



National Institute for Public Health  
and the Environment  
*Ministry of Health, Welfare and Sport*

**Congener specific transfer model for  
dioxins (PCDD/Fs and dl-PCBs) in  
laying hens, version 1.4 - model  
documentation.**

2024

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## Colophon

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## Summary

The fundamentals of a congener specific feed-food transfer model for PCDD/F and dl-PCB concentrations in body fat and egg yolk fat in laying hens are presented. The model, which is available as a webtool application (<https://feedfoodtransfer.nl/>), can be used to compare simulated concentrations with regulatory limits for these food matrices.

# 1 Introduction

Polychlorinated dibenzo-p-dioxins and dibenzofurans (PCDD/Fs) and dioxin-like polychlorinated biphenyls (dl-PCBs) are persistent environmental pollutants (POPs) that may accumulate in fatty tissues and the liver (“hepatic sequestration”) of animals and humans. One of the main sources of human exposure to PCDD/Fs and dl-PCBs is the consumption of animal products, such as meat, milk and eggs. In turn, animal feed is an important contributor to the accumulation of PCDD/Fs and dl-PCBs in animal products used for human consumption.

This report presents the congener-specific transfer model that estimates PCDD/F and dl-PCB concentrations in body fat and egg yolk fat of laying hens exposed to these compounds via feed.

The concentration of the sum of PCDD/Fs and dl-PCBs is expressed in total toxic equivalents of 2,3,7,8-TCDD (total TEQ) using Toxic Equivalence Factors (TEFs) for the different PCDD/F and dl-PCB congeners (van den Berg et al. 2006). The estimated concentrations can be compared to the regulatory limits that have been defined by regulatory agencies in various countries.

For all congeners the same model structure was used, but parameter values were calibrated separately for each congener. The model is available as a webtool application (<https://feedfoodtransfer.nl/>).

For simulations based on total TEQ levels in feed, a total TEQ transfer model is also available as a webtool application. The calibration of this latter model is based on the total TEQ concentration, i.e. the concentration of PCDD/Fs and dl-PCBs expressed in terms of equivalents of 2,3,7,8-TCDD.

## 2 Model description

### 2.1 General overview

The transfer model used to estimate PCDD/Fs and dl-PCBs concentrations in egg yolk comprises two compartments representing a central compartment and a fat compartment (Fig 1). Intake of PCDD/Fs and dl-PCBs is modelled as a constant intake amount,  $A_i$ , of which a fraction ( $F_{abs}$ ) is absorbed over the gut wall into the central compartment on a daily basis. PCDD/Fs and dl-PCBs that have been absorbed by the central compartment can migrate to the fat compartment ( $q_c$ ), and vice versa ( $q_f$ ). PCDD/Fs and dl-PCBs can leave the laying hen's body through two processes. The first is excretion to egg yolk fat ( $\varepsilon y$ ), with  $\varepsilon$  being the laying efficiency, and  $y$  being the excretion rate constant. The second is hepatic clearance ( $k$ ).

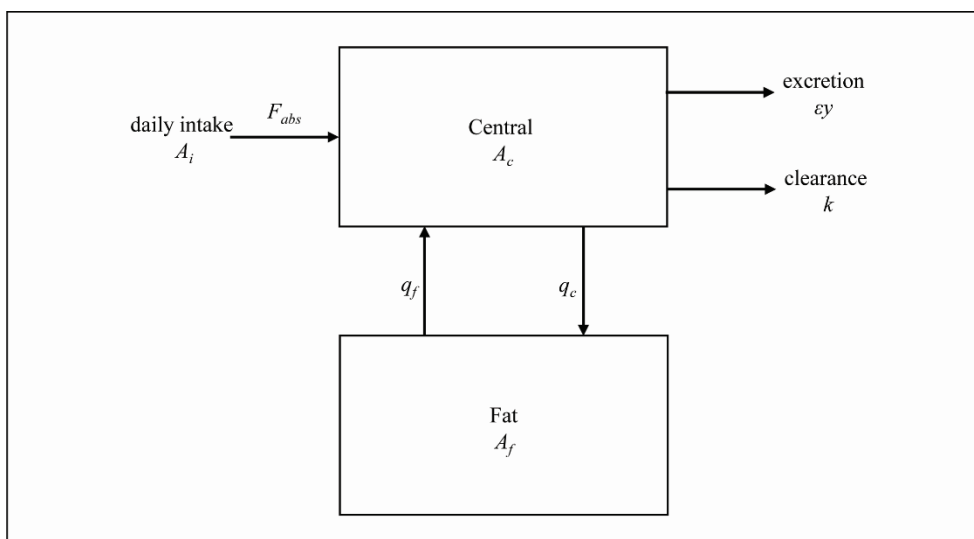


Figure 1. Two compartments comprised kinetic model for the PCDD/F and dl-PCB congeners in the laying hen (Figure taken from Notenboom et al. 2023).

### 2.2 Model equations

The transfer model described in this report consists of a set of coupled ordinary differential equations (ODEs). These ODEs describe the distribution of PCDD/Fs and dl-PCBs between the central compartment and the fat compartment over time. For both compartments of the models, an ODE was formulated. Specifically, equations 1 and 2 describe the change in the amount of PCDD/Fs and dl-PCBs in the central compartment and the fat compartment, respectively.

$$\frac{dA_c(t)}{dt} = F_{abs}A_i - (q_c + \varepsilon y + k)A_c(t) + q_f A_f(t) \quad (1)$$

$$\frac{dA_f(t)}{dt} = q_c A_c(t) - q_f A_f(t) \quad (2)$$

$A_c(t)$  [pg]: Amount of substance in the central compartment at time  $t$

$A_f(t)$  [pg]: Amount of substance in the fat compartment at time  $t$

$F_{abs}$  [-]: Absorption fraction

$A_i$  [pg day<sup>-1</sup>]: Daily intake amount of substance

$q_c$  [day<sup>-1</sup>]: Transfer rate constant from central compartment to fat compartment

$q_f$  [day<sup>-1</sup>]: Transfer rate constant from fat compartment to central compartment

$\varepsilon$  [-]: Laying efficiency

$y$  [day<sup>-1</sup>]: Excretion rate constant from central compartment to egg yolk fat

$k$  [day<sup>-1</sup>]: Hepatic clearance rate constant

The transfer rate parameters used in equations 1 and 2 can be expressed as unknown model parameters (van Eijkeren et al., 2006):

$$q_c = \frac{Q}{P_c V_c} \quad (3)$$

$$q_f = \frac{Q}{P_f V_f} \quad (4)$$

$$y = \frac{P_{y,f} W_{y,f}}{P_c V_c} \quad (5)$$

$$k = \frac{CL}{P_c V_c} \quad (6)$$

Here,  $Q$  represents the compartment blood flow.  $V_c$  and  $V_f$  represent the volumes of the central and fat compartment, respectively.  $P_c$  and  $P_f$  represent the blood-body partition coefficient and the blood-fat partition coefficients, respectively.  $CL$  represents the hepatic clearance rate.  $W_{y,f}$  is the amount of fat in the egg yolk and  $P_{y,f}$  is the partition coefficient between the blood and the egg yolk fat.

The amount of PCDD/F and dl-PCB congeners in the body and fat compartment can be converted into concentrations by dividing the amount by the volume of the respective compartments,  $V_c$  and  $V_f$ .

Finally, the change in the amount of PCDD/F and dl-PCB congeners in eggs at a given time,  $A_{yf}(t)$ , can be calculated as follows:

$$\frac{dA_{yf}(t)}{dt} = \varepsilon y A_c(t) - A_{yf}(t) \quad (7)$$

## 2.3 Model assumptions

The following assumptions were made in the presented model:

- PCDD/Fs and dl-PCBs homogeneously distribute over the fat compartment.
- PCDD/F and dl-PCB concentrations measured in abdominal fat are representative of the PCDD/F and dl-PCB concentrations in the fat compartment.
- Hepatic sequestration was neglected
- The amount of fat in the egg yolk,  $W_{y,f}$  is constant over time and can be measured.
- The laying hens are assumed to weigh 1840 grams ( $V_{total}$ ). The sizes of the two compartments (central and fat) are calibrated.
- It is assumed that the hens get fed once a day with a constant amount of feed per day.
- The volume of the central compartment can be derived by taking the difference between the total volume and the volume of the fat compartment (which was calibrated (see section 2.5)).
- The density of the compartments is 1 g/cm<sup>3</sup>. The volume of the model compartments,  $V_c$  and  $V_f$ , are thus equal to the weights of the compartments ( $W_c$  and  $W_f$ ).
- Limitations of the available experimental data prevented the calibration of 1,2,3,4,6,7,8,9-OCDF, 1,2,3,4,6,7,8-HpCDD, 1,2,3,4,6,7,8,9-OCDD and PCB123. For these congeners the simulation is performed using the parameters for the total TEQ model.

## 2.4 Generic parameters

The remaining parameters (*Table 1*) are not specific to PCDD/Fs or dl-PCBs and can all be obtained from literature.

*Table 1. Generic parameter values*

Parameter	Value	Unit	Source
$\epsilon$	0.9	day <sup>-1</sup>	Mean of exposure groups in Kan and Jonker-Den Rooyen (1978)
$V_{total}$	1840	cm <sup>3</sup>	expert opinion
$W_{egg}$	60	g	Kan and Jonker-Den Rooyen (1978)
$W_y$	19.2	g	Gilbert (1971)
$W_{y,f}$	5.76	g	Gilbert (1971)

## 2.5 System-dependent parameters

As explained by van Eijkeren et al. (2006), the presented transfer model contains two parameters,  $q_c$  and  $q_f$ , that can be identified unconditionally from the available experimental data, whereas it contains four parameters,  $y$ ,  $k$ ,  $F_{abs}$ , and  $W_f$ , that are conditionally identifiable. The four conditionally identifiable parameters cannot be directly fitted to the data.



However, they can be determined in relation with each other (van Eijkeren et al., 2006):

$$c_1 = r = \varepsilon y + k \quad (8)$$

$$c_2 = yF_{abs} \quad (9)$$

$$c_3 = \frac{F_{abs}}{W_f} \quad (10)$$

Here, parameters  $c_1$ ,  $c_2$ , and  $c_3$  can be fitted to the available experimental data. Although the four conditionally identifiable parameters cannot be directly fitted to the data and it is thus impossible to find a single value they should take on, it is possible to find the possible range of values they might take on. This can be done by defining boundary conditions on the parameter values. More specifically, the hepatic clearance,  $k$ , cannot be lower than  $0 \text{ day}^{-1}$ , whereas the absorption fraction,  $F_{abs}$  cannot exceed 1. If the model is fitted with the first boundary condition, i.e.,  $k \geq 0$ , then it follows that  $y \leq \frac{c_1}{\varepsilon}$ ,  $F_{abs} \geq \frac{c_2}{y}$ , and  $W_f \geq \frac{F_{abs}}{c_3}$ . Similarly, from the second boundary condition, i.e.,  $F_{abs} \leq 1$ , it follows that  $y \Rightarrow c_2$ ,  $k \leq c_1 - \varepsilon c_2$  and  $W_f \leq \frac{1}{c_3}$ .

The true parameter values are thus mathematically bound to be within the boundaries described above. However, in order to find definitive parameter values for the transfer model, assumptions were necessary. Therefore, as a conservative estimate for the substance concentrations in egg yolk fat, an hepatic clearance of 0 was assumed, i.e.,  $k = 0$ . From this assumption, it follows that  $y = \frac{c_1}{\varepsilon}$ ,  $F_{abs} = \frac{\varepsilon c_2}{c_1}$  and  $W_f = \frac{\varepsilon c_2}{c_1 c_3}$ . Based on these assumptions, Notenboom et al. (2023) calibrated these model parameters using the experimental data reported by Hoogenboom et al. (2006) and Traag et al. (2006) for the PCDD/F and dl-PCB toxic equivalent (TEQ) as well as for each of the individual congeners. The calibrated parameters used in the transfer model are shown in Table 2. Note that calibration of the parameters was not possible for 1,2,3,4,6,7,8,9-OCDF, 1,2,3,4,6,7,8-HpCDD, 1,2,3,4,6,7,8,9-OCDD and PCB 123. For these compounds, a web tool user can either choose to use the parameter values calibrated for PCDD/F and dl-PCB TEQ, or to exclude these compounds from the analyses.

Table 2. Calibrated parameter values used in the transfer model for each of the 29 congeners

Compound	$q_c$ [day <sup>-1</sup> ] Mass transfer rate from central compartment to fat compartment.*	$q_f$ [day <sup>-1</sup> ] Mass transfer rate from fat compartment to central compartment.*	$F_{abs}$ [-] Absorption fraction. Calibrated.*	$\gamma$ [day <sup>-1</sup> ] Excretion rate constant to egg yolk fat	$k$ [day <sup>-1</sup> ] Hepatic clearance rate	$V_f$ [g]
PCDD/F and dl-PCB TEQ	0.14	0.06	0.78	0.057	0	230
2,3,7,8-TCDF	0.31	0.205	0.70	0.040	0	200
1,2,3,7,8-PeCDF	0.19	0.073	0.71	0.078	0	210
2,3,4,7,8-PeCDF	0.10	0.057	0.71	0.055	0	190
1,2,3,4,7,8-HxCDF	0.08	0.029	0.60	0.110	0	180
1,2,3,6,7,8-HxCDF	0.08	0.031	0.55	0.109	0	180
2,3,4,6,7,8-HxCDF	0.10	0.034	0.45	0.131	0	200
1,2,3,7,8,9-HxCDF	0.10	0.040	0.54	0.103	0	180
1,2,3,4,6,7,8-HpCDF	0.06	0.034	0.18	0.182	0	140
1,2,3,4,7,8,9-HpCDF	0.04	0.018	0.24	0.167	0	150
1,2,3,4,6,7,8,9-OCDF**	-	-	-	-	-	-
2,3,7,8-TCDD	0.35	0.230	0.78	0.042	0	210
1,2,3,7,8-PeCDD	0.14	0.070	0.75	0.055	0	220
1,2,3,4,7,8-HxCDD	0.09	0.030	0.61	0.101	0	190
1,2,3,6,7,8-HxCDD	0.09	0.036	0.59	0.106	0	170
1,2,3,7,8,9-HxCDD	0.07	0.032	0.42	0.118	0	150
1,2,3,4,6,7,8-HpCDD**	-	-	-	-	-	-
1,2,3,4,6,7,8,9-OCDD**	-	-	-	-	-	-
PCB 81	0.11	0.121	0.92	0.024	0	190
PCB 77	0.25	0.136	0.89	0.044	0	240
PCB 126	0.13	0.067	1.00	0.038	0	270

Compound	$q_c$ [day <sup>-1</sup> ] Mass transfer rate from central compartment to fat compartment.*	$q_f$ [day <sup>-1</sup> ] Mass transfer rate from fat compartment to central compartment.*	$F_{abs}$ [-] Absorption fraction. Calibrated.*	$\gamma$ [day <sup>-1</sup> ] Excretion rate constant to egg yolk fat	$k$ [day <sup>-1</sup> ] Hepatic clearance rate	$V_f$ [g]
PCB 169	0.11	0.029	0.85	0.081	0	220
PCB 123**	-	-	-	-	-	-
PCB 118	0.12	0.063	0.98	0.041	0	230
PCB 114	0.20	0.090	0.89	0.061	0	180
PCB 105	0.12	0.084	0.92	0.037	0	200
PCB 167	0.10	0.095	1.00	0.062	0	70
PCB 156	0.11	0.039	0.92	0.063	0	220
PCB 157	0.16	0.051	0.86	0.094	0	190
PCB 189	0.06	0.017	0.80	0.102	0	190

\* Notenboom et al., 2023

\*\* No calibration possible. For these congeners the simulation is performed using the parameters for the total TEQ model (PCDD/F and dl-PCB TEQ).

### 3 Software details

The transfer model simulations were developed and run using the R modelling language and using the deSolve package. Specifications on the programming packages are listed below:

Name software: R (tested with version 4.0.5)  
Manufacturer: The R Foundation for Statistical Computing  
Place of manufacture: online  
Year of manufacture: 2021  
Description: A programming language for statistical computing

Name software: DeSolve (tested with version 1.30)  
Manufacturer: Karline Soetaert, Thomas Petzoldt and R. Woodrow Setzer  
Place of manufacture: online  
Year of manufacture: 2023  
Description: Package to solve systems of differential equations  
url: <https://cran.r-project.org/web/packages/deSolve/index.html>

Name software: dplyr (tested with version 1.1.4)  
Manufacturer: Hadley Wickham, Romain François, Lionel Henry, Kirill Müller, Davis Vaughan, Ryan Dickerson, Posit Software, PBC  
Place of manufacture: online  
Year of manufacture: 2023  
Description: A fast, consistent tool for working with data frame like objects, both in memory and out of memory.  
url: <https://cran.r-project.org/web/packages/dplyr/index.html>

## 4 Model applicability

The transfer model presented in this report can be used to simulate the carry-over of PCDD/Fs and dl-PCBs from feed to body fat and egg yolk fat of laying hens. As such, the model enables comparison of the estimated concentration to regulatory limits of these food matrices. Similarly the model can be used to estimate the wash-out period needed to comply with regulatory limits in case the concentrations exceeded such regulatory limits.

An example of a model application is given in Figure 2. The grey line depicts the dioxin concentration in egg yolk fat based on the sum of the transfer of the individual congeners.

In addition, the black line shows the model calculations based on the total TEQ model, i.e. based on the total TEQ concentration in feed. This total TEQ model is also available as a separate model on the website [feedfoodtransfer.nl](http://feedfoodtransfer.nl).

Exposure to various congeners was simulated for an exposure duration of 56 days. Concentrations of congeners in the contaminated feed are given in Table 3. Feed intake was 0.113 kg per day. After the 56 days of exposure to contaminated feed, an additional 200 days were simulated in which only clean feed was provided (i.e. feed not containing any PCDD/F and dl-PCB congeners).

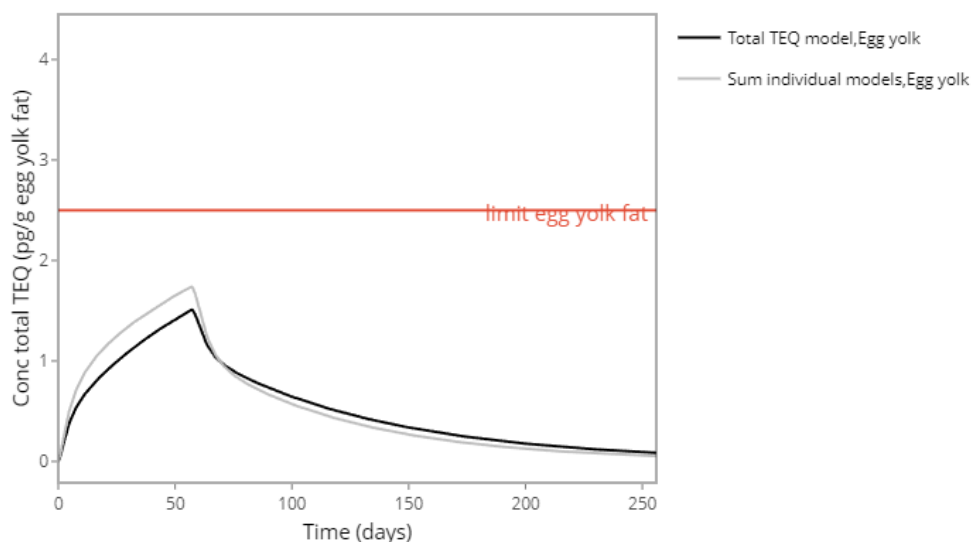


Figure 2 Simulated total TEQ concentration in egg yolk of laying hens fed contaminated feed during 56 days followed by clean feed for 200 days. Laying hens were fed 0.113 kg dry feed per day.

*Table 3 Congener concentrations in feed used to illustrate the simulation of the total TEQ concentration in egg yolk.*

<b>Congener</b>	<b>Concentration (ng kg<sup>-1</sup> dry feed)</b>
2,3,7,8-TCDF	0.12
2,3,4,7,8-PeCDF	0.34
1,2,3,6,7,8-HxCDF	0.21
1,2,3,7,8,9-HxCDF	0.10
1,2,3,4,6,7,8-HpCDF	0.22
1,2,3,6,7,8-HxCDD	0.51

## 5 References

Gilbert, A. (1971) The egg: its physical and chemical aspects. In "Physiology and Biochemistry of the Domestic Fowl" Vol. 3, eds. Bell, DJ, and Freeman, BM. Academic, New York.

Hoogenboom, LAP, Kan CA, Zeilmaker MJ, van Eijkeren JCH, Traag WA. (2006). Carry-over of dioxins and PCBs from feed and soil to eggs at low contamination levels. *Food Additives and Contaminants* 23:518–527. <https://doi.org/10.1080/02652030500512037>.

Kan, CA and JC. Jonker-Den Rooyen, JC. (1978) Accumulation and depletion of some organochlorine pesticides in high-producing laying hens. *Journal of Agricultural and Food Chemistry*. 26(4): 935-940. <https://doi.org/10.1021/jf60218a007>.

Notenboom S, Punt A, Hoogenveen R, Zeilmaker MJ, Hoogenboom LAP, Bokkers BGH. (2023) A congener-specific modelling approach for the transfer of polychlorinated dibenzo-p-dioxins and dibenzofurans and dioxin-like polychlorinated biphenyls from feed to eggs of laying hens, *Food Additives & Contaminants: Part A*, 40:1, 96-109. <https://doi.org/10.1080/19440049.2022.2137301>.

Traag, WA, Kan, CA, van der Weg, G, Onstenk, C, Hoogenboom, LAP. (2006). Residues of dioxins (PCDD/Fs) and PCBs in eggs, fat and livers of laying hens following consumption of contaminated feed. *Chemosphere* 65:9, 1518-1525. <https://doi.org/10.1016/j.chemosphere.2006.04.001>

Van den Berg M, Birnbaum LS, Denison M, De Vito M, Farland W, Feeley M, Fiedler H, Hakansson H, Hanberg A, Haws L, Rose M, Safe S, Schrenk D, Tohyama C, Tritscher A, Tuomisto J, Tysklind M, Walker N, Peterson RE. (2006). The 2005 World Health Organization reevaluation of human and mammalian toxic equivalency factors for dioxins and dioxin-like compounds. *Toxicol Sci*. 93(2):223-241. <https://doi.org/10.1093/toxsci/kfl055>

Van Eijkeren JCH, Zeilmaker MJ, Kan CA, Traag WA, Hoogenboom LAP. (2006) A toxicokinetic model for the carry-over of dioxins and PCBs from feed and soil to eggs, *Food Additives & Contaminants*, 23:5, 509-517. <https://doi.org/10.1080/02652030500512045>.

## Annex I: R-Code

The code below illustrates the basic implementation of the congener specific transfer model for dioxins (PCDD/Fs and dl-PCBs) in laying hens, v1.3. This code can be used freely and is provided "as is" without warranty of any kind. The National Institute of Public Health and the Environment (RIVM) expressly rejects all liability for the accuracy, completeness, or suitability of the information provided. Use of the information is entirely at your own risk.

### Model code (dioxin-congener-laying-hen.R):

---

```
library(deSolve)

assign_parameters <- function(cpd) {
  #' Assign default parameters for the model
  #'
  #' @param cpd name of the compound for which the parameters are
  #' needed
  #'
  #' @return parameter vector

  inputParameters <- modelParameters |>
    mutate(
      contaminationLevel = input$contaminationLevel,
      dose = Fabs * contaminationLevel * 1000 * input$feedIntake * tef
    )
  inputParameters[30, "dose"] <- sum(inputParameters$dose, na.rm =
  TRUE)

  # return all variables in this function's environment
  as.list(inputParameters |> filter(compound == cpd))
}

calculate_variables <- function(parameters) {
  #' Calculate derived parameters from the input parameters, e.g.
  #' scaling.
  #'
  #' @param parameters vector containing the model parameters
  #'
  #' @return parameter vector updated with derived parameters

  # calculate derived parameters from the input parameters, e.g.
  # scaling.
  with(parameters, {
    # return all variables in this function's environment
    as.list(sys.frame(sys.nframe()))
  }) # end with
}
```



```

# END!INITIAL

# DYNAMIC

# DERIVATIVE

derivative <- function(t, y, parameters, ...) {
  #' ODEs defining the model
  #'
  #' @param current time step
  #' @param y current state in a named list: `y <- c(D=dose, Ac=0,
  Af=0, AEgg=0)`
  #' @param parameters vector containing the model parameters
  #'
  #' @return derivative of each variable

  # define the derivatives of the model
  with(as.list(c(y, parameters)), {
    dD <- -D
    dAc <- D - (qcentral + k + e * yy) * Ac + qfat * Af
    dAf <- qcentral * Ac - qfat * Af
    dAEgg <- (e * yy) * Ac - AEgg

    return(list(c(dD, dAc, dAf, dAEgg),
      Cf = Af / Vf,
      Cegg = AEgg / 5.76
    ))
  })
}

run_model <- function(parameters) {
  #' Run model
  #'
  #' @param parameters vector containing the model parameters
  #'
  #' @return simulation results
  parameters <- calculate_variables(parameters)

  with(parameters, {
    tout <- seq(0, input$tdoseoff + input$tstop, by = 1)
    y0 <- c(D = dose, Ac = 0, Af = 0, AEgg = 0)
    dosing <- data.frame(
      var = c("D"),
      time = c(seq(0, input$tdoseoff, by = 1)), #
      value = c(dose),
      method = c("add")
    )
    solution <- ode(
      y = y0, times = tout, events = list(data = dosing),
      func = derivative, parms = parameters, method = "rk4"
    )
  })
}

```

```
    return(as.matrix(unclass(solution)))
  })
}
```

---

## Running the model (example)

---

```
library(dplyr)
library(ggplot2)

source("dioxin-congener-laying-hen.R")

modelParameters <- read.csv("modelInputParameters.csv", header =
TRUE)

### User input ###
compounds <- c("C1", "C3", "C5", "C7", "C8", "C14")
contaminationLevel <- c("C1"=0.12, "C3"=0.34, "C5"=0.21, "C7"=0.10,
"C8"=0.22, "C14"=0.51) # ng / kg
feedIntake <- 0.113 # kg
tstop <- 200 # days
tdoseoff <- 56 # days

### Run model ###
result <- list()
for (c in 1:length(compounds)){
  cpd <- compounds[c]
  input <- c(feedIntake = feedIntake, tstop = tstop, tdoseoff = tdoseoff,
contaminationLevel = list(contaminationLevel[[cpd]]))
  p <- assign_parameters(cpd)
  p <- calculate_variables(p)
  result[[c]] <- as.data.frame(run_model(p))
}

### Visualizing sum of individual models ###
total_teq_egg <- data.frame(result[[1]][["time"], Reduce(`+`,
lapply(result, `[`, 'Cegg'))))
total_teq_fat <- data.frame(result[[1]][["time"], Reduce(`+`,
lapply(result, `[`, 'Cf'))))
total_teq_egg %>% ggplot(aes(time,Cegg)) +
  geom_line()
```

---

**modellnputParameters.csv**

---

compound,name,tef, qcentral, qfat ,e,yy,k,Fabs,Vf,Vc,Vtotal
C1,"1: 2,3,7,8-TCDF",0.1,0.31,0.205,0.9,0.04,0,0.7,200,1640,1840
C2,"2: 1,2,3,7,8-PeCDF",0.03,0.19,0.073,0.9,0.078,0,0.71,210,1630,1840
C3,"3: 2,3,4,7,8-PeCDF",0.3,0.1,0.057,0.9,0.055,0,0.71,190,1650,1840
C4,"4: 1,2,3,4,7,8-HxCDF",0.1,0.08,0.029,0.9,0.11,0,0.6,180,1660,1840
C5,"5: 1,2,3,6,7,8-HxCDF",0.1,0.08,0.031,0.9,0.109,0,0.55,180,1660,1840
C6,"6: 2,3,4,6,7,8-HxCDF",0.1,0.1,0.034,0.9,0.131,0,0.45,200,1640,1840
C7,"7: 1,2,3,7,8,9-HxCDF",0.1,0.1,0.04,0.9,0.103,0,0.54,180,1660,1840
C8,"8: 1,2,3,4,6,7,8-HpCDF",0.01,0.06,0.034,0.9,0.182,0,0.18,140,1700,1840
C9,"9: 1,2,3,4,7,8,9-HpCDF",0.01,0.04,0.018,0.9,0.167,0,0.24,150,1690,1840
C10,"10: 1,2,3,4,6,7,8,9-OCDF",0.0003,0.14,0.06,0.9,0.057,0,0.78,230,1610,1840
C11,"11: 2,3,7,8-TCDD",1,0.35,0.23,0.9,0.042,0,0.78,210,1630,1840
C12,"12: 1,2,3,7,8-PeCDD",1,0.14,0.07,0.9,0.055,0,0.75,220,1620,1840
C13,"13: 1,2,3,4,7,8-HxCDD",0.1,0.09,0.03,0.9,0.101,0,0.61,190,1650,1840
C14,"14: 1,2,3,6,7,8-HxCDD",0.1,0.09,0.036,0.9,0.106,0,0.59,170,1670,1840
C15,"15: 1,2,3,7,8,9-HxCDD",0.1,0.07,0.032,0.9,0.118,0,0.42,150,1690,1840
C16,"16: 1,2,3,4,6,7,8-HpCDD",0.01,0.14,0.06,0.9,0.057,0,0.78,230,1610,1840
C17,"17: 1,2,3,4,6,7,8,9-OCDD",0.0003,0.14,0.06,0.9,0.057,0,0.78,230,1610,1840
C18,18: PCB 81,0.0003,0.11,0.121,0.9,0.024,0,0.92,190,1650,1840
C19,19: PCB 77,0.0001,0.25,0.136,0.9,0.044,0,0.89,240,1600,1840
C20,20: PCB 126 ,0.1,0.13,0.067,0.9,0.038,0,1,270,1570,1840
C21,21: PCB 169,0.03,0.11,0.029,0.9,0.081,0,0.85,220,1620,1840
C22,22: PCB 123,0.00003,0.14,0.06,0.9,0.057,0,0.78,230,1610,1840
C23,23: PCB 118,0.00003,0.12,0.063,0.9,0.041,0,0.98,230,1610,1840
C24,24: PCB 114,0.00003,0.2,0.09,0.9,0.061,0,0.89,180,1660,1840
C25,25: PCB 105,0.00003,0.12,0.084,0.9,0.037,0,0.92,200,1640,1840
C26,26: PCB 167,0.00003,0.1,0.095,0.9,0.062,0,1,70,1770,1840
C27,27: PCB 156,0.00003,0.11,0.039,0.9,0.063,0,0.92,220,1620,1840
C28,28: PCB 157,0.00003,0.16,0.051,0.9,0.094,0,0.86,190,1650,1840
C29,29: PCB 189,0.00003,0.06,0.017,0.9,0.102,0,0.8,190,1650,1840
totalTeq,Total TEQ model,1,0.14,0.06,0.9,0.057,0,0.78,230,1640,1840

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