

Example evaluation of FOCUS dataset Z

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Key words: Kinetics, FOCUS, nonlinear optimisation

1 The data

The following code defines the example dataset from Appendix 7 to the FOCUS kinetics report ([FOCUS Work Group on Degradation Kinetics, 2011](#)), p.350.

```
require(mkin)
LOD = 0.5
FOCUS_2006_Z = data.frame(
  t = c(0, 0.04, 0.125, 0.29, 0.54, 1, 2, 3, 4, 7, 10, 14, 21,
        42, 61, 96, 124),
  Z0 = c(100, 81.7, 70.4, 51.1, 41.2, 6.6, 4.6, 3.9, 4.6, 4.3, 6.8,
        2.9, 3.5, 5.3, 4.4, 1.2, 0.7),
  Z1 = c(0, 18.3, 29.6, 46.3, 55.1, 65.7, 39.1, 36, 15.3, 5.6, 1.1,
        1.6, 0.6, 0.5 * LOD, NA, NA, NA),
  Z2 = c(0, NA, 0.5 * LOD, 2.6, 3.8, 15.3, 37.2, 31.7, 35.6, 14.5,
        0.8, 2.1, 1.9, 0.5 * LOD, NA, NA, NA),
  Z3 = c(0, NA, NA, NA, NA, 0.5 * LOD, 9.2, 13.1, 22.3, 28.4, 32.5,
        25.2, 17.2, 4.8, 4.5, 2.8, 4.4))

FOCUS_2006_Z_mkin <- mkin_wide_to_long(FOCUS_2006_Z)
```

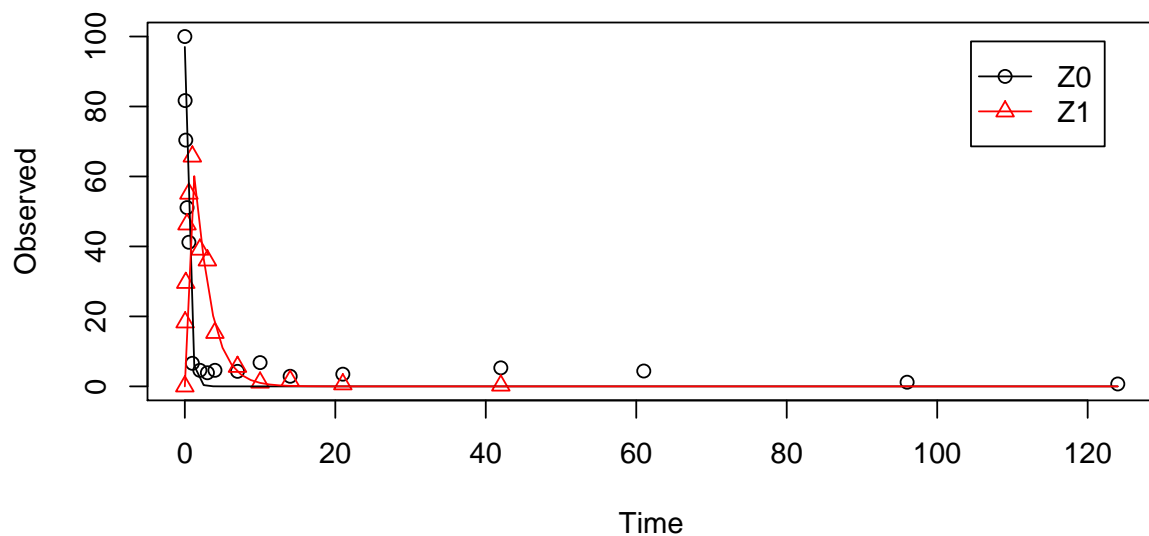
2 Parent compound and one metabolite

The next step is to set up the models used for the kinetic analysis. As the simultaneous fit of parent and the first metabolite is usually straightforward, Step 1 (SFO for parent only) is skipped here. We start with the model 2a, with formation and decline of metabolite Z1 and the pathway from parent directly to sink included (default in mkin).

```

Z.2a <- mkinmod(Z0 = list(type = "SF0", to = "Z1"),
               Z1 = list(type = "SF0"))
m.Z.2a <- mkinfit(Z.2a, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.2a)

```



```

summary(m.Z.2a, data = FALSE)

## mkin version:      0.9.33
## R version:        3.1.1
## Date of fit:       Sat Oct 11 10:01:48 2014
## Date of summary:   Sat Oct 11 10:01:48 2014
##
## Equations:
## d_Z0 = - k_Z0_sink * Z0 - k_Z0_Z1 * Z0
## d_Z1 = + k_Z0_Z1 * Z0 - k_Z1_sink * Z1
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 47 model solutions performed in 0.548 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##          value      type

```

```

## Z0_0      100.0000  state
## k_Z0_sink  0.1000 deparm
## k_Z0_Z1    0.1001 deparm
## k_Z1_sink  0.1002 deparm
##
## Starting values for the transformed parameters actually optimised:
##           value lower upper
## Z0_0      100.000  -Inf   Inf
## log_k_Z0_sink -2.303  -Inf   Inf
## log_k_Z0_Z1  -2.302  -Inf   Inf
## log_k_Z1_sink -2.301  -Inf   Inf
##
## Fixed parameter values:
##      value  type
## Z1_0      0  state
##
## Optimised, transformed parameters:
##           Estimate Std. Error Lower Upper t value Pr(>|t|) Pr(>t)
## Z0_0           97.000          NA     NA     NA      NA      NA      NA
## log_k_Z0_sink  -36.400          NA     NA     NA      NA      NA      NA
## log_k_Z0_Z1      0.805          NA     NA     NA      NA      NA      NA
## log_k_Z1_sink   -0.730          NA     NA     NA      NA      NA      NA
##
## Parameter correlation:
## Could not estimate covariance matrix; singular system:
##
## Residual standard error: 5.06 on 27 degrees of freedom
##
## Backtransformed parameters:
##           Estimate Lower Upper
## Z0_0      9.70e+01     NA     NA
## k_Z0_sink 1.62e-16     NA     NA
## k_Z0_Z1    2.24e+00     NA     NA
## k_Z1_sink 4.82e-01     NA     NA
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data    17.9      4 26
## Z0          18.0      3 14
## Z1          15.1      1 12
##
## Resulting formation fractions:

```

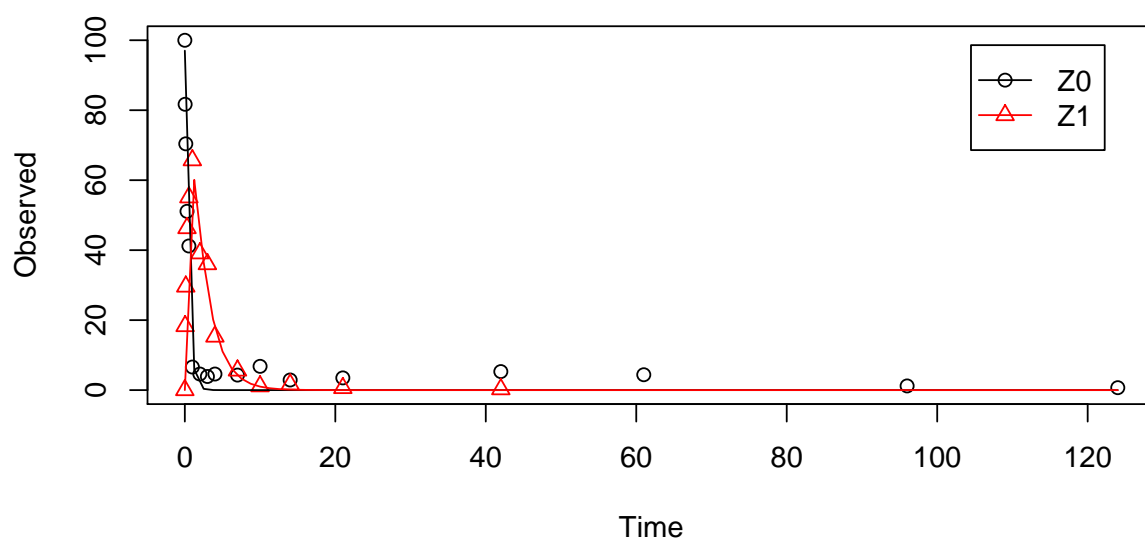
```
##          ff
## Z0_sink 7.23e-17
## Z0_Z1   1.00e+00
## Z1_sink 1.00e+00
##
## Estimated disappearance times:
##      DT50 DT90
## Z0 0.31 1.03
## Z1 1.44 4.78
```

As obvious from the summary, the kinetic rate constant from parent compound Z to sink is negligible. Accordingly, the exact magnitude of the fitted parameter $\log k_{Z_sink}$ is ill-defined and the covariance matrix is not returned. This suggests, in agreement with the analysis in the FOCUS kinetics report, to simplify the model by removing the pathway to sink.

A similar result can be obtained when formation fractions are used in the model formulation:

```
Z.2a.ff <- mkinmod(Z0 = list(type = "SFO", to = "Z1"),
                  Z1 = list(type = "SFO"),
                  use_of_ff = "max")

m.Z.2a.ff <- mkinfit(Z.2a.ff, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.2a.ff)
```



```

summary(m.Z.2a.ff, data = FALSE)

## mkin version:      0.9.33
## R version:        3.1.1
## Date of fit:       Sat Oct 11 10:01:49 2014
## Date of summary:  Sat Oct 11 10:01:49 2014
##
## Equations:
## d_Z0 = - k_Z0 * Z0 d_Z1 = + f_Z0_to_Z1 * k_Z0 * Z0 - k_Z1 * Z1
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 49 model solutions performed in 0.572 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##           value  type
## Z0_0         100.0000 state
## k_Z0           0.1000 deparm
## k_Z1           0.1001 deparm
## f_Z0_to_Z1    0.5000 deparm
##
## Starting values for the transformed parameters actually optimised:
##           value lower upper
## Z0_0         100.000  -Inf  Inf
## log_k_Z0      -2.303  -Inf  Inf
## log_k_Z1      -2.302  -Inf  Inf
## f_Z0_ilr_1     0.000  -Inf  Inf
##
## Fixed parameter values:
##           value  type
## Z1_0           0 state
##
## Optimised, transformed parameters:
##           Estimate Std. Error Lower Upper t value Pr(>|t|) Pr(>t)
## Z0_0           97.000          NA    NA    NA    NA      NA      NA
## log_k_Z0         0.805          NA    NA    NA    NA      NA      NA
## log_k_Z1        -0.730          NA    NA    NA    NA      NA      NA
## f_Z0_ilr_1      23.900          NA    NA    NA    NA      NA      NA
##
## Parameter correlation:

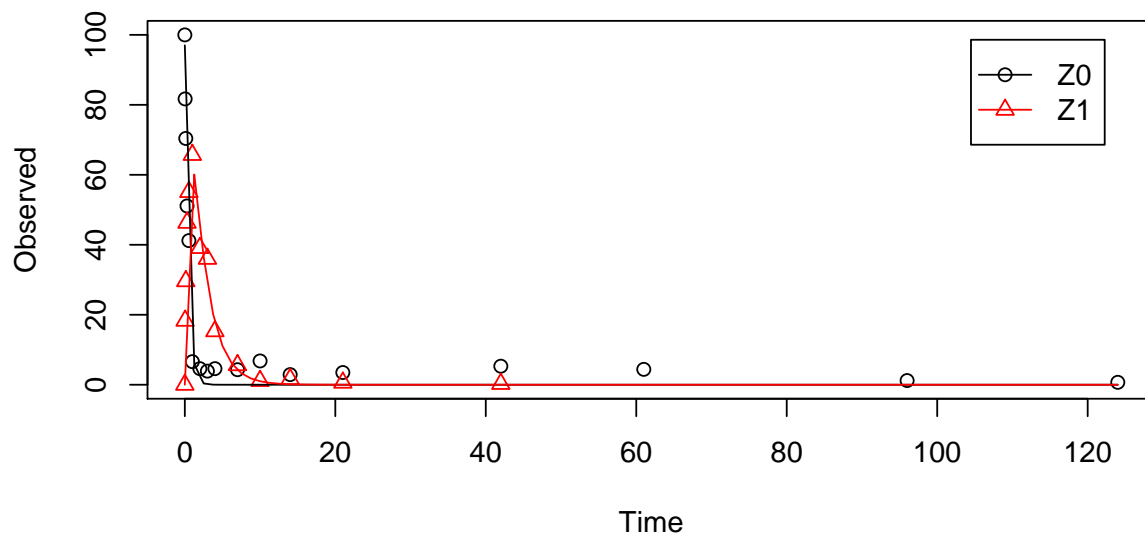
```

```
## Could not estimate covariance matrix; singular system:
##
## Residual standard error: 5.06 on 27 degrees of freedom
##
## Backtransformed parameters:
##           Estimate Lower Upper
## Z0_0          97.000    NA    NA
## k_Z0           2.240    NA    NA
## k_Z1           0.482    NA    NA
## f_Z0_to_Z1     1.000    NA    NA
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data      17.9      4 26
## Z0             17.6      2 15
## Z1             15.6      2 11
##
## Resulting formation fractions:
##           ff
## Z0_Z1      1e+00
## Z0_sink    2e-15
##
## Estimated disappearance times:
##      DT50 DT90
## Z0 0.31 1.03
## Z1 1.44 4.78
```

Here, the ilr transformed formation fraction fitted in the model takes a very large value, and the backtransformed formation fraction from parent Z to Z1 is practically unity. Again, the covariance matrix is not returned as the model is overparameterised.

The simplified model is obtained by setting the list component `sink` to `FALSE`.

```
Z.3 <- mkinmod(Z0 = list(type = "SFO", to = "Z1", sink = FALSE),
               Z1 = list(type = "SFO"), use_of_ff = "max")
m.Z.3 <- mkinfit(Z.3, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.3)
```



```
summary(m.Z.3, data = FALSE)

## mkin version:    0.9.33
## R version:      3.1.1
## Date of fit:     Sat Oct 11 10:01:49 2014
## Date of summary: Sat Oct 11 10:01:49 2014
##
## Equations:
## d_Z0 = - k_Z0 * Z0 d_Z1 = + k_Z0 * Z0 - k_Z1 * Z1
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 30 model solutions performed in 0.346 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##      value  type
## Z0_0 100.0000 state
## k_Z0  0.1000 deparm
## k_Z1  0.1001 deparm
##
## Starting values for the transformed parameters actually optimised:
##      value lower upper
```



```

## Z0_0      100.000  -Inf   Inf
## log_k_Z0  -2.303  -Inf   Inf
## log_k_Z1  -2.302  -Inf   Inf
##
## Fixed parameter values:
##      value  type
## Z1_0      0 state
##
## Optimised, transformed parameters:
##      Estimate Std. Error  Lower  Upper t value Pr(>|t|)  Pr(>t)
## Z0_0        97.000      2.6800 91.500 103.000   36.20 4.73e-25 2.36e-25
## log_k_Z0      0.805      0.0657  0.670   0.939   12.30 9.12e-13 4.56e-13
## log_k_Z1     -0.730      0.0885 -0.911  -0.548   -8.24 5.74e-09 2.87e-09
##
## Parameter correlation:
##      Z0_0 log_k_Z0 log_k_Z1
## Z0_0      1.000   0.1063   0.4104
## log_k_Z0  0.106   1.0000   0.0434
## log_k_Z1  0.410   0.0434   1.0000
##
## Residual standard error: 4.97 on 28 degrees of freedom
##
## Backtransformed parameters:
##      Estimate  Lower  Upper
## Z0_0    97.000 91.500 103.000
## k_Z0     2.240  1.950   2.560
## k_Z1     0.482  0.402   0.578
##
## Chi2 error levels in percent:
##      err.min n.optim df
## All data    17.6      3 27
## Z0           17.6      2 15
## Z1           15.1      1 12
##
## Estimated disappearance times:
##      DT50 DT90
## Z0  0.31 1.03
## Z1  1.44 4.78

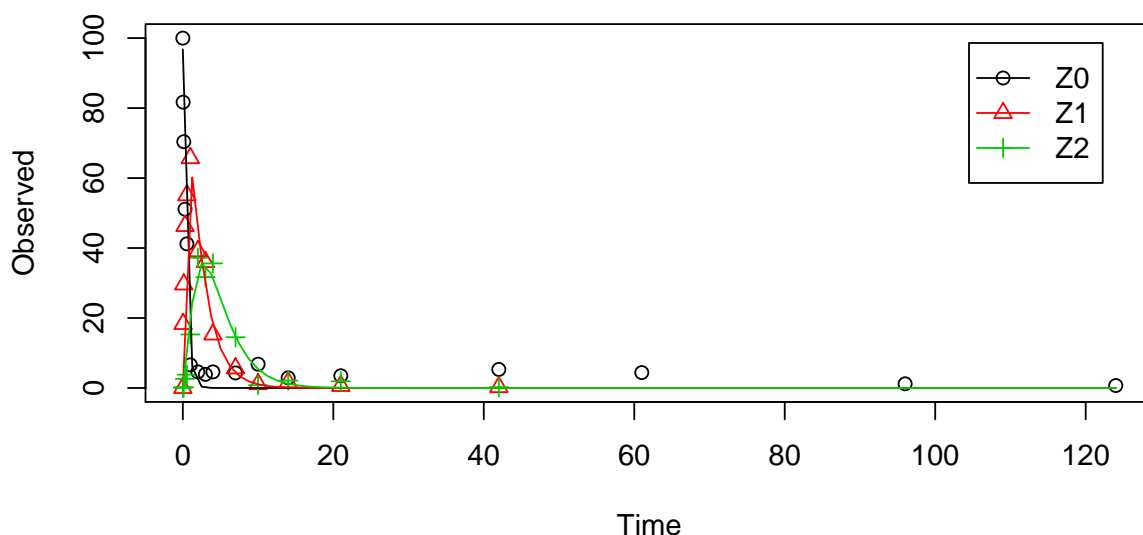
```

As there is only one transformation product for Z0 and no pathway to sink, the formation fraction is internally fixed to unity.

3 Including metabolites Z2 and Z3

As suggested in the FOCUS report, the pathway to sink was removed for metabolite Z1 as well in the next step. While this step appears questionable on the basis of the above results, it is followed here for the purpose of comparison. Also, in the FOCUS report, it is assumed that there is additional empirical evidence that Z1 quickly and exclusively hydrolyses to Z2.

```
Z.5 <- mkinmod(Z0 = list(type = "SF0", to = "Z1", sink = FALSE),
               Z1 = list(type = "SF0", to = "Z2", sink = FALSE),
               Z2 = list(type = "SF0"))
m.Z.5 <- mkinfit(Z.5, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.5)
```



```
summary(m.Z.5, data = FALSE)

## mkin version:      0.9.33
## R version:         3.1.1
## Date of fit:        Sat Oct 11 10:01:50 2014
## Date of summary:    Sat Oct 11 10:01:50 2014
##
## Equations:
## d_Z0 = - 0 - k_Z0_Z1 * Z0 d_Z1 = + k_Z0_Z1 * Z0 - 0 - k_Z1_Z2 * Z1
## d_Z2 = + k_Z1_Z2 * Z1 - k_Z2_sink * Z2
##
```

```

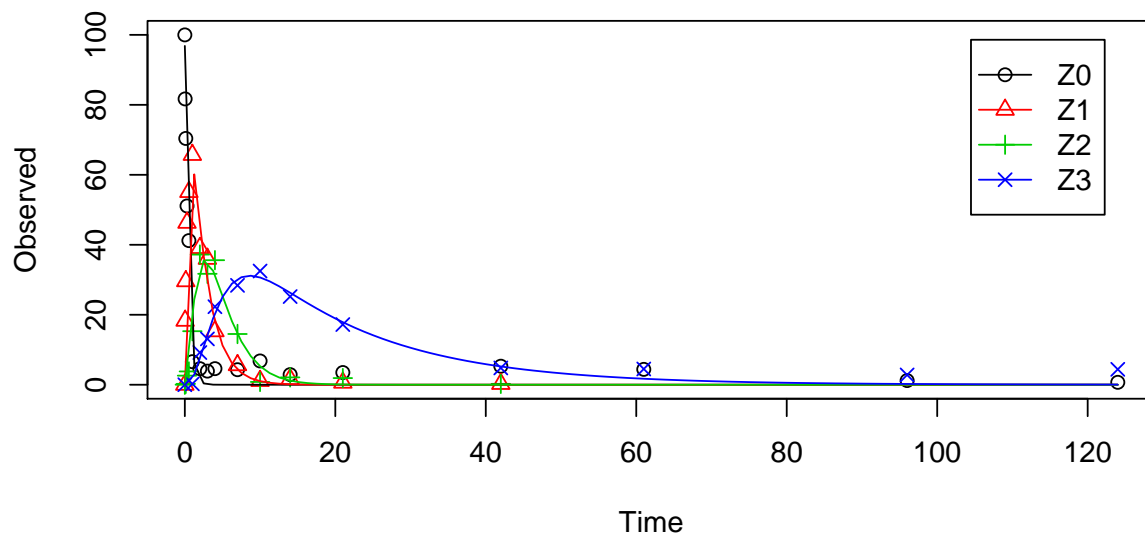
## Model predictions using solution type eigen
##
## Fitted with method Marq using 42 model solutions performed in 0.672 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##      value  type
## Z0_0      100.0000 state
## k_Z0_Z1    0.1000 deparm
## k_Z1_Z2    0.1001 deparm
## k_Z2_sink  0.1002 deparm
##
## Starting values for the transformed parameters actually optimised:
##      value lower upper
## Z0_0      100.000 -Inf  Inf
## log_k_Z0_Z1 -2.303 -Inf  Inf
## log_k_Z1_Z2 -2.302 -Inf  Inf
## log_k_Z2_sink -2.301 -Inf  Inf
##
## Fixed parameter values:
##      value  type
## Z1_0      0 state
## Z2_0      0 state
##
## Optimised, transformed parameters:
##      Estimate Std. Error Lower Upper t value Pr(>|t|)
## Z0_0      96.800    2.2700 92.200 101.000  42.70 5.43e-35
## log_k_Z0_Z1  0.795    0.0584  0.677  0.913  13.60 1.36e-16
## log_k_Z1_Z2 -0.741    0.0682 -0.879 -0.603 -10.90 1.68e-13
## log_k_Z2_sink -0.803    0.1110 -1.030 -0.579  -7.24 8.79e-09
##      Pr(>t)
## Z0_0      2.72e-35
## log_k_Z0_Z1 6.80e-17
## log_k_Z1_Z2 8.41e-14
## log_k_Z2_sink 4.39e-09
##
## Parameter correlation:
##      Z0_0 log_k_Z0_Z1 log_k_Z1_Z2 log_k_Z2_sink
## Z0_0      1.0000    0.0578    0.2875    0.3179
## log_k_Z0_Z1 0.0578    1.0000   -0.0436    0.0121
## log_k_Z1_Z2 0.2875   -0.0436    1.0000    0.2402

```

```
## log_k_Z2_sink 0.3179      0.0121      0.2402      1.0000
##
## Residual standard error: 4.49 on 40 degrees of freedom
##
## Backtransformed parameters:
##           Estimate Lower Upper
## Z0_0          96.800 92.200 101.000
## k_Z0_Z1        2.210  1.970  2.490
## k_Z1_Z2        0.477  0.415  0.547
## k_Z2_sink      0.448  0.358  0.561
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data      19.1      4 38
## Z0             17.4      2 15
## Z1             15.3      1 12
## Z2             19.6      1 11
##
## Resulting formation fractions:
##           ff
## Z0_Z1      1
## Z1_Z2      1
## Z2_sink    1
##
## Estimated disappearance times:
##           DT50 DT90
## Z0 0.313 1.04
## Z1 1.454 4.83
## Z2 1.547 5.14
```

Finally, metabolite Z3 is added to the model. The fit is accelerated by using the starting parameters from the previous fit.

```
Z.FOCUS <- mkinmod(Z0 = list(type = "SFO", to = "Z1", sink = FALSE),
                  Z1 = list(type = "SFO", to = "Z2", sink = FALSE),
                  Z2 = list(type = "SFO", to = "Z3"),
                  Z3 = list(type = "SFO"))
m.Z.FOCUS <- mkinfit(Z.FOCUS, FOCUS_2006_Z_mkin,
                   parms.ini = m.Z.5$bparms.ode,
                   quiet = TRUE)
plot(m.Z.FOCUS)
```



```
summary(m.Z.FOCUS, data = FALSE)

## mkin version:    0.9.33
## R version:      3.1.1
## Date of fit:     Sat Oct 11 10:01:52 2014
## Date of summary: Sat Oct 11 10:01:52 2014
##
## Equations:
## d_Z0 = - 0 - k_Z0_Z1 * Z0 d_Z1 = + k_Z0_Z1 * Z0 - 0 - k_Z1_Z2 * Z1
## d_Z2 = + k_Z1_Z2 * Z1 - k_Z2_sink * Z2 - k_Z2_Z3 * Z2
## d_Z3 = + k_Z2_Z3 * Z2 - k_Z3_sink * Z3
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 65 model solutions performed in 1.331 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##      value  type
## Z0_0      100.0000 state
## k_Z0_Z1     2.2140 deparm
## k_Z1_Z2     0.4766 deparm
## k_Z2_sink    0.4481 deparm
```

```

## k_Z2_Z3      0.1000 deparm
## k_Z3_sink    0.1001 deparm
##
## Starting values for the transformed parameters actually optimised:
##              value lower upper
## Z0_0          100.0000 -Inf   Inf
## log_k_Z0_Z1    0.7948 -Inf   Inf
## log_k_Z1_Z2   -0.7410 -Inf   Inf
## log_k_Z2_sink -0.8027 -Inf   Inf
## log_k_Z2_Z3   -2.3026 -Inf   Inf
## log_k_Z3_sink -2.3016 -Inf   Inf
##
## Fixed parameter values:
##      value type
## Z1_0      0 state
## Z2_0      0 state
## Z3_0      0 state
##
## Optimised, transformed parameters:
##      Estimate Std. Error  Lower  Upper t value Pr(>|t|)
## Z0_0          96.800     2.0600  92.700 101.000   47.00 1.12e-43
## log_k_Z0_Z1     0.795     0.0533   0.688   0.902   14.90 3.08e-20
## log_k_Z1_Z2    -0.738     0.0612  -0.860  -0.615  -12.00 1.57e-16
## log_k_Z2_sink  -1.430     0.1720  -1.780  -1.090   -8.35 4.16e-11
## log_k_Z2_Z3    -1.550     0.1230  -1.790  -1.300  -12.60 2.60e-17
## log_k_Z3_sink  -2.840     0.2440  -3.320  -2.350  -11.60 5.64e-16
##
##      Pr(>t)
## Z0_0      5.58e-44
## log_k_Z0_Z1 1.54e-20
## log_k_Z1_Z2 7.84e-17
## log_k_Z2_sink 2.08e-11
## log_k_Z2_Z3 1.30e-17
## log_k_Z3_sink 2.82e-16
##
## Parameter correlation:
##      Z0_0 log_k_Z0_Z1 log_k_Z1_Z2 log_k_Z2_sink
## Z0_0      1.0000      0.0539      0.2727      0.3701
## log_k_Z0_Z1 0.0539      1.0000     -0.0521      0.0244
## log_k_Z1_Z2 0.2727     -0.0521      1.0000      0.2938
## log_k_Z2_sink 0.3701      0.0244      0.2938      1.0000
## log_k_Z2_Z3 -0.0730     -0.0358     -0.1213     -0.1889
## log_k_Z3_sink -0.1135     -0.0252     -0.1915     -0.6430

```

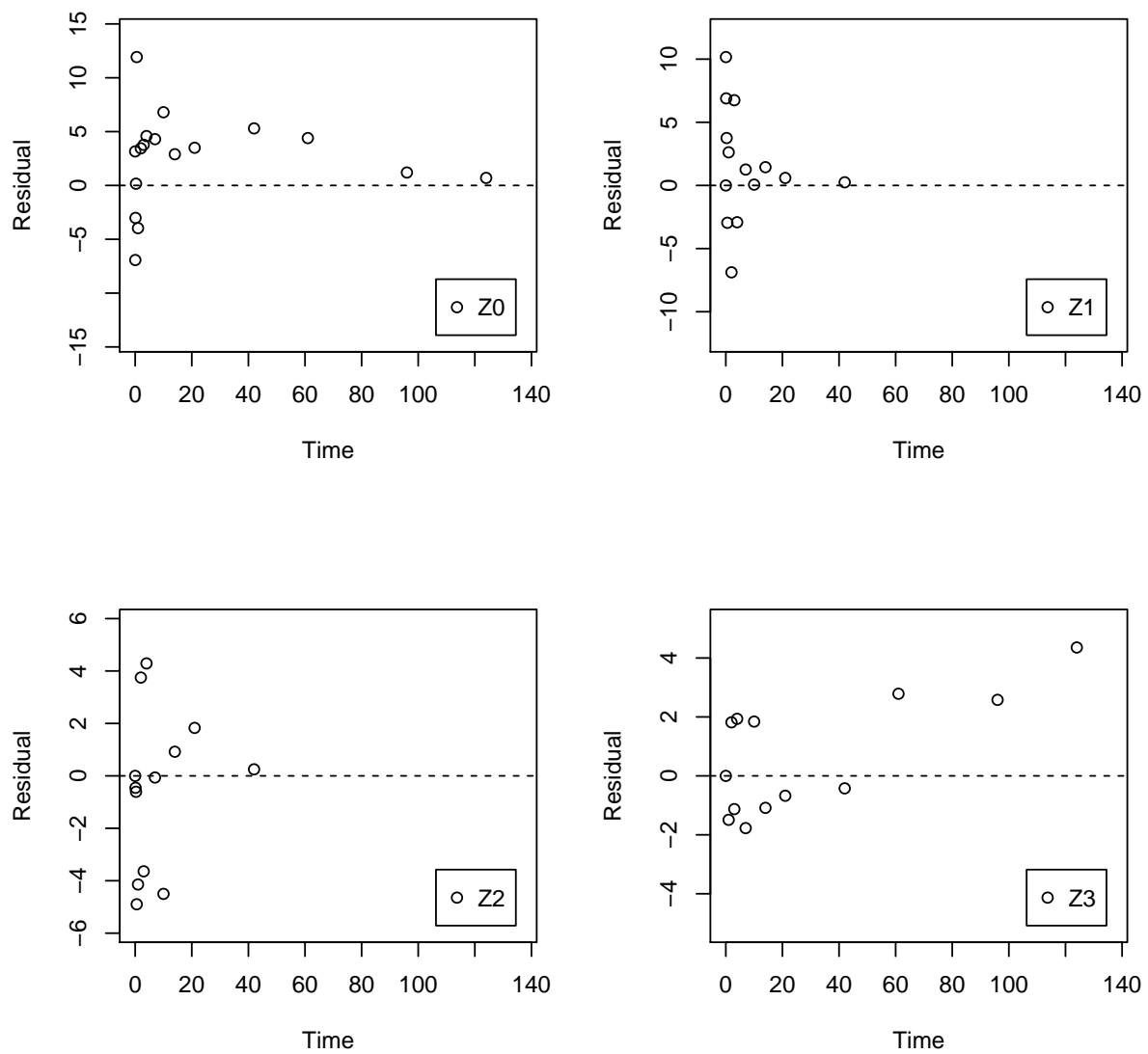
```

##          log_k_Z2_Z3 log_k_Z3_sink
## Z0_0          -0.0730      -0.1135
## log_k_Z0_Z1    -0.0358      -0.0252
## log_k_Z1_Z2    -0.1213      -0.1915
## log_k_Z2_sink  -0.1889      -0.6430
## log_k_Z2_Z3     1.0000       0.5516
## log_k_Z3_sink   0.5516       1.0000
##
## Residual standard error: 4.1 on 51 degrees of freedom
##
## Backtransformed parameters:
##          Estimate Lower Upper
## Z0_0          96.8000 92.700 101.0000
## k_Z0_Z1        2.2200  1.990  2.4700
## k_Z1_Z2        0.4780  0.423  0.5410
## k_Z2_sink      0.2390  0.169  0.3370
## k_Z2_Z3        0.2130  0.166  0.2720
## k_Z3_sink      0.0587  0.036  0.0957
##
## Chi2 error levels in percent:
##          err.min n.optim df
## All data      19.2        6 48
## Z0             17.4         2 15
## Z1             15.2         1 12
## Z2             20.3         2 10
## Z3             11.9         1 11
##
## Resulting formation fractions:
##          ff
## Z0_Z1      1.000
## Z1_Z2      1.000
## Z2_sink    0.528
## Z2_Z3      0.472
## Z3_sink    1.000
##
## Estimated disappearance times:
##          DT50 DT90
## Z0  0.313  1.04
## Z1  1.449  4.81
## Z2  1.535  5.10
## Z3 11.810 39.23

```

This is the fit corresponding to the final result chosen in Appendix 7 of the FOCUS report. The residual plots can be obtained by

```
par(mfrow = c(2, 2))
mkinresplot(m.Z.FOCUS, "Z0", lpos = "bottomright")
mkinresplot(m.Z.FOCUS, "Z1", lpos = "bottomright")
mkinresplot(m.Z.FOCUS, "Z2", lpos = "bottomright")
mkinresplot(m.Z.FOCUS, "Z3", lpos = "bottomright")
```

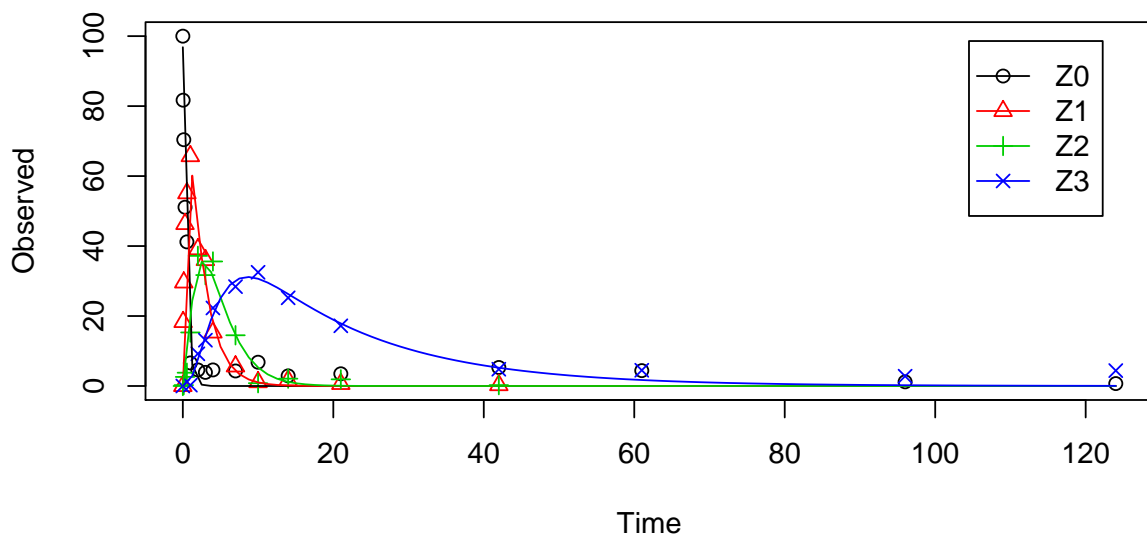


We can also investigate the confidence interval for the formation fraction from Z2 to Z3 by specifying the model using formation fractions.


```

Z.FOCUS.ff <- mkinmod(Z0 = list(type = "SFO", to = "Z1", sink = FALSE),
  Z1 = list(type = "SFO", to = "Z2", sink = FALSE),
  Z2 = list(type = "SFO", to = "Z3"),
  Z3 = list(type = "SFO"),
  use_of_ff = "max")
m.Z.FOCUS.ff <- mkinfit(Z.FOCUS.ff, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.FOCUS.ff)

```



```

summary(m.Z.FOCUS.ff, data = FALSE)

## mkin version:      0.9.33
## R version:         3.1.1
## Date of fit:       Sat Oct 11 10:01:53 2014
## Date of summary:   Sat Oct 11 10:01:53 2014
##
## Equations:
## d_Z0 = - k_Z0 * Z0 d_Z1 = + k_Z0 * Z0 - k_Z1 * Z1
## d_Z2 = + k_Z1 * Z1 - k_Z2 * Z2
## d_Z3 = + f_Z2_to_Z3 * k_Z2 * Z2 - k_Z3 * Z3
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 65 model solutions performed in 1.372 s
##

```

```

## Weighting: none
##
## Starting values for parameters to be optimised:
##           value  type
## Z0_0       100.0000  state
## k_Z0        0.1000 deparm
## k_Z1        0.1001 deparm
## k_Z2        0.1002 deparm
## k_Z3        0.1003 deparm
## f_Z2_to_Z3  0.5000 deparm
##
## Starting values for the transformed parameters actually optimised:
##           value lower upper
## Z0_0       100.000  -Inf   Inf
## log_k_Z0    -2.303  -Inf   Inf
## log_k_Z1    -2.302  -Inf   Inf
## log_k_Z2    -2.301  -Inf   Inf
## log_k_Z3    -2.300  -Inf   Inf
## f_Z2_ilr_1   0.000  -Inf   Inf
##
## Fixed parameter values:
##           value  type
## Z1_0         0  state
## Z2_0         0  state
## Z3_0         0  state
##
## Optimised, transformed parameters:
##           Estimate Std. Error  Lower  Upper t value Pr(>|t|)
## Z0_0          96.8000    2.0600  92.700 101.000  47.000 1.12e-43
## log_k_Z0       0.7950    0.0533   0.688   0.902  14.900 3.08e-20
## log_k_Z1      -0.7380    0.0612  -0.860  -0.615 -12.000 1.57e-16
## log_k_Z2      -0.7950    0.0979  -0.991  -0.598  -8.120 9.44e-11
## log_k_Z3      -2.8400    0.2440  -3.320  -2.350 -11.600 5.64e-16
## f_Z2_ilr_1    -0.0807    0.1620  -0.406   0.244  -0.498 6.20e-01
##           Pr(>t)
## Z0_0          5.58e-44
## log_k_Z0       1.54e-20
## log_k_Z1       7.84e-17
## log_k_Z2       4.72e-11
## log_k_Z3       2.82e-16
## f_Z2_ilr_1     3.10e-01
##

```

```

## Parameter correlation:
##           Z0_0 log_k_Z0 log_k_Z1 log_k_Z2 log_k_Z3 f_Z2_ilr_1
## Z0_0      1.0000  0.05386   0.2727   0.29977  -0.1135   -0.3164
## log_k_Z0   0.0539  1.00000  -0.0521   0.00149  -0.0252   -0.0375
## log_k_Z1   0.2727 -0.05210   1.0000   0.20061  -0.1915   -0.2852
## log_k_Z2   0.2998  0.00149   0.2006   1.00000  -0.2701   -0.3886
## log_k_Z3  -0.1135 -0.02522  -0.1915  -0.27013   1.0000    0.7772
## f_Z2_ilr_1 -0.3164 -0.03748  -0.2852 -0.38860   0.7772    1.0000
##
## Residual standard error: 4.1 on 51 degrees of freedom
##
## Backtransformed parameters:
##           Estimate Lower Upper
## Z0_0      96.8000 92.700 101.0000
## k_Z0       2.2200  1.990  2.4700
## k_Z1       0.4780  0.423  0.5410
## k_Z2       0.4520  0.371  0.5500
## k_Z3       0.0587  0.036  0.0957
## f_Z2_to_Z3  0.4720  0.360  0.5860
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data    19.2      6 48
## Z0          17.4      2 15
## Z1          15.2      1 12
## Z2          19.6      1 11
## Z3          12.3      2 10
##
## Resulting formation fractions:
##           ff
## Z2_Z3    0.472
## Z2_sink  0.528
##
## Estimated disappearance times:
##           DT50 DT90
## Z0    0.313  1.04
## Z1    1.449  4.81
## Z2    1.535  5.10
## Z3   11.809 39.23

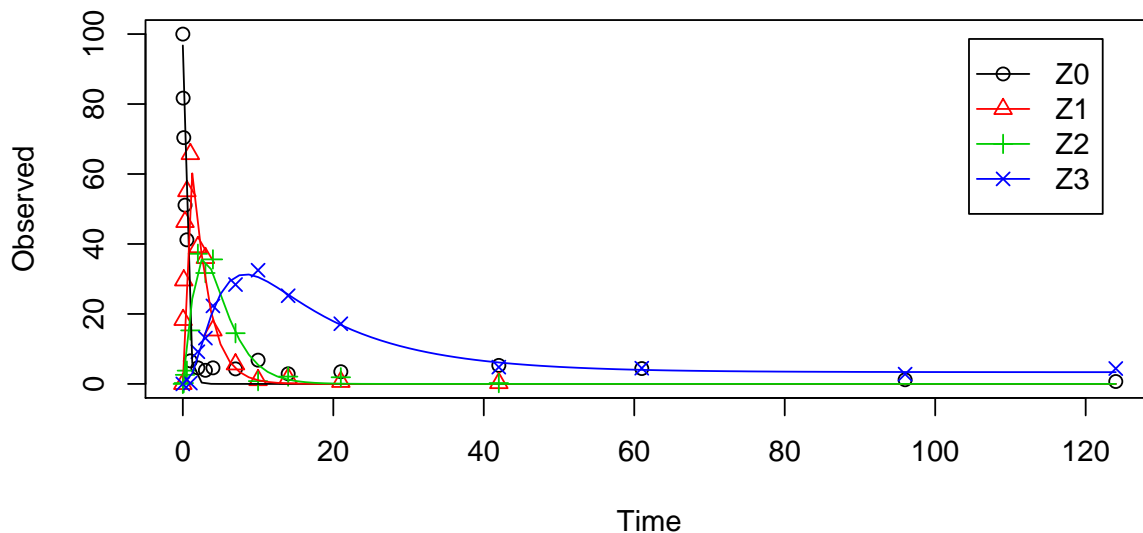
```

4 Using the SFORB model for parent and metabolites

As the FOCUS report states, there is a certain tailing of the time course of metabolite Z3. Also, the time course of the parent compound is not fitted very well using the SFO model, as residues at a certain low level remain.

Therefore, an additional model is offered here, using the single first-order reversible binding (SFORB) model for metabolite Z3. As expected, the χ^2 error level is lower for metabolite Z3 using this model and the graphical fit for Z3 is improved. However, the covariance matrix is not returned.

```
Z.mkin.1 <- mkinmod(Z0 = list(type = "SFO", to = "Z1", sink = FALSE),
  Z1 = list(type = "SFO", to = "Z2", sink = FALSE),
  Z2 = list(type = "SFO", to = "Z3"),
  Z3 = list(type = "SFORB"))
m.Z.mkin.1 <- mkinfit(Z.mkin.1, FOCUS_2006_Z_mkin,
  parms.ini = c(k_Z0_Z1 = 0.5, k_Z1_Z2 = 0.3),
  quiet = TRUE)
plot(m.Z.mkin.1)
```



```
summary(m.Z.mkin.1, data = FALSE)
## mkin version:    0.9.33
## R version:       3.1.1
## Date of fit:     Sat Oct 11 10:01:58 2014
```

```

## Date of summary: Sat Oct 11 10:01:58 2014
##
## Equations:
## d_Z0 = - 0 - k_Z0_Z1 * Z0 d_Z1 = + k_Z0_Z1 * Z0 - 0 - k_Z1_Z2 * Z1
## d_Z2 = + k_Z1_Z2 * Z1 - k_Z2_sink * Z2 - k_Z2_Z3_free * Z2
## d_Z3_free = + k_Z2_Z3_free * Z2 - k_Z3_free_sink * Z3_free -
##             k_Z3_free_bound * Z3_free + k_Z3_bound_free *
##             Z3_bound
## d_Z3_bound = + k_Z3_free_bound * Z3_free - k_Z3_bound_free *
##             Z3_bound
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 201 model solutions performed in 4.364 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##             value   type
## Z0_0          100.0000 state
## k_Z0_Z1         0.5000 deparm
## k_Z1_Z2         0.3000 deparm
## k_Z2_sink       0.1000 deparm
## k_Z2_Z3_free    0.1001 deparm
## k_Z3_free_sink  0.1002 deparm
## k_Z3_free_bound 0.1000 deparm
## k_Z3_bound_free 0.0200 deparm
##
## Starting values for the transformed parameters actually optimised:
##             value lower upper
## Z0_0          100.0000 -Inf   Inf
## log_k_Z0_Z1    -0.6931 -Inf   Inf
## log_k_Z1_Z2    -1.2040 -Inf   Inf
## log_k_Z2_sink  -2.3026 -Inf   Inf
## log_k_Z2_Z3_free -2.3016 -Inf   Inf
## log_k_Z3_free_sink -2.3006 -Inf   Inf
## log_k_Z3_free_bound -2.3026 -Inf   Inf
## log_k_Z3_bound_free -3.9120 -Inf   Inf
##
## Fixed parameter values:
##             value   type
## Z1_0           0 state

```

```

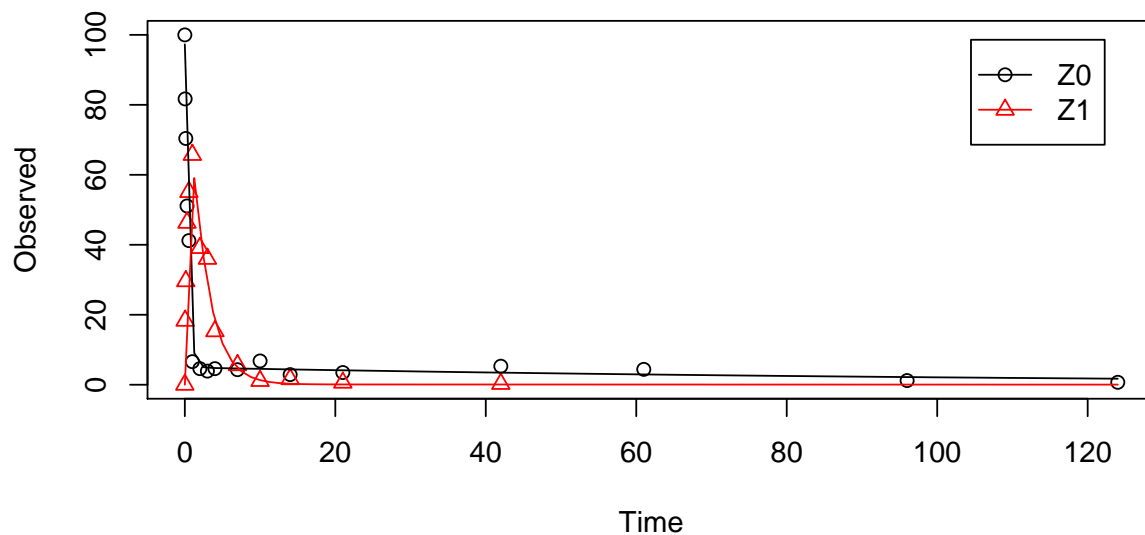
## Z2_0      0 state
## Z3_free_0  0 state
## Z3_bound_0 0 state
##
## Optimised, transformed parameters:
##           Estimate Std. Error Lower Upper t value Pr(>|t|)
## Z0_0      96.700      NA      NA      NA      NA      NA
## log_k_Z0_Z1  0.795      NA      NA      NA      NA      NA
## log_k_Z1_Z2 -0.743      NA      NA      NA      NA      NA
## log_k_Z2_sink -1.490      NA      NA      NA      NA      NA
## log_k_Z2_Z3_free -1.500      NA      NA      NA      NA      NA
## log_k_Z3_free_sink -2.650      NA      NA      NA      NA      NA
## log_k_Z3_free_bound -5.240      NA      NA      NA      NA      NA
## log_k_Z3_bound_free -21.400      NA      NA      NA      NA      NA
##           Pr(>t)
## Z0_0      NA
## log_k_Z0_Z1  NA
## log_k_Z1_Z2  NA
## log_k_Z2_sink  NA
## log_k_Z2_Z3_free  NA
## log_k_Z3_free_sink  NA
## log_k_Z3_free_bound  NA
## log_k_Z3_bound_free  NA
##
## Parameter correlation:
## Could not estimate covariance matrix; singular system:
##
## Residual standard error: 4.11 on 49 degrees of freedom
##
## Backtransformed parameters:
##           Estimate Lower Upper
## Z0_0      9.67e+01  NA      NA
## k_Z0_Z1    2.21e+00  NA      NA
## k_Z1_Z2    4.76e-01  NA      NA
## k_Z2_sink  2.24e-01  NA      NA
## k_Z2_Z3_free 2.22e-01  NA      NA
## k_Z3_free_sink 7.03e-02  NA      NA
## k_Z3_free_bound 5.28e-03  NA      NA
## k_Z3_bound_free 5.06e-10  NA      NA
##
## Chi2 error levels in percent:
##           err.min n.optim df

```

```
## All data      19.41      8 47
## Z0           17.43      2 15
## Z1           15.27      1 12
## Z2           20.28      2 10
## Z3           8.56       3 10
##
## Estimated Eigenvalues of SFORB model(s):
##      Z3_b1      Z3_b2
## 7.56e-02 4.71e-10
##
## Resulting formation fractions:
##                ff
## Z0_Z1          1.000
## Z1_Z2          1.000
## Z2_sink        0.502
## Z2_Z3_free     0.498
## Z3_free_sink   1.000
##
## Estimated disappearance times:
##      DT50  DT90 DT50_Z3_b1 DT50_Z3_b2
## Z0  0.313  1.04          NA          NA
## Z1  1.457  4.84          NA          NA
## Z2  1.552  5.16          NA          NA
## Z3 10.198 45.33          9.17    1.47e+09
```

Therefore, a further stepwise model building is performed starting from the stage of parent and one metabolite, starting from the assumption that the model fit for the parent compound can be improved by using the SFORB model.

```
Z.mkin.2 <- mkinmod(Z0 = list(type = "SFORB", to = "Z1", sink = FALSE),
                  Z1 = list(type = "SFO"))
m.Z.mkin.2 <- mkinfit(Z.mkin.2, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.mkin.2)
```



```
summary(m.Z.mkin.2, data = FALSE)

## mkin version:    0.9.33
## R version:      3.1.1
## Date of fit:     Sat Oct 11 10:01:59 2014
## Date of summary: Sat Oct 11 10:01:59 2014
##
## Equations:
## d_Z0_free = - 0 - k_Z0_free_bound * Z0_free + k_Z0_bound_free
##              * Z0_bound - k_Z0_free_Z1 * Z0_free
## d_Z0_bound = + k_Z0_free_bound * Z0_free - k_Z0_bound_free *
##              Z0_bound d_Z1 = + k_Z0_free_Z1 * Z0_free - k_Z1_sink * Z1
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 50 model solutions performed in 0.621 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##              value  type
## Z0_free_0      100.0000 state
## k_Z0_free_bound  0.1000 deparm
## k_Z0_bound_free  0.0200 deparm
```



```

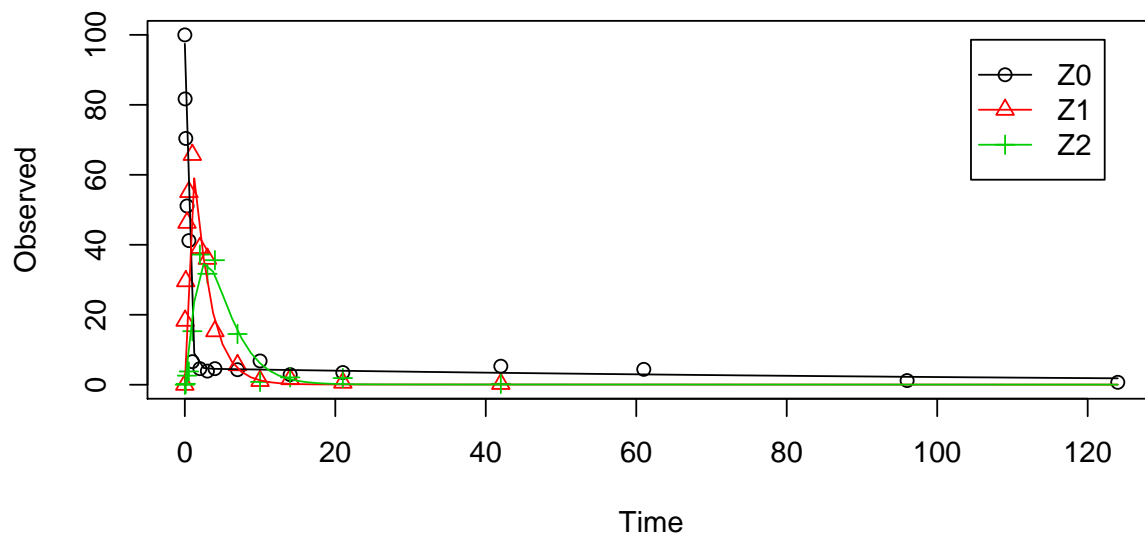
## k_Z0_free_Z1      0.1002 deparm
## k_Z1_sink         0.1003 deparm
##
## Starting values for the transformed parameters actually optimised:
##               value lower upper
## Z0_free_0       100.000 -Inf   Inf
## log_k_Z0_free_bound -2.303 -Inf   Inf
## log_k_Z0_bound_free -3.912 -Inf   Inf
## log_k_Z0_free_Z1   -2.301 -Inf   Inf
## log_k_Z1_sink      -2.300 -Inf   Inf
##
## Fixed parameter values:
##               value type
## Z0_bound_0       0 state
## Z1_0              0 state
##
## Optimised, transformed parameters:
##               Estimate Std. Error Lower Upper t value
## Z0_free_0         97.300      2.4000 92.400 102.000  40.60
## log_k_Z0_free_bound -2.080      0.4320 -2.970  -1.190  -4.82
## log_k_Z0_bound_free -4.720      1.6000 -8.020  -1.420  -2.94
## log_k_Z0_free_Z1     0.855      0.0643  0.723   0.987  13.30
## log_k_Z1_sink       -0.793      0.0851 -0.968  -0.619  -9.33
##               Pr(>|t|) Pr(>t)
## Z0_free_0         4.73e-25 2.36e-25
## log_k_Z0_free_bound 5.44e-05 2.72e-05
## log_k_Z0_bound_free 6.78e-03 3.39e-03
## log_k_Z0_free_Z1   4.18e-13 2.09e-13
## log_k_Z1_sink       8.86e-10 4.43e-10
##
## Parameter correlation:
##               Z0_free_0 log_k_Z0_free_bound log_k_Z0_bound_free
## Z0_free_0         1.00000          0.00649          0.0332
## log_k_Z0_free_bound 0.00649          1.00000          0.5465
## log_k_Z0_bound_free 0.03324          0.54647          1.0000
## log_k_Z0_free_Z1   0.11182          0.41393          0.1584
## log_k_Z1_sink       0.39155         -0.29191         -0.1260
##               log_k_Z0_free_Z1 log_k_Z1_sink
## Z0_free_0         0.1118          0.3916
## log_k_Z0_free_bound 0.4139         -0.2919
## log_k_Z0_bound_free 0.1584         -0.1260
## log_k_Z0_free_Z1   1.0000         -0.0419

```

```
## log_k_Z1_sink          -0.0419          1.0000
##
## Residual standard error: 4.44 on 26 degrees of freedom
##
## Backtransformed parameters:
##           Estimate      Lower      Upper
## Z0_free_0      97.30000 9.24e+01 102.000
## k_Z0_free_bound 0.12500 5.13e-02 0.303
## k_Z0_bound_free 0.00891 3.29e-04 0.241
## k_Z0_free_Z1    2.35000 2.06e+00 2.680
## k_Z1_sink       0.45200 3.80e-01 0.539
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data      15.6         5 25
## Z0             14.7         4 13
## Z1             14.3         1 12
##
## Estimated Eigenvalues of SFORB model(s):
##   Z0_b1  Z0_b2
## 2.47631 0.00846
##
## Resulting formation fractions:
##           ff
## Z0_free_Z1 1
## Z1_sink     1
##
## Estimated disappearance times:
##      DT50 DT90 DT50_Z0_b1 DT50_Z0_b2
## Z0 0.302 1.19         0.28         81.9
## Z1 1.532 5.09          NA          NA
```

When metabolite Z2 is added, the additional sink for Z1 is turned off again, for the same reasons as in the original analysis.

```
Z.mkin.3 <- mkinmod(Z0 = list(type = "SFORB", to = "Z1", sink = FALSE),
                  Z1 = list(type = "SFO", to = "Z2", sink = FALSE),
                  Z2 = list(type = "SFO"))
m.Z.mkin.3 <- mkinfit(Z.mkin.3, FOCUS_2006_Z_mkin, quiet = TRUE)
plot(m.Z.mkin.3)
```



```
summary(m.Z.mkin.3, data = FALSE)

## mkin version:    0.9.33
## R version:      3.1.1
## Date of fit:     Sat Oct 11 10:02:01 2014
## Date of summary: Sat Oct 11 10:02:01 2014
##
## Equations:
## d_Z0_free = - 0 - k_Z0_free_bound * Z0_free + k_Z0_bound_free
##              * Z0_bound - k_Z0_free_Z1 * Z0_free
## d_Z0_bound = + k_Z0_free_bound * Z0_free - k_Z0_bound_free *
##              Z0_bound
## d_Z1 = + k_Z0_free_Z1 * Z0_free - 0 - k_Z1_Z2 * Z1
## d_Z2 = + k_Z1_Z2 * Z1 - k_Z2_sink * Z2
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 58 model solutions performed in 1.613 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##              value    type
## Z0_free_0      100.0000 state
```

```

## k_Z0_free_bound    0.1000 deparm
## k_Z0_bound_free    0.0200 deparm
## k_Z0_free_Z1       0.1002 deparm
## k_Z1_Z2            0.1003 deparm
## k_Z2_sink          0.1004 deparm
##
## Starting values for the transformed parameters actually optimised:
##               value lower upper
## Z0_free_0      100.000  -Inf   Inf
## log_k_Z0_free_bound -2.303  -Inf   Inf
## log_k_Z0_bound_free -3.912  -Inf   Inf
## log_k_Z0_free_Z1   -2.301  -Inf   Inf
## log_k_Z1_Z2        -2.300  -Inf   Inf
## log_k_Z2_sink      -2.299  -Inf   Inf
##
## Fixed parameter values:
##               value type
## Z0_bound_0      0 state
## Z1_0            0 state
## Z2_0            0 state
##
## Optimised, transformed parameters:
##               Estimate Std. Error Lower Upper t value
## Z0_free_0        97.400     2.0700 93.200 102.000  47.00
## log_k_Z0_free_bound -2.150     0.4040 -2.970  -1.330  -5.32
## log_k_Z0_bound_free -4.840     1.6100 -8.100  -1.580  -3.00
## log_k_Z0_free_Z1     0.846     0.0583  0.728   0.964  14.50
## log_k_Z1_Z2        -0.781     0.0649 -0.912  -0.650 -12.00
## log_k_Z2_sink       -0.861     0.1060 -1.070  -0.647  -8.14
##               Pr(>|t|) Pr(>t)
## Z0_free_0        2.70e-35 1.35e-35
## log_k_Z0_free_bound 4.88e-06 2.44e-06
## log_k_Z0_bound_free 4.71e-03 2.35e-03
## log_k_Z0_free_Z1   4.50e-17 2.25e-17
## log_k_Z1_Z2        1.52e-14 7.61e-15
## log_k_Z2_sink       7.47e-10 3.73e-10
##
## Parameter correlation:
##               Z0_free_0 log_k_Z0_free_bound log_k_Z0_bound_free
## Z0_free_0      1.0000                0.075      0.0708
## log_k_Z0_free_bound 0.0750                1.000      0.5425
## log_k_Z0_bound_free 0.0708                0.543      1.0000

```

```

## log_k_Z0_free_Z1      0.0908      0.425      0.1632
## log_k_Z1_Z2           0.2572     -0.228     -0.0863
## log_k_Z2_sink         0.2888     -0.211     -0.0792
##           log_k_Z0_free_Z1 log_k_Z1_Z2 log_k_Z2_sink
## Z0_free_0            0.0908      0.2572      0.2888
## log_k_Z0_free_bound   0.4245     -0.2276     -0.2105
## log_k_Z0_bound_free   0.1632     -0.0863     -0.0792
## log_k_Z0_free_Z1      1.0000     -0.1008     -0.0490
## log_k_Z1_Z2           -0.1008      1.0000      0.2728
## log_k_Z2_sink         -0.0490      0.2728      1.0000
##
## Residual standard error: 4.08 on 38 degrees of freedom
##
## Backtransformed parameters:
##           Estimate      Lower      Upper
## Z0_free_0      97.40000 9.32e+01 102.000
## k_Z0_free_bound 0.11700 5.15e-02  0.264
## k_Z0_bound_free 0.00792 3.04e-04  0.207
## k_Z0_free_Z1   2.33000 2.07e+00  2.620
## k_Z1_Z2         0.45800 4.02e-01  0.522
## k_Z2_sink       0.42300 3.41e-01  0.524
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data      17.3      6 36
## Z0             14.7      4 13
## Z1             14.4      1 12
## Z2             20.3      1 11
##
## Estimated Eigenvalues of SFORB model(s):
##   Z0_b1  Z0_b2
## 2.44664 0.00754
##
## Resulting formation fractions:
##           ff
## Z0_free_Z1  1
## Z1_Z2       1
## Z2_sink     1
##
## Estimated disappearance times:
##   DT50 DT90 DT50_Z0_b1 DT50_Z0_b2
## Z0 0.304 1.18      0.283      91.9

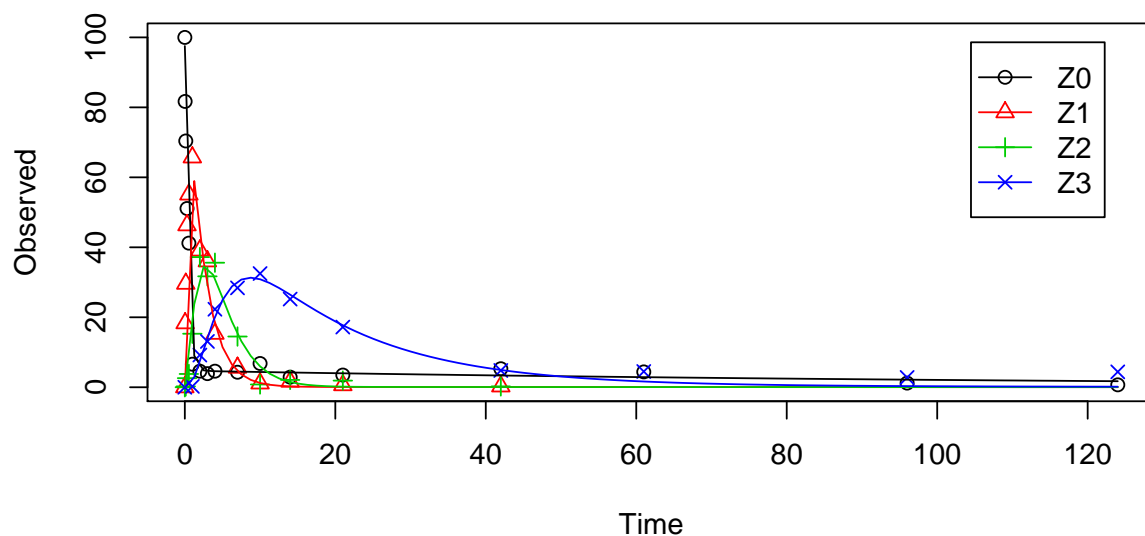
```

```
## Z1 1.514 5.03      NA      NA
## Z2 1.639 5.44      NA      NA
```

This results in a much better representation of the behaviour of the parent compound Z0.

Finally, Z3 is added as well. These models appear overparameterised (no covariance matrix returned) if the sink for Z1 is left in the models.

```
Z.mkin.4 <- mkinmod(Z0 = list(type = "SFORB", to = "Z1", sink = FALSE),
  Z1 = list(type = "SFO", to = "Z2", sink = FALSE),
  Z2 = list(type = "SFO", to = "Z3"),
  Z3 = list(type = "SFO"))
m.Z.mkin.4 <- mkinfit(Z.mkin.4, FOCUS_2006_Z_mkin,
  parms.ini = c(k_Z1_Z2 = 0.05),
  quiet = TRUE)
plot(m.Z.mkin.4)
```



```
summary(m.Z.mkin.4, data = FALSE)

## mkin version:    0.9.33
## R version:       3.1.1
## Date of fit:      Sat Oct 11 10:02:05 2014
## Date of summary:  Sat Oct 11 10:02:06 2014
##
## Equations:
```

```

## d_Z0_free = - 0 - k_Z0_free_bound * Z0_free + k_Z0_bound_free
##           * Z0_bound - k_Z0_free_Z1 * Z0_free
## d_Z0_bound = + k_Z0_free_bound * Z0_free - k_Z0_bound_free *
##           Z0_bound
## d_Z1 = + k_Z0_free_Z1 * Z0_free - 0 - k_Z1_Z2 * Z1
## d_Z2 = + k_Z1_Z2 * Z1 - k_Z2_sink * Z2 - k_Z2_Z3 * Z2
## d_Z3 = + k_Z2_Z3 * Z2 - k_Z3_sink * Z3
##
## Model predictions using solution type eigen
##
## Fitted with method Marq using 207 model solutions performed in 4.775 s
##
## Weighting: none
##
## Starting values for parameters to be optimised:
##           value   type
## Z0_free_0      100.0000 state
## k_Z1_Z2         0.0500 deparm
## k_Z0_free_bound 0.1000 deparm
## k_Z0_bound_free 0.0200 deparm
## k_Z0_free_Z1    0.1002 deparm
## k_Z2_sink       0.1003 deparm
## k_Z2_Z3         0.1004 deparm
## k_Z3_sink       0.1005 deparm
##
## Starting values for the transformed parameters actually optimised:
##           value lower upper
## Z0_free_0      100.000 -Inf   Inf
## log_k_Z1_Z2     -2.996 -Inf   Inf
## log_k_Z0_free_bound -2.303 -Inf   Inf
## log_k_Z0_bound_free -3.912 -Inf   Inf
## log_k_Z0_free_Z1  -2.301 -Inf   Inf
## log_k_Z2_sink    -2.300 -Inf   Inf
## log_k_Z2_Z3      -2.299 -Inf   Inf
## log_k_Z3_sink    -2.298 -Inf   Inf
##
## Fixed parameter values:
##           value   type
## Z0_bound_0       0 state
## Z1_0              0 state
## Z2_0              0 state
## Z3_0              0 state

```

```

##
## Optimised, transformed parameters:
##      Estimate Std. Error Lower Upper t value
## Z0_free_0      97.500      1.8900 93.700 101.000  51.70
## log_k_Z1_Z2     -0.777      0.0583 -0.894 -0.660 -13.30
## log_k_Z0_free_bound -2.140      0.3680 -2.880 -1.400  -5.80
## log_k_Z0_bound_free -4.760      1.4200 -7.610 -1.920  -3.36
## log_k_Z0_free_Z1      0.847      0.0534  0.740  0.954  15.90
## log_k_Z2_sink     -1.560      0.1830 -1.930 -1.190  -8.55
## log_k_Z2_Z3     -1.530      0.1140 -1.760 -1.300 -13.50
## log_k_Z3_sink     -2.770      0.2250 -3.220 -2.320 -12.30
##      Pr(>|t|) Pr(>t)
## Z0_free_0      2.07e-44 1.03e-44
## log_k_Z1_Z2      6.66e-18 3.33e-18
## log_k_Z0_free_bound 4.71e-07 2.36e-07
## log_k_Z0_bound_free 1.52e-03 7.58e-04
## log_k_Z0_free_Z1      6.13e-21 3.06e-21
## log_k_Z2_sink      2.79e-11 1.40e-11
## log_k_Z2_Z3      4.49e-18 2.24e-18
## log_k_Z3_sink      1.25e-16 6.23e-17
##
## Parameter correlation:
##      Z0_free_0 log_k_Z1_Z2 log_k_Z0_free_bound
## Z0_free_0      1.0000      0.2424      0.0782
## log_k_Z1_Z2      0.2424      1.0000      -0.2274
## log_k_Z0_free_bound 0.0782     -0.2274      1.0000
## log_k_Z0_bound_free 0.0692     -0.0894      0.5398
## log_k_Z0_free_Z1      0.0888     -0.1084      0.4276
## log_k_Z2_sink      0.3299      0.3405     -0.2633
## log_k_Z2_Z3     -0.0749     -0.1489      0.0670
## log_k_Z3_sink     -0.1046     -0.2249      0.1384
##      log_k_Z0_bound_free log_k_Z0_free_Z1
## Z0_free_0      0.0692      0.0888
## log_k_Z1_Z2     -0.0894     -0.1084
## log_k_Z0_free_bound 0.5398      0.4276
## log_k_Z0_bound_free 1.0000      0.1628
## log_k_Z0_free_Z1      0.1628      1.0000
## log_k_Z2_sink     -0.1275     -0.0531
## log_k_Z2_Z3      0.0608     -0.0128
## log_k_Z3_sink      0.1252      0.0186
##      log_k_Z2_sink log_k_Z2_Z3 log_k_Z3_sink
## Z0_free_0      0.3299     -0.0749     -0.1046

```



```

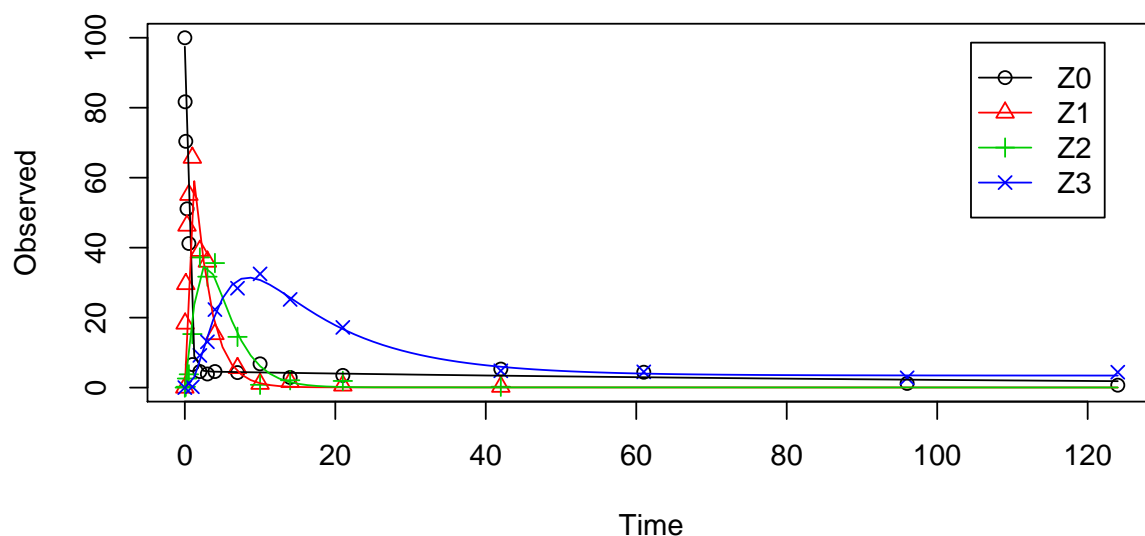
## log_k_Z1_Z2          0.3405      -0.1489      -0.2249
## log_k_Z0_free_bound  -0.2633       0.0670       0.1384
## log_k_Z0_bound_free  -0.1275       0.0608       0.1252
## log_k_Z0_free_Z1     -0.0531      -0.0128       0.0186
## log_k_Z2_sink        1.0000      -0.2547      -0.6832
## log_k_Z2_Z3          -0.2547       1.0000       0.5639
## log_k_Z3_sink        -0.6832       0.5639       1.0000
##
## Residual standard error: 3.74 on 49 degrees of freedom
##
## Backtransformed parameters:
##           Estimate      Lower      Upper
## Z0_free_0    97.50000 9.37e+01 101.0000
## k_Z1_Z2       0.46000 4.09e-01  0.5170
## k_Z0_free_bound 0.11800 5.64e-02  0.2480
## k_Z0_bound_free 0.00852 4.93e-04  0.1470
## k_Z0_free_Z1   2.33000 2.10e+00  2.6000
## k_Z2_sink      0.21000 1.45e-01  0.3030
## k_Z2_Z3        0.21700 1.73e-01  0.2730
## k_Z3_sink      0.06270 3.99e-02  0.0985
##
## Chi2 error levels in percent:
##           err.min n.optim df
## All data    17.5      8 46
## Z0          14.7      4 13
## Z1          14.4      1 12
## Z2          21.0      2 10
## Z3          11.8      1 11
##
## Estimated Eigenvalues of SFORB model(s):
##   Z0_b1  Z0_b2
## 2.45127 0.00811
##
## Resulting formation fractions:
##           ff
## Z0_free_Z1 1.000
## Z1_Z2      1.000
## Z2_sink    0.492
## Z2_Z3      0.508
## Z3_sink    1.000
##
## Estimated disappearance times:

```

##	DT50	DT90	DT50_Z0_b1	DT50_Z0_b2
## Z0	0.304	1.19	0.283	85.4
## Z1	1.507	5.01	NA	NA
## Z2	1.623	5.39	NA	NA
## Z3	11.051	36.71	NA	NA

The error level of the fit, but especially of metabolite Z3, can be improved if the SFORB model is chosen for this metabolite, as this model is capable of representing the tailing of the metabolite decline phase.

```
Z.mkin.5 <- mkinmod(Z0 = list(type = "SFORB", to = "Z1", sink = FALSE),
  Z1 = list(type = "SFO", to = "Z2", sink = FALSE),
  Z2 = list(type = "SFO", to = "Z3"),
  Z3 = list(type = "SFORB"))
m.Z.mkin.5 <- mkinfit(Z.mkin.5, FOCUS_2006_Z_mkin,
  parms.ini = m.Z.mkin.4$bparms.ode[1:5],
  quiet = TRUE)
plot(m.Z.mkin.5)
```



```
summary(m.Z.mkin.5, data = FALSE)$bpar
```

##		Estimate	Lower	Upper
## Z0_free_0		9.742e+01	NA	NA
## k_Z0_free_bound		1.168e-01	NA	NA
## k_Z0_bound_free		7.890e-03	NA	NA

```
## k_Z0_free_Z1      2.330e+00    NA    NA
## k_Z1_Z2           4.576e-01    NA    NA
## k_Z2_sink         1.957e-01    NA    NA
## k_Z2_Z3_free      2.266e-01    NA    NA
## k_Z3_free_sink    7.479e-02    NA    NA
## k_Z3_free_bound   5.218e-03    NA    NA
## k_Z3_bound_free   5.013e-22    NA    NA
```

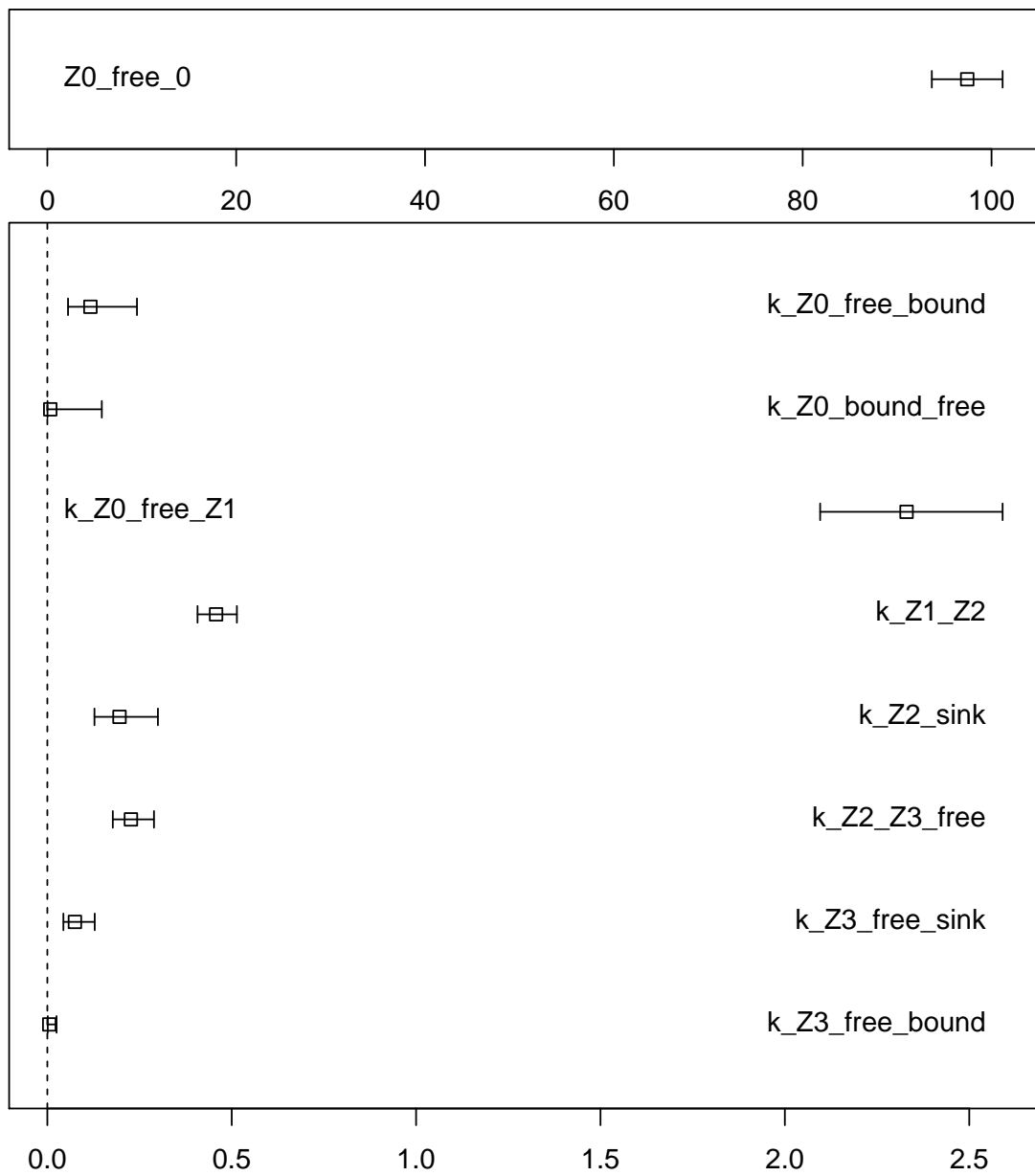
The summary view of the backtransformed parameters shows that we get no confidence intervals due to overparameterisation. As the optimized `k_Z3_bound_free` is excessively small, it is reasonable to fix it to zero.

```
m.Z.mkin.5a <- mkinfit(Z.mkin.5, FOCUS_2006_Z_mkin,
                      parms.ini = c(m.Z.mkin.4$bparms.ode[1:5],
                                   k_Z3_bound_free = 0),
                      fixed_parms = "k_Z3_bound_free",
                      quiet = TRUE)
summary(m.Z.mkin.5a, data = FALSE)$bpar
```

##	Estimate	Lower	Upper
## Z0_free_0	97.424939	9.368e+01	101.17374
## k_Z0_free_bound	0.116755	5.608e-02	0.24306
## k_Z0_bound_free	0.007889	4.213e-04	0.14772
## k_Z0_free_Z1	2.329999	2.096e+00	2.59050
## k_Z1_Z2	0.457590	4.074e-01	0.51402
## k_Z2_sink	0.195710	1.277e-01	0.29984
## k_Z2_Z3_free	0.226585	1.775e-01	0.28920
## k_Z3_free_sink	0.074789	4.354e-02	0.12848
## k_Z3_free_bound	0.005218	1.093e-03	0.02492

A graphical representation of the confidence intervals can finally be obtained.

```
mkinparplot(m.Z.mkin.5a)
```



The endpoints obtained with this model are

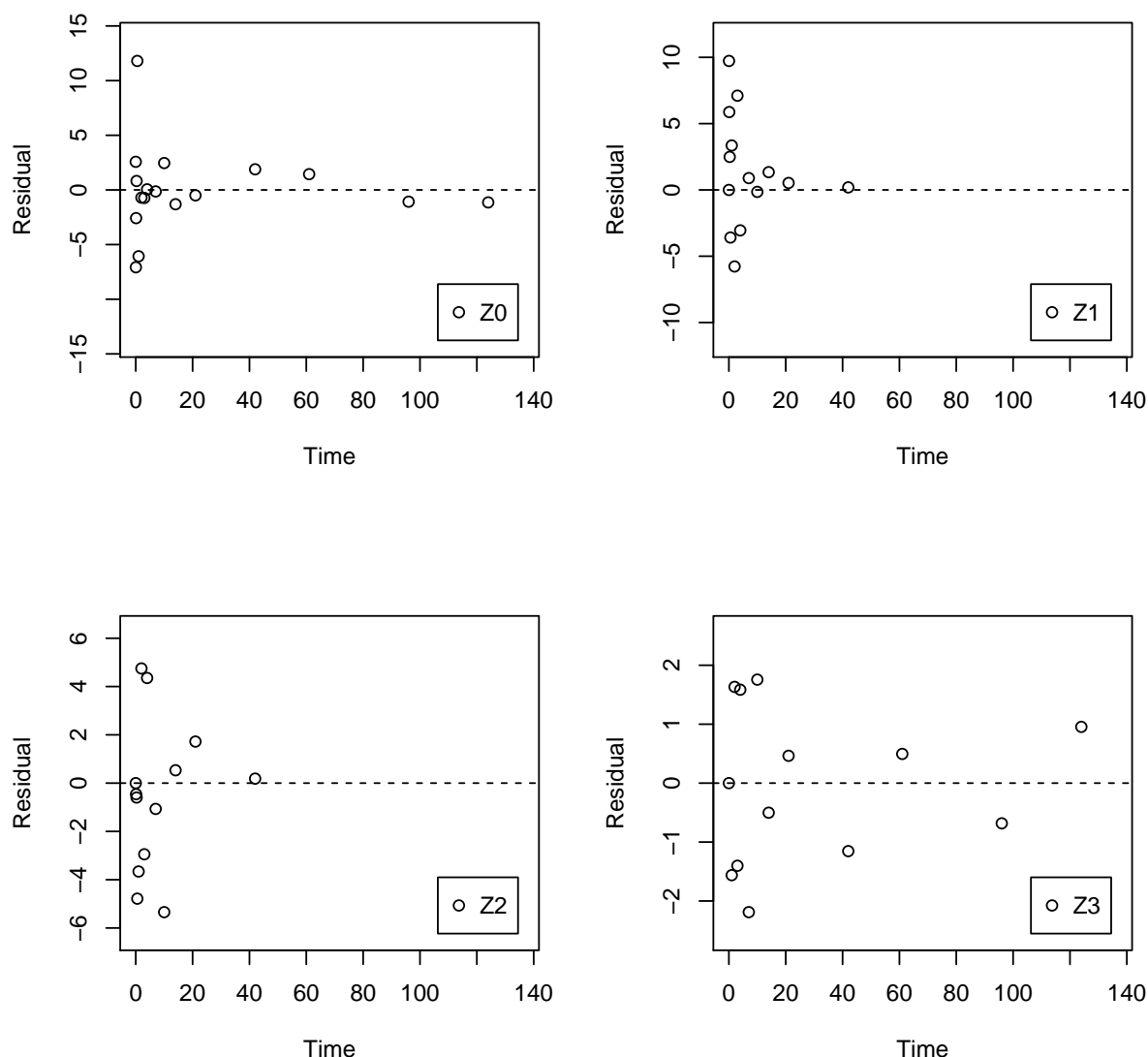
```
endpoints(m.Z.mkin.5a)

## $ff
##   Z0_free_Z1      Z1_Z2      Z2_sink      Z2_Z3_free Z3_free_sink
##   1.0000      1.0000      0.4634      0.5366      1.0000
##
## $SFORB
##   Z0_b1      Z0_b2      Z3_b1      Z3_b2
## 2.447132 0.007511 0.080007 0.000000
```

```
##
## $distimes
##      DT50    DT90 DT50_Z0_b1 DT50_Z0_b2 DT50_Z3_b1 DT50_Z3_b2
## Z0 0.3043  1.185    0.2832    92.28         NA         NA
## Z1 1.5148  5.032         NA         NA         NA         NA
## Z2 1.6414  5.453         NA         NA         NA         NA
## Z3 9.5675 41.137         NA         NA         8.664        Inf
```

It is clear the degradation rate of Z3 towards the end of the experiment is very low as DT50_Z3_b2 is reported to be infinity. However, this appears to be a feature of the data.

```
par(mfrow = c(2, 2))
mkinresplot(m.Z.mkin.5, "Z0", lpos = "bottomright")
mkinresplot(m.Z.mkin.5, "Z1", lpos = "bottomright")
mkinresplot(m.Z.mkin.5, "Z2", lpos = "bottomright")
mkinresplot(m.Z.mkin.5, "Z3", lpos = "bottomright")
```



As expected, the residual plots are much more random than in the case of the all SFO model for which they were shown above. In conclusion, the model `Z.mkin.5` is proposed as the best-fit model for the dataset from Appendix 7 of the FOCUS report.

References

FOCUS Work Group on Degradation Kinetics. *Generic guidance for estimating persistence and degradation kinetics from environmental fate studies on pesticides in EU registration*, 1.0 edition, November 2011. URL <http://focus.jrc.ec.europa.eu/dk>.