

SAS CODE FOR IMPLEMENTING THE DK SELECTION MODEL AND THE LOCAL INFLUENCE
UNDER THE DK SELECTION MODEL
SAS VERSION: 9.5

1. SAS implementation:

The SAS code was applied to CD4 count measurement data (IMPI_29_2016.sas) from the IMPI trial.

2. Data structure:

The longitudinal data should be in a long format:

```
Data IMPI_2016;
input id sqcd4 transage art pred time;
CARDS;
1      15.26434      33      0      1      0
1      11.7047       33      0      1      1
1      15.52417      33      0      1      0.5
1      16.8226       33      1      1      3
1      18.02776      33      1      1      6
2      15.32971      32      0      1      0
2      14.79865      32      0      1      1
2      15.32971      32      0      1      0.5
2      21.56386      32      1      1      3
2      25.17936      32      1      1      6
.      .            .      .      .      .
```

RUN;

3. Data variables description:

Id: subject identification number.

sqcd4: square root of CD4 count.

transage: age of a subject.

art: anti-retroviral therapy.

```
pred: prednisolone
```

```
time: month
```

NB: other forms of variables can be added depending on the model to be fitted.

4. Create the design matrix for the covariates x and a vector for the response variable y :

```
Proc iml;
use IMPI_2016;
read all var {id sqcd4 transage art pred time} into data;
  id = data[,1];
  time = data[,6];
  treat = data[,5]; /*prednisolone*/
  timetreat =time#treat; /*prednisolone x time interaction*/
  art=data[,4];
  predart= treat#art; /*prednisolone x time interaction*/
  transage = data[,3];
  intercept=j(nrow(data),1,1);

create x var {intercept time treat timetreat art predart transage};
append;
  y = data[,2];
create y var {y};
append;
```

5. Now supply the number of subjects (nsub), number of time points (ntime), and initial values for parameter estimates and variance-covariance structure; eg,

```
/*initial values for parameter estimates*/
beta= 24.3408//0.4241//0.2943//0.02986//1.9891//-0.05294//-3.2065;

/*variance-covariance matrix*/
sigma11=27.5557;
sigma21=23.1566;
sigma22=29.7099;
sigma31=21.7018;
sigma32=22.8297;
sigma33=29.6190;
sigma41=17.7755;
sigma42=17.6218;
sigma43=20.0637;
```

```

sigma44=25.7221;
sigma51 = 18.4084;
sigma52 = 18.7202;
sigma53 = 20.3257;
sigma54 = 22.7242;
sigma55 = 26.2859;
v = j(5,5,1);
v[1,1] = sigma11;
v[1,2] = sigma21;
v[2,1] = sigma21;
v[2,2] = sigma22;
v[1,3] = sigma31;
v[3,1] = sigma31;
v[2,3] = sigma32;
v[3,2] = sigma32;
v[3,3] = sigma33;
v[1,4] = sigma41;
v[4,1] = sigma41;
v[2,4] = sigma42;
v[4,2] = sigma42;
v[3,4] = sigma43;
v[4,3] = sigma43;
v[4,4] = sigma44;
v[5,1] = sigma51;
v[1,5] = sigma51;
v[5,2] = sigma52;
v[2,5] = sigma52;
v[5,3] = sigma53;
v[3,5] = sigma53;
v[5,4] = sigma54;
v[4,5] = sigma54;
v[5,5] = sigma55;
u=root(v);
v2=t(u)*u;
uvec=colvec(u);
nozero=loc(uvec<>0);
uvec=uvec[nozero];
psi= 1; /*initial value for  $\psi_0$  in the dropout model*/
/*For  $\psi_0$ ,  $\psi_1$ , and  $\psi_2$ , initial values are provided in a vector form as [1:3]*/
This means that under MCAR, only  $\psi_0$  is required,  $\psi_0$  and  $\psi_1$  are required for MAR

```

```

        and  $\psi_0$ ,  $\psi_1$ , and  $\psi_2$  are required for NMAR.*/
        initial=beta//uvec//psi;
create initial var {initial};
append;
        nsub=137; /*number of subjects*/
        ntime=5; /*number of time points*/
create nsub var {nsub};
append;
create ntime var {ntime};
append;
quit;

```

The above information is then used to fit the DK selection the local influence models under MCAR, MAR, and NMAR mechanisms.