

# Pumas.jl Workshop Solutions

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## 1 Problem 1: Simulate a first-order absorption model with linear elimination after a 100 mg oral dose in 24 subjects

Parameters are:  $K_a = 1 \text{ hr}^{-1}$ ,  $CL = 1 \text{ L/hr}$ ,  $V = 20 \text{ L/hr}$ .

### 1.1 Part 1: Setup the population

```
using Pumas, Plots, CSV, Random
Random.seed!(0)
```

```
Random.MersenneTwister(UInt32[0x00000000], Random.DSFMT.DSFMT_state{Int32}[7
48398797, 1073523691, -1738140313, 1073664641, -1492392947, 1073490074, -16
25281839, 1073254801, 1875112882, 1073717145 ... 943540191, 1073626624, 109
1647724, 1073372234, -1273625233, -823628301, 835224507, 991807863, 382, 0]
), [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0 ... 0.0, 0.0, 0.0, 0.0
, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0], UInt128[0x00000000000000000000000000000000
, 0x00000000000000000000000000000000, 0x00000000000000000000000000000000, 0
x00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x00
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x00000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x000000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x00000000
00000000000000000000000000000000 ... 0x00000000000000000000000000000000, 0x000000000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x000000000000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x000000000000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x000000000000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x000000000000
00000000000000000000000000000000, 0x00000000000000000000000000000000, 0x000000000000
000000000000], 1002, 0)
```

```
single_dose_regimen = DosageRegimen(100, time=0)
first(single_dose_regimen.data)
```

	time	cmt	amt	evid	ii	addl	rate	duration	ss
	Float64	Int64	Float64	Int8	Float64	Int64	Float64	Float64	Int8
1	0.0	1	100.0	1	0.0	0	0.0	0.0	0

to build a single subject

```
s1 = Subject(id=1, evs=single_dose_regimen, cvs=(Wt=70,))
```

```
Subject
  ID: 1
  Events: 1
  Covariates: (Wt = 70,)
```

let's first define a function to choose body weight randomly

```
choose_covariates() = (Wt = rand(55:80),)
```

```
choose_covariates (generic function with 1 method)
```

Then, we use generate a population of subjects with a random weight generated from the covariate function above

```
pop = Population(map(i -> Subject(id = i, evs = single_dose_regimen, cvs =
choose_covariates()), 1:24))
```

```
Population
  Subjects: 24
  Covariates: Wt
```

You can view the generated population using by calling a random subject by index and look at the subject's

- covariates
- events
- id numbers
- observations
- time

Let us us peek at the first subject's covariates

```
pop[1].covariates
(Wt = 55,)
```

## 1.2 Part 2: Write the model

```
mymodel = @model begin
  @param begin
    tvcl ∈ RealDomain(lower=0, init = 1.0)
    tvv ∈ RealDomain(lower=0, init = 20)
    tvka ∈ RealDomain(lower = 0, init= 1)
    Ω ∈ PDiagDomain(init=[0.09,0.09, 0.09])
    σ_prop ∈ RealDomain(lower=0,init=0.04)
  end

  @random begin
    η ~ MvNormal(Ω)
  end

  @pre begin
    CL = tvcl * (Wt/70)^0.75 * exp(η[1])
    V = tvv * (Wt/70) * exp(η[2])
```

```

    Ka = tvka * exp( $\eta$ [3])
end
@covariates Wt

@analytics Depots1Central1
  #@analytics begin
  #   Depot' = -Ka*Depot
  #   Central' = Ka*Depot - (CL/V)*Central
  #end

@derived begin
  cp = @. 1000*(Central / V)
  dv ~ @. Normal(cp, sqrt(cp^2* $\sigma$ _prop))
end
end

PumasModel
  Parameters: tvcl, tvv, tvka,  $\Omega$ ,  $\sigma$ _prop
  Random effects:  $\eta$ 
  Covariates: Wt
  Dynamical variables: Depot, Central
  Derived: cp, dv
  Observed: cp, dv

```

Note that above, we are using the analytical solution in `@analytics`. You can switch to using the differential equation system if you prefer.

### 1.3 Part 3: Simulate

Let's first extract the model parameters

```

param = init_param(mymodel)

(tvcl = 1.0, tvv = 20, tvka = 1,  $\Omega$  = PDMats.PDiagMat{Float64,Array{Float64,1}}(3, [0.09, 0.09, 0.09], [11.111111111111111, 11.111111111111111, 11.111111111111111]),  $\sigma$ _prop = 0.04)

```

Then using the `simobs` function, carry out the simulation and visualize the simulation output

```

obs = simobs(mymodel, pop, param, obstimes=0:1:72)
plot(obs)

```

where

- `mymodel` is the model setup in the Part 2,
- `pop` is the population of subjects that was setup in Part 1
- `param` is the specified set of model parameters
- `obstimes` specifies the simulation time period.

## 2 Problem 2: Perform Non-compartmental analysis

We will start by generating a dataframe of the results from the simulation step

```
simdf = DataFrame(obs)
first(simdf, 6)
```

	id	time	cp	dv	amt	evid	cmt	rate	Wt
	String	Int64	Float64	Float64	Float64	Int8	Int64	Float64	Int64
1	1	0	0.0	0.0	100.0	1	1	0.0	55
2	1	0	0.0	0.0	0.0	0		0.0	55
3	1	1	5993.99	6699.63	0.0	0		0.0	55
4	1	2	6866.37	6459.5	0.0	0		0.0	55
5	1	3	6662.28	7583.15	0.0	0		0.0	55
6	1	4	6253.33	6887.26	0.0	0		0.0	55

For the purpose of NCA, let us use the `cp` (output without residual error) as our observed value

To prepare the dataset for NCA analysis, let us use the `read_nca` function. The NCA datasets in Pumas requires a `route` specification which can either be `iv` or `ev`. Since this is an oral drug administration, lets add that to the `simdf`.

```
simdf[:, :route] .= "ev"
```

```
1776-element Array{String,1}:
```

```
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
⋮
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
"ev"
```

Next we can define time, concentration and dose units so the report includes the units for the pharmacokinetic parameters. The general syntax for units are `u` followed by the unit in quotes `"`.

```
timeu = u"hr"
concu = u"mg/L"
amtu = u"mg"
```

```
mg
```

```
nca_df = read_nca(simdf, id=:id, time=:time, conc=:cp, amt=:amt,
    route=:route, timeu=timeu, concu=concu, amtu=amtu, lloq=0.4concu)
```

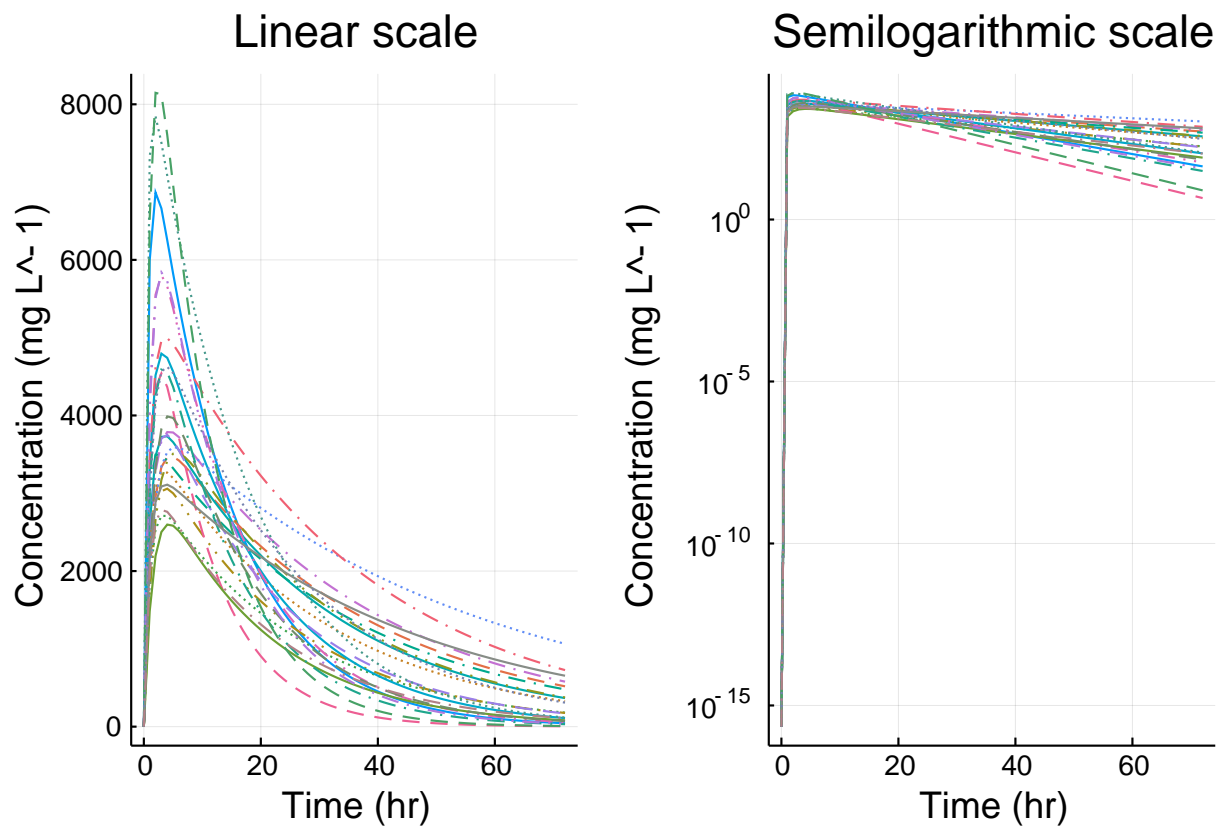
```
NCAPopulation (24 subjects):
```

```
ID: ["1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12", "13",
```

```
"14", "15", "16", "17", "18", "19", "20", "21", "22", "23", "24"]
concentration: mg L-1
time:         hr
auc:          mg hr L-1
aumc:         mg hr2 L-1
λz:           hr-1
dose:         mg
```

You can view the concentration-time plots by doing

```
plot(ncadf)
```



You can then generate `cmax` and `auc` for each subject

```
auc = NCA.auc(ncadf)
```

	id	auc
	String	Unitful...
1	1	108523.0 mg hr L <sup>-1</sup>
2	2	1.37362e5 mg hr L <sup>-1</sup>
3	3	77472.5 mg hr L <sup>-1</sup>
4	4	1.51225e5 mg hr L <sup>-1</sup>
5	5	84021.7 mg hr L <sup>-1</sup>
6	6	1.2242e5 mg hr L <sup>-1</sup>
7	7	59389.0 mg hr L <sup>-1</sup>
8	8	1.07756e5 mg hr L <sup>-1</sup>
9	9	130008.0 mg hr L <sup>-1</sup>
10	10	1.22717e5 mg hr L <sup>-1</sup>
11	11	1.02494e5 mg hr L <sup>-1</sup>
12	12	96274.4 mg hr L <sup>-1</sup>
13	13	2.12502e5 mg hr L <sup>-1</sup>
14	14	1.93418e5 mg hr L <sup>-1</sup>
15	15	1.04152e5 mg hr L <sup>-1</sup>
16	16	61961.3 mg hr L <sup>-1</sup>
17	17	84879.5 mg hr L <sup>-1</sup>
18	18	1.43681e5 mg hr L <sup>-1</sup>
19	19	79255.8 mg hr L <sup>-1</sup>
20	20	98306.3 mg hr L <sup>-1</sup>
21	21	1.46144e5 mg hr L <sup>-1</sup>
22	22	1.03207e5 mg hr L <sup>-1</sup>
23	23	1.33058e5 mg hr L <sup>-1</sup>
24	24	67737.9 mg hr L <sup>-1</sup>

`cmax` = `NCA.cmax(ncadf)`

	id	cmax
	String	Unitful...
1	1	6866.37 mg L <sup>-1</sup>
2	2	3469.66 mg L <sup>-1</sup>
3	3	2710.07 mg L <sup>-1</sup>
4	4	3786.48 mg L <sup>-1</sup>
5	5	3059.08 mg L <sup>-1</sup>
6	6	3733.26 mg L <sup>-1</sup>
7	7	4540.05 mg L <sup>-1</sup>
8	8	3265.54 mg L <sup>-1</sup>
9	9	3496.55 mg L <sup>-1</sup>
10	10	3511.88 mg L <sup>-1</sup>
11	11	4795.13 mg L <sup>-1</sup>
12	12	3749.97 mg L <sup>-1</sup>
13	13	3590.13 mg L <sup>-1</sup>
14	14	4993.79 mg L <sup>-1</sup>
15	15	5804.5 mg L <sup>-1</sup>
16	16	2597.4 mg L <sup>-1</sup>
17	17	3987.81 mg L <sup>-1</sup>
18	18	7845.09 mg L <sup>-1</sup>
19	19	4590.03 mg L <sup>-1</sup>
20	20	5839.47 mg L <sup>-1</sup>
21	21	3110.65 mg L <sup>-1</sup>
22	22	8147.68 mg L <sup>-1</sup>
23	23	4624.67 mg L <sup>-1</sup>
24	24	2785.83 mg L <sup>-1</sup>

Or generate the entire NCA report using

```
report = NCAReport(ncadf)
report = NCA.to_dataframe(report)
first(report,6)
```

	id	doseamt	lambda_z	half_life	tmax	tlag	cmax	clast
	String	Unitful...	Unitful...	Unitful...	Unitful...	Unitful...	Unitful...	Unitful...
1	1	100.0 mg	0.0730531 hr <sup>-1</sup>	9.48826 hr	2 hr	0 hr	6866.37 mg L <sup>-1</sup>	43.6488 m
2	2	100.0 mg	0.028807 hr <sup>-1</sup>	24.0618 hr	5 hr	0 hr	3469.66 mg L <sup>-1</sup>	518.298 m
3	3	100.0 mg	0.0402099 hr <sup>-1</sup>	17.2382 hr	3 hr	0 hr	2710.07 mg L <sup>-1</sup>	180.311 m
4	4	100.0 mg	0.0283742 hr <sup>-1</sup>	24.4288 hr	4 hr	0 hr	3786.48 mg L <sup>-1</sup>	578.314 m
5	5	100.0 mg	0.0426007 hr <sup>-1</sup>	16.2708 hr	4 hr	0 hr	3059.08 mg L <sup>-1</sup>	176.002 m
6	6	100.0 mg	0.0344511 hr <sup>-1</sup>	20.1197 hr	4 hr	0 hr	3733.26 mg L <sup>-1</sup>	366.833 m

### 3 Problem 3: Estimate using Non-linear mixed effects

We can use the simulated dataset in the Problem 1 for our estimation. We need a couple of data manipulation steps

1. missing `cmt` should be converted to 2 to reflect central compartment
2. data rows where `time` = 0, and `cp`=0 should be removed

```
simdf.cmt = ifelse.(ismissing.(simdf.cmt), 2, simdf.cmt)
est_df = simdf[!((simdf.dv == 0.0) & (simdf.cmt == 2)),:]
first(est_df,6)
```

	id	time	cp	dv	amt	evid	cmt	rate	Wt	route
	String	Int64	Float64	Float64	Float64	Int8	Int64	Float64	Int64	String
1	1	0	0.0	0.0	100.0	1	1	0.0	55	ev
2	1	1	5993.99	6699.63	0.0	0	2	0.0	55	ev
3	1	2	6866.37	6459.5	0.0	0	2	0.0	55	ev
4	1	3	6662.28	7583.15	0.0	0	2	0.0	55	ev
5	1	4	6253.33	6887.26	0.0	0	2	0.0	55	ev
6	1	5	5825.83	5759.5	0.0	0	2	0.0	55	ev

### 3.1 Part 1: Read datasets for NLME estimation

We can use the `read_pumas` function to prepare the dataset for NLME estimation

```
data = read_pumas(est_df ,cvs = [:Wt], dvs=[:dv])
```

```
Population
Subjects: 24
Covariates: Wt
Observables: dv
```

where

- `cvs` takes an array of covariates
- `dvs` takes an array of the dependent variables
- since the dataframe has `time` as the variable, the function does not need a specific input

### 3.2 Part 2: Perform a model fit

We now use the

- `mymodel` model that we wrote earlier
- the set of parameters specified in `param` as initial estimates
- `data` that was read in using the `read_pumas` function

to fit the model.

```
res = fit(mymodel,data,param,Pumas.FOCEI())
```

```
FittedPumasModel
```

```
Successful minimization: true
```

```
Likelihood approximation: Pumas.FOCEI
Deviance: 19742.767
```



```
Total number of observation records: 1728
Number of active observation records: 1728
Number of subjects: 24
```

```
-----
              Estimate
-----
tvcl      0.95056
tvv       20.923
tvka      0.8943
 $\Omega_{1,1}$     0.11207
 $\Omega_{2,2}$     0.08522
 $\Omega_{3,3}$     0.1822
 $\sigma_{prop}$   0.042688
-----
```

### 3.3 Part 3: Infer the results

infer provides the model inference

```
infer(res)
```

```
Calculating: variance-covariance matrix. Done.
FittedPumasModelInference
```

```
Successful minimization: true
```

```
Likelihood approximation: Pumas.FOCEI
Deviance: 19742.767
Total number of observation records: 1728
Number of active observation records: 1728
Number of subjects: 24
```

```
-----
              Estimate      RSE      95.0% C.I.
-----
tvcl      0.95056      6.8651    [ 0.82266 ; 1.0785 ]
tvv       20.923      6.0007    [18.462   ; 23.384   ]
tvka      0.8943     10.371    [ 0.71253 ; 1.0761   ]
 $\Omega_{1,1}$     0.11207     28.011    [ 0.050543; 0.1736   ]
 $\Omega_{2,2}$     0.08522     29.941    [ 0.03521 ; 0.13523   ]
 $\Omega_{3,3}$     0.1822      35.976    [ 0.053727; 0.31067   ]
 $\sigma_{prop}$   0.042688      3.2558    [ 0.039964; 0.045412 ]
-----
```

### 3.4 Part 4: Inspect the results

inspect gives you the

- model predictions
- residuals
- Empirical Bayes estimates

```
preds = DataFrame(predict(res))
first(preds, 6)
```

	id	time	Wt	dv_pred	dv_ipred	pred_approx
	String	Float64	Int64	Float64	Float64	Pumas...
1	1	1.0	55	3251.17	5535.34	FOCEI()
2	1	2.0	55	4842.08	6469.77	FOCEI()
3	1	3.0	55	5289.64	6334.61	FOCEI()
4	1	4.0	55	5288.21	5969.44	FOCEI()
5	1	5.0	55	5139.73	5572.61	FOCEI()
6	1	6.0	55	4948.98	5189.74	FOCEI()

```
resids = DataFrame(wresiduals(res))
first(resids, 6)
```

	id	time	Wt	dv_wres	dv_iwres	wres_approx
	String	Float64	Int64	Float64	Float64	Pumas...
1	1	1.0	55	1.57625	1.01804	FOCEI()
2	1	2.0	55	-0.346817	-0.00768109	FOCEI()
3	1	3.0	55	0.471787	0.95396	FOCEI()
4	1	4.0	55	0.0874083	0.744159	FOCEI()
5	1	5.0	55	-0.491189	0.162325	FOCEI()
6	1	6.0	55	-1.94495	-1.57674	FOCEI()

```
ebes = DataFrame(empirical_bayes(res))
first(ebes, 6)
```

	id	time	Wt	ebe_1	ebes_approx
	String	Float64	Int64	Array...	Pumas...
1	1	1.0	55	[0.178176, -0.221974, 0.4724]	FOCEI()
2	1	2.0	55	[0.178176, -0.221974, 0.4724]	FOCEI()
3	1	3.0	55	[0.178176, -0.221974, 0.4724]	FOCEI()
4	1	4.0	55	[0.178176, -0.221974, 0.4724]	FOCEI()
5	1	5.0	55	[0.178176, -0.221974, 0.4724]	FOCEI()
6	1	6.0	55	[0.178176, -0.221974, 0.4724]	FOCEI()

There is an `inspect` function that provides all the results at once

*Note that this function below fails to convert into a dataframe due to a bug. Will be fixed soon*

```
resout = DataFrame(inspect(res))
first(resout, 6)
```