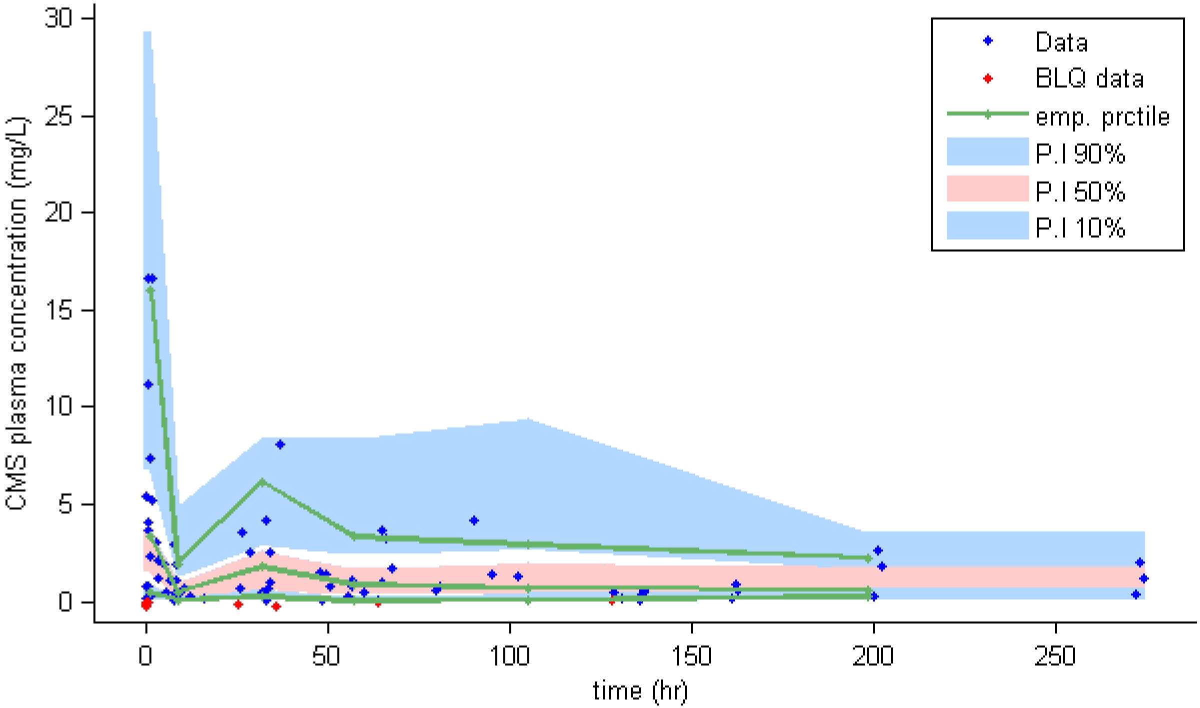
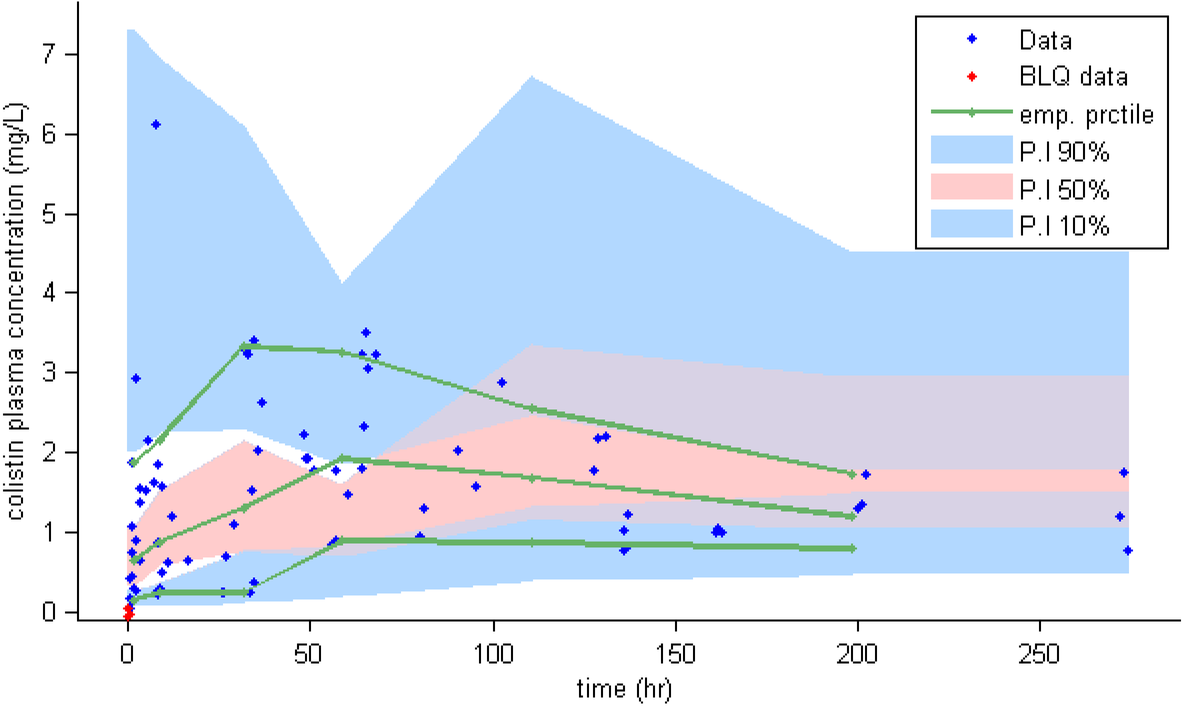
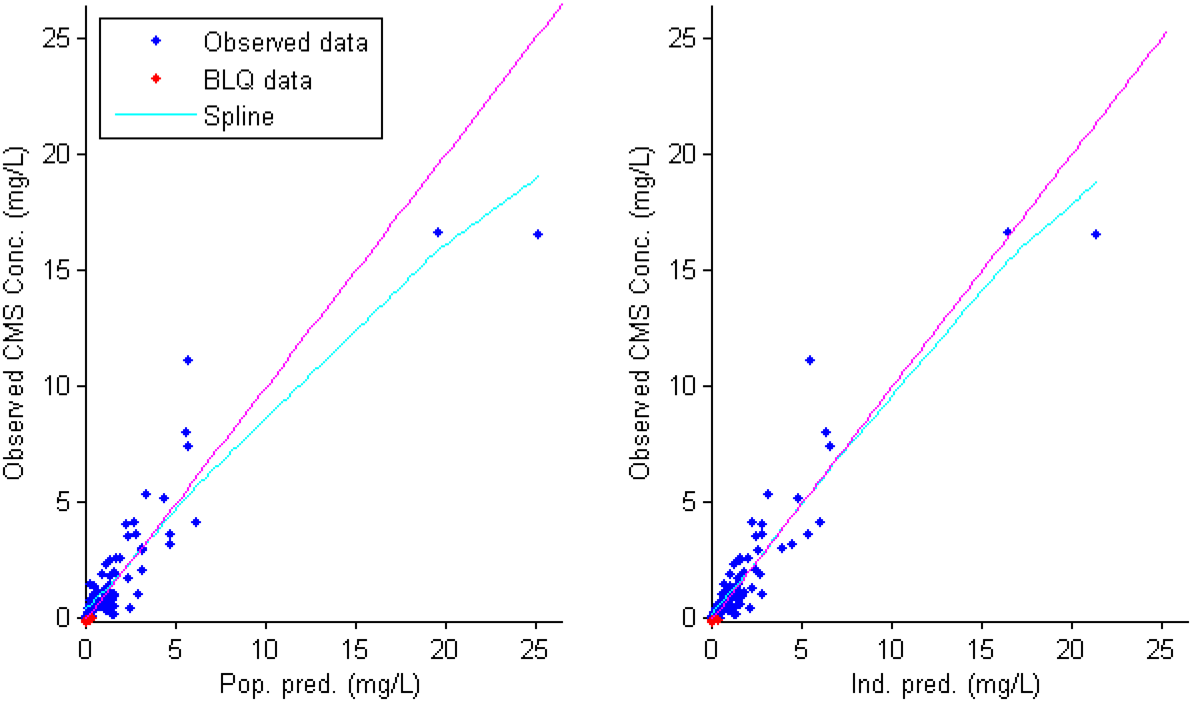
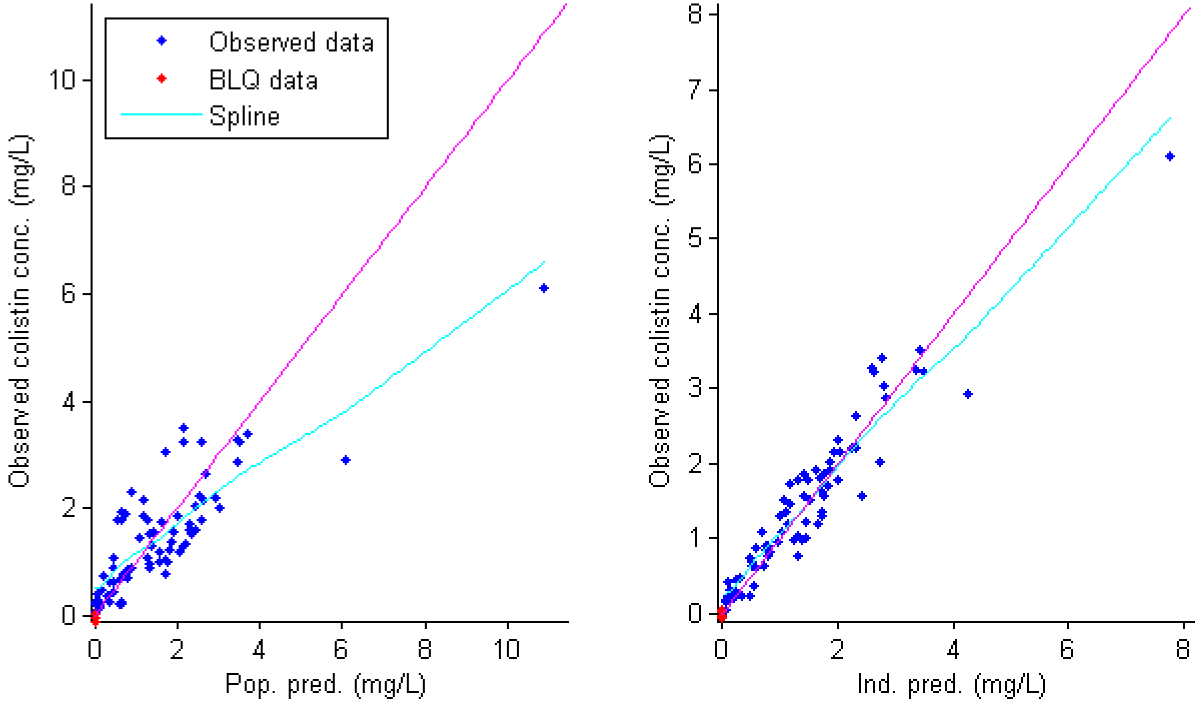

CMS plasma concentration (mg/L)
30
25
20
15
10
5
0
0
50
100
150
200
250
time (hr)
Data
BLQ data
emp. prctile
P.I 90%
P.I 50%
P.I 10%


colistin plasma concentration (mg/L)
0
1
2
3
4
5
6
7
time (hr)
0
50
100
150
200
250
Data
BLQ data
emp. prctile
P.I 90%
P.I 50%
P.I 10%


Observed data
BLQ data
Spline
Observed CMS Conc. (mg/L)
0
5
10
15
20
25
Pop. pred. (mg/L)
Observed CMS Conc. (mg/L)
Ind. pred. (mg/L)


Observed data
BLQ data
Spline
Observed colistin conc. (mg/L)
0
2
4
6
8
10
Pop. pred. (mg/L)
0
2
4
6
8
10
Observed colistin conc. (mg/L)
0
1
2
3
4
5
6
7
8
Ind. pred. (mg/L)
0
2
4
6
8

```
DESCRIPTION:
PK model for CMS (YTYPE=1) 1 cpt, colistine (YTYPE=2) 1 cpt, with aerosol, with hemodialysis

INPUT:
parameter={Faero,CLincms,CLoutcms,CLincol,CLoutcol,CLbiotrans,Vbal,Vcms,CLnrcms,CLcol,Vcol,CLHDcms,CLHDcol}
regressor={collect,seance}

PK:
compartment(cmt=1,amount=Qcms)
compartment(cmt=2,amount=Acms)
compartment(cmt=3,amount=Acol)
compartment(cmt=4,amount=Qcol)

iv(adm=1, cmt=1)
iv(adm=2, cmt=2, p=Faero)

EQUATION:
pcol=1166.8 ; masse mol colistine
pcms=1631.97 ; masse mol CMS
rlm=pcol/pcms

ddt_Acms = -(CLbiotrans+CLoutcms)*Acms/Vbal  + CLincms*Qcms/Vcms
ddt_Acol = -CLoutcol*Acol/Vbal+CLbiotrans*Acms/Vbal*rlm  + CLincol*Qcol/Vcol

ddt_Qcms = -(CLincms+CLnrcms+CLHDcms*seance)*Qcms/Vcms + CLoutcms*Acms*Vbal
ddt_Qcol = -(CLincol+CLcol+CLHDcol*seance)*Qcol/Vcol  + CLnrcms*rlm*Qcms/Vcms+CLoutcol*Acol/Vbal

Ccms = Qcms/Vcms
Ccol = Qcol/Vcol

ddt_AUCcms=Ccms
ddt_AUCcol=Ccol

OUTPUT:
output =  {Ccms,Ccol}
table = {AUCcms, AUCcol}
```

Fig. S1. Visual predictive check of CMS plasma concentrations for the final model. Dots represent the observed data (red for concentrations below the limit of quantification) and lines represent the 10th, 50th and 90th percentiles of the observed data. The shaded areas are the 95% CI of the 10th, 50th and 90th percentiles for the final model.

Fig. S2. Visual predictive check of colistin plasma concentrations for the final model. Dots represent the observed data (red for concentrations below the limit of quantification) and lines represent the 10th, 50th and 90th percentiles of the observed data. The shaded areas are the 95% CI of the 10th, 50th and 90th percentiles for the final model.

Fig. S3. Observed data *versus* population (left) and individual (right) predictions of CMS concentrations.

Fig. S4. Observed data *versus* population (left) and individual (right) predictions of colistin concentrations.

Doc. S1. Control stream for the final model in Monolix software