

```
my_packages <- c('kableExtra', 'readxl', 'readr', 'knitr', 'tidyverse')
pacman::p_load(char = my_packages)
```

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet='16', range="B2:D12") %>%
  kable()
```

Variable Name	Situation	Meaning
ID	At all time	NM-TRAN infers that the data are population
DV	At all time	Dependent Variable (Observation to be fitted)
MDV	At all time	Missing data variable (MDV = 1)
TIME	PREDPP	Time
AMT	PREDPP	Dosing amount
RATE	PREDPP	Dosing rate (infusion) - amount dosed during unit time
ADDL	PREDPP	Number of additional doses just like initial dose
II	PREDPP	Interdose interval (Used with ADDL)
SS	PREDPP	Steady-state dose (55=1)
CMT	PREDPP	Compartment

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet='22', range="B2:H6") %>%
  mutate(Description = gsub("\r\n", "<br/>", Description)) %>%
  kable(format='markdown')
```

TIME	AMT	RATE	ADDL	ss	II	Description
8	10	.	3	3	8	Non steady state, 10mg bolus at 8hr, 3 additional dose every 8hr
8	10	10	3	3	8	Non steady state, 10mg infusion for 1hr at 8hr, 3 additional dose every 8hr
64	10	.	3	3	8	Steady state, 10mg bolus at 64hr, 3 additional dose every 8hr
64	10	10	3	3	8	Steady state, 10mg infusion for 1hr at 64hr 3 additional dose every 8hr

```
#kable(format = 'html')
```

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet='28', range="B2:E23") %>%
  kable()
```

ADVAN subroutine	TRANS subroutine	Required parameters	Select additional parameters
ADVAN1	TRANS1	K	S1, S2, F1, R1, D1, ALAG1
NA	TRANS2	CL, V	NA
ADVAN2	TRANS1	K, KA	S1, S2, S3, F1, F2, R1, R2, D1, I
NA	TRANS2	CL, V, KA	NA
ADVAN3	TRANS1	K, K12, K21	NA
NA	TRANS3	CL, V, Q, VSS	NA
NA	TRANS4	CL, V1, Q, V2	NA
NA	TRANS5	AOB, ALPHA, BETA	NA
NA	TRANS6	ALPHA, BETA, K21	NA
ADVAN4	TRANS1	K, K23, K, KA	S1, S2, S3, S4, F1, F2, F3, R1, F
NA	TRANS3	CL, V, Q, VSS, KA	NA
NA	TRANS4	CL, V2, Q, V3, KA	NA
NA	TRANS5	AOB, ALPHA, BETA, KA	NA
NA	TRANS6	ALPHA, BETA, K31, KA	NA
ADVAN10	TRANS1	VM, KM	S1, S2, F1, R1, D1, ALAG1
ADVAN11	TRANS1	K, K12, K21, K13, K31	S1, S2, S3, S4, F1, F2, F3, R1, F
NA	TRANS4	CL, V1, Q2, V2, Q3, V3	NA
NA	TRANS6	ALPHA, BETA, GAMMA, K21, K31	NA
ADVAN12	TRANS1	K, K23, K32, K24, K42, KA	S1, S2, S3, S4, S5, F1, F2, F3, F
NA	TRANS4	CL, V2, Q3, V3, Q4, V4, KA	NA
NA	TRANS6	ALPHA, BETA, GAMMA, K32, K42, KA	NA

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet='47', range="B2:D39") %>%
  kable()
```

```
## New names:
## * `` -> ...2
```

Alternative Parameters	...2	Reparameterization Lines
ADVAN1	TRANS2	NA
CL	Clearance	$K=CL/V$
V	Volume of distribution	NA
ADVAN2	TRANS2	NA
CL	Clearance	$K=CL/V$
V	Volume of distribution	$KA=KA$
KA	Absorption rate	NA
ADVAN3	TRANS3	NA
CL	Clearance	$K=CL/V$
V	Central Volume	$K12=Q/V$
Q	Intercompartmental clearance	$K21=Q/(VSS-V)$
VSS	Volume of distribution at steady state	NA
ADVAN3	TRANS4	NA
CL	Clearance	$K=CL/V1$
V1	Central Volume	$K12=Q/V1$
Q	Intercompartmental clearance	$K21=Q/V2$
V2	Peripheral volume	NA
ADVAN3	TRANS5	NA
AOB	A/B	$K21=(AOB*BETA+ALPHA)/(AOB+1)$
ALPHA	alpha	$K=ALPHA*BETA/K21$
BETA	beta	$K12=ALPHA+BETA-K21-K$
ADVAN3	TRANS6	NA
ALPHA	alpha	$K=ALPHA*BETA/K21$
BETA	beta	$K12=ALPHA+BETA-K21-K$
K21	Rate constant from periph. to central	$K21=K21$
ADVAN4	TRANS3	NA
CL	Clearance	$K=CL/V$
V	Central Volume	$K23=Q/V$
Q	Intercompartmental clearance	$K32=Q/(VSS-V)$
VSS	Volume of distribution at steady state	$KA=KA$
KA	Absorption rate	NA
ADVAN4	TRANS4	NA
CL	Clearance	$K=CL/V2$
V2	Central Volume	$K23=Q/V2$
Q	Intercompartmental clearance	$K32=Q/V3$
V3	Peripheral volume	$KA=KA$
KA	Absorption rate	NA

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet="50", range="B2:E36") %>%
  kable()
```

```
## New names:
## * `` -> ...4
```

ADVAN	Compartments	Basic and additional PK parameters	...4
ADVAN1	1 = Central	K	Rate constant of elimination
NA	2 = Output	S1	Scale for central compartment
NA	NA	S2	Scale for output compartment
NA	NA	F1	Bioavailability for central compartment
NA	NA	F0	Output Fraction
ADVAN2	1 = Depot	KA	Absorption rate constant
NA	2 = Central	K	Rate constant of elimination
NA	3 = Output	S1	Scale for depot compartment
NA	NA	S2	Scale for central compartment
NA	NA	S3	Scale for output compartment
NA	NA	F1	Bioavailability for depot compartment
NA	NA	F2	Bioavailability for central compartment
NA	NA	F0	Output Fraction
ADVAN3	1 = Central	K	Rate constant of elimination
NA	2 = Peripheral	K12	Rate constant from central to peripheral
NA	3 = Output	K21	Rate constant from peripheral to central
NA	NA	S1	Scale for central compartment
NA	NA	S2	Scale for peripheral compartment
NA	NA	S3	Scale for output compartment
NA	NA	F1	Bioavailability for central compartment
NA	NA	F2	Bioavailability for peripheral compartment
NA	NA	F0	Output Fraction
ADVAN4	1 = Depot	KA	Absorption rate constant
NA	2 = Central	K	Rate constant of elimination
NA	3 = Peripheral	K23	Rate constant from central to Peripheral
NA	4 = Output	K32	Rate constant from peripheral to central
NA	NA	S1	Scale for depot compartment
NA	NA	S2	Scale for central compartment
NA	NA	S3	Scale for Peripheral compartment
NA	NA	S4	Scale for output compartment
NA	NA	F1	Bioavailability for depot compartment
NA	NA	F2	Bioavailability for central compartment
NA	NA	F3	Bioavailability for Peripheral compartment
NA	NA	F0	Output Fraction

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet="71", range="B2:F20") %>%
  kable()
```

```
## Warning in read_fun(path = enc2native(normalizePath(path))), sheet_i = sheet, :
## Expecting numeric in D19 / R19C4: got a date

## Warning in read_fun(path = enc2native(normalizePath(path))), sheet_i = sheet, :
## Expecting numeric in D20 / R20C4: got a date

## New names:
## * `` -> ...2
## * `` -> ...3
## * `` -> ...4
## * `` -> ...5
```

i	...2	...3	...4	...5
NA	NA	NA	NA	NA
Starting Value: 0.70	NA	NA	NA	NA
1	0.70	-13.19	22.16	NA
2	1.30	17.85	52.24	NA
3	0.95	-2.72	56.64	NA
4	1.00	0.09	60.09	NA
Starting Value: 1.60	NA	NA	NA	NA
1	1.60	25.80	-7.68	4.96
2	4.96	16956.16	25498.56	4.30
3	4.30	5419.61	10714.92	3.79
4	3.79	1696.52	4601.51	3.42
5	3.42	507.53	2070.60	3.18
6	3.18	135.68	1036.75	3.04
7	3.04	26.45	649.51	3.00
8	3.00	2.08	548.97	3.00
9	3.00	0.02	540.07	3.00
10	3.00	0.00	540.00	3.00
11	3.00	0.00	540.00	3.00

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet="112", range="B2:E7") %>%
  kable()
```

```
## New names:
## * `` -> ...3
## * `` -> ...4
```

Δ No. of parameter	Δ -2LL by p-value	...3	...4
NA	p = 0.05	p = 0.01	p = 0.001
1	3.84	6.63	10.8
2	5.99	9.2100000000000009	13.8
3	7.81	11.3	16.3
4	9.49	13.3	18.5

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet="125", range="B2:C6") %>%
  kable()
```

Δ Parameters	Δ -2LL
1	3.84
2	5.99
3	7.81
4	9.49

```
readxl::read_excel("data-raw/fig-tab.xlsx", sheet="187", range="B2:F6") %>%
  kable()
```

```
## New names:
## * `` -> ...1
```

...1	PK-PD 연결 방법	PK data	Population PK parameter	In
Simultaneous PK-PD analysis	SIM (Simultaneous)	O	Estimate	E
Sequential PK-PD analysis	PPP&D (Population PK Parameter & Data)	O	Fix	E
NA	PPP (Population PK Parameters)	X	Fix	E
NA	IPP (Individual PK Parameters)	X	- (not considered)	F

```
read_csv('../assets/media-13/tab1.csv') %>%
  rename(`Fitted  $\hat{Y}_i$ ` = 3) %>%
  kable(booktabs=TRUE, escape=FALSE) %>%
```

```
kable_styling("striped") %>%
add_header_above(c(" " = 1, "Plot of i Versus" = 3))

## Parsed with column specification:
## cols(
##   `Unsatisfactory Plot` = col_character(),
##   `Time order` = col_character(),
##   `Fitted <U+0176>i` = col_character(),
##   `Xji Values` = col_character()
## )

## Warning in env_bind_impl(env, dots$named): unable to translate 'Fitted
## <U+0176>i' to native encoding
```

Unsatisfactory Plot	Time order	Fitted \hat{Y}_i
Funnel indicating nonconstant variance	Use weighted least squares	Use weighted least squares
Ascending or descending band	Consider adding first-order term in time	Error in analysis or wrong model
Curved band	Consider adding first- and second- order terms in time	Consider adding extra terms