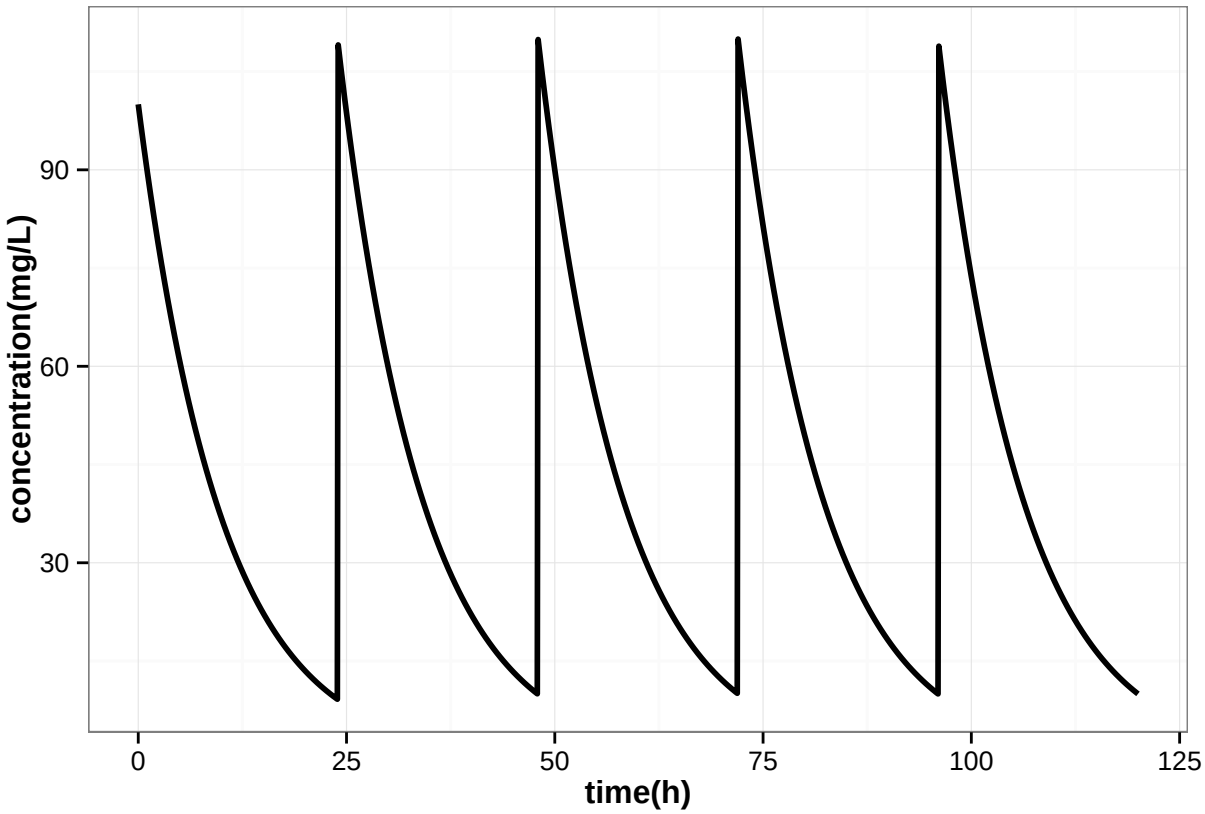
2. pk profile of 100 mg iv bolus, ld (t = 0), md (q= 6 hr), cl = 0.1 L/hr, v = 1 L



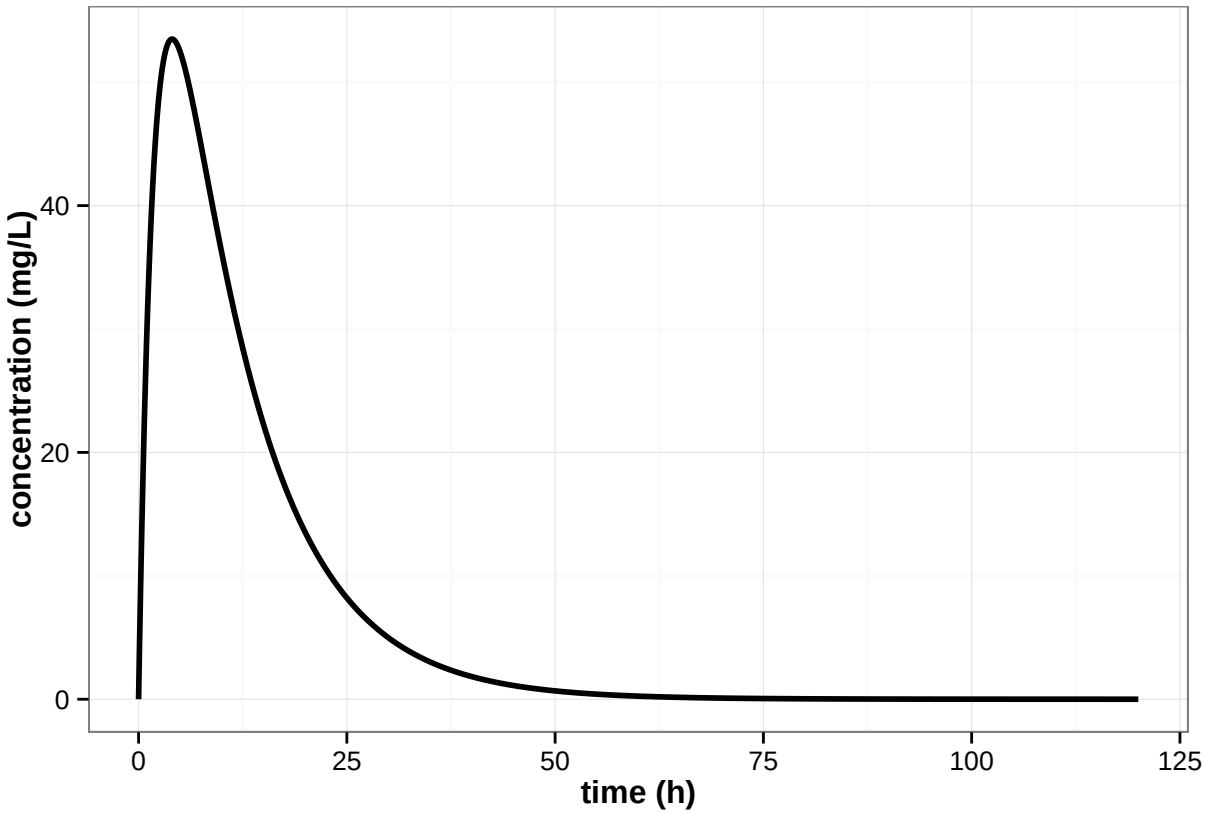
3. pk profile of 100 mg iv bolus, ld (t=0), md (q=12 hr), cl =0.1 l/hr, v = 1l



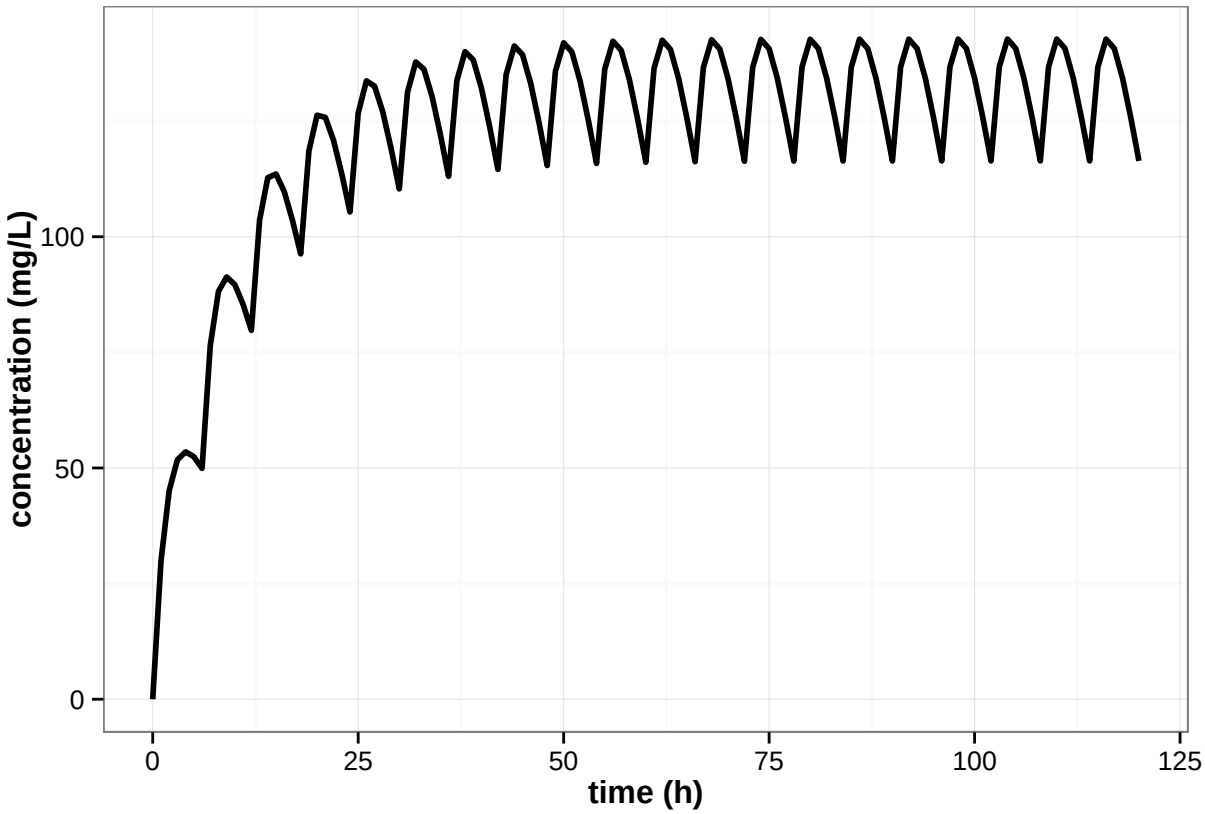
4. pk profile of 100 mg iv bolus, ld (t=0), md (q=24 hr), cl=0.1 l/hr, v=1l



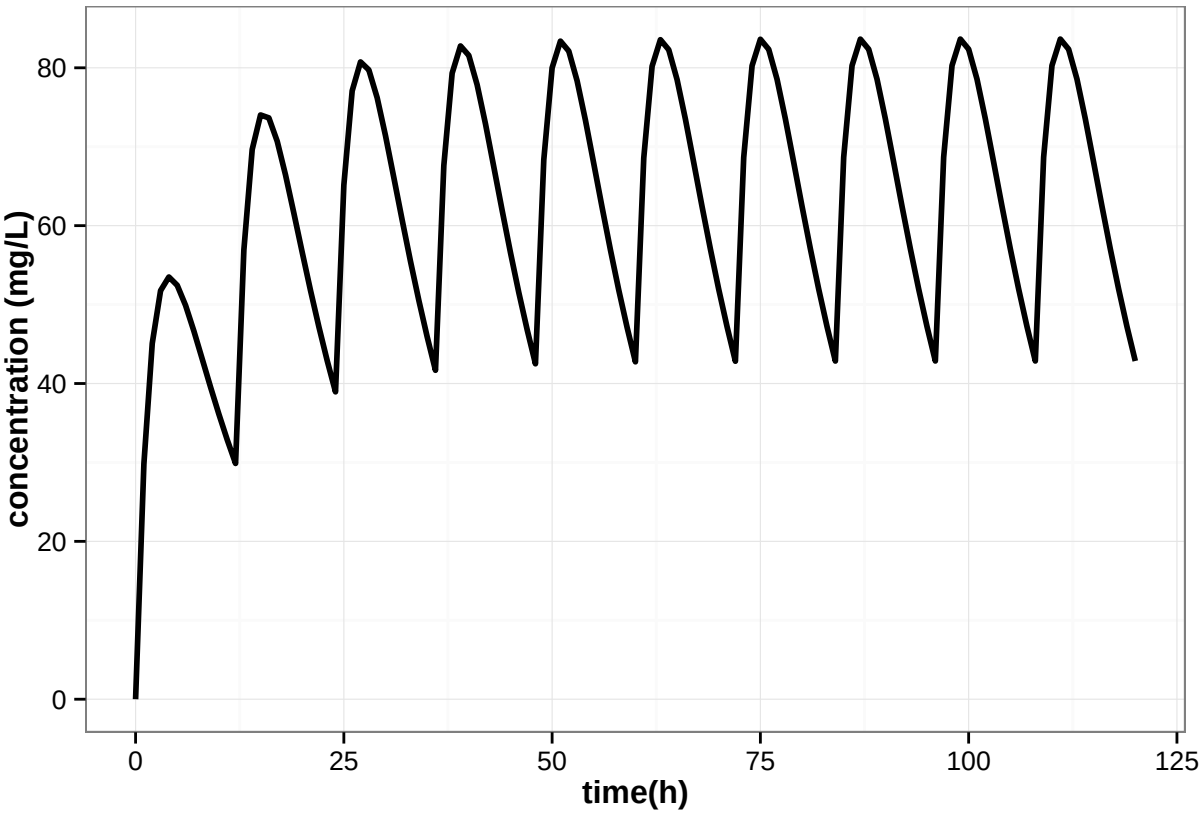
5. pk profile of 100 mg oral (sd), Cl = 0.1 L/hr, V = 1 L, ka = 0.5/hr, F = 0.8



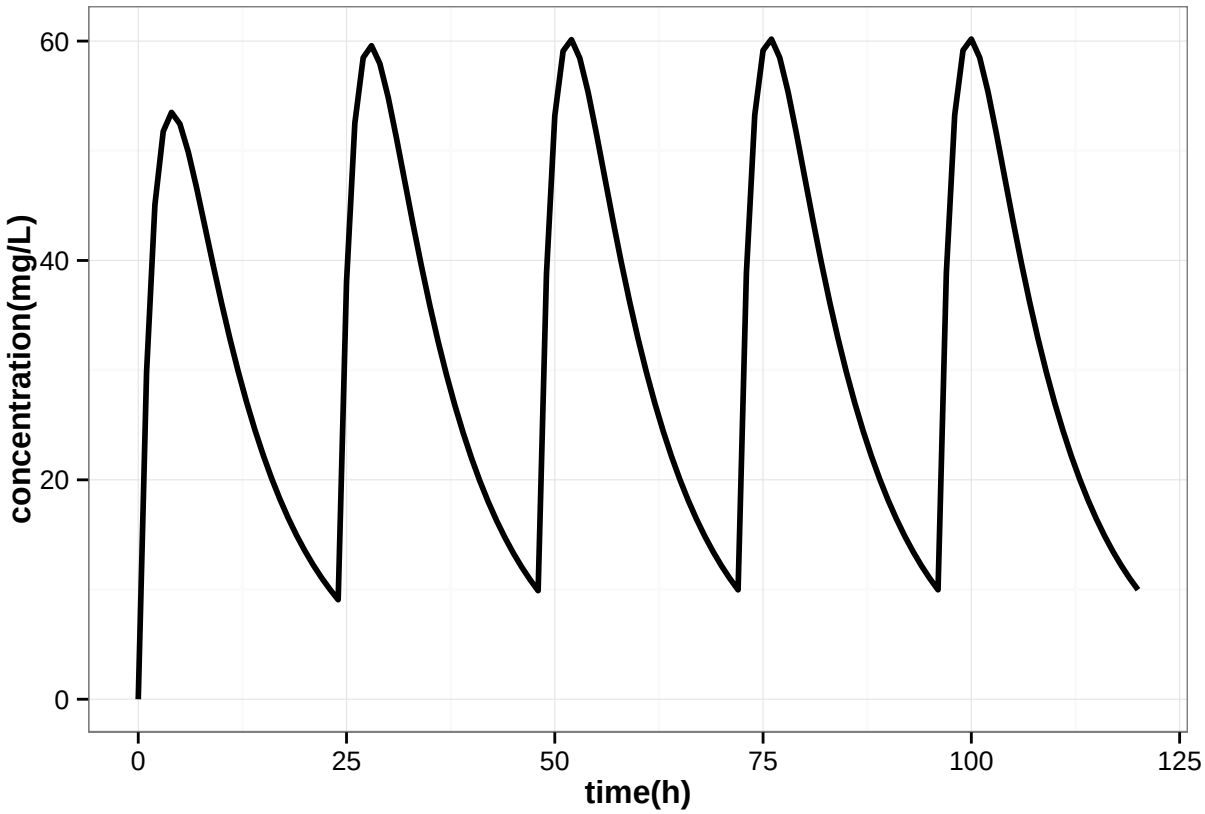
6. pk profile of 100 mg oral, ld (t=0), md (q= 6 hr), Cl = 0.1 L/hr, V = 1 L, ka = 0.5/hr, F = 0.8



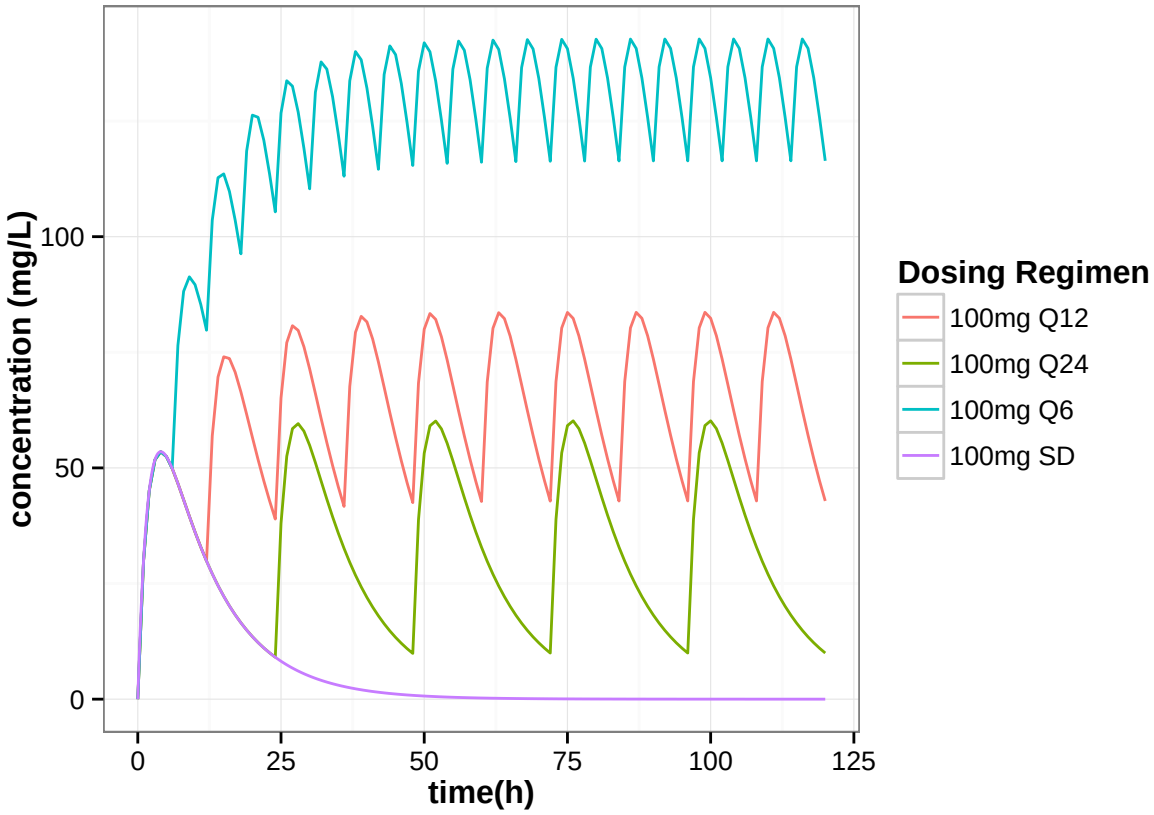
7. pk profile of 100 mg oral, ld (t=0), md (q=12 hr), cl=0.1 l/hr, v=1l, ka=0.5/hr, f=0.8



8. pk profile of 100 mg oral, ld (t=0), md (q=24 hr), cl = 0.1 l/hr, v=1l, ka=0.5/hr, f=0.8



9. Overlay plots - oral



10. Overlay plots - iv