corti model

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```r
parameters <- c(ks_Rm = 2.90, IC50_Rm = 26.2, kon = 0.00329, kT = 0.63, kre = 0.57, Rf = 0.49, kd_R = 0
                kd_Rm = 0.612, ks_r = 3.22, D = 53, Rm0 = 4.74, DR = 0, DRN = 0)

Glucocorticoid_func <- function(t, y, parms) {
    with(as.list(c(y, parms)),{

      # Dit model bevat 4 afgeleide functies:
      # Afgeleide 1:

      dmRNAr_dt <- ks_Rm * ( 1 - (DRN / (IC50_Rm + DRN))) - kd_Rm * mRNAr

      # Afgeleide 2:

      dR_dt <- ks_r * mRNAr + Rf * kre * DRN - kon * D * R - kd_R * R

      # Afgeleide 3:

      dDR_dt <- kon * D * R - kT * DR

      # Afgeleide 4:

      dDRN_dt <- kT * DR - kre * DRN

      return(list(c(dmRNAr_dt, dR_dt, dDR_dt, dDRN_dt)))
       }
       )
}

state <- c(mRNAr = 4.74, R = 267, DR = 0, DRN = 0)
t <- seq(0, 48, by = 0.5)

out <- deSolve::ode(times = t, y = state, parms = parameters, func = Glucocorticoid_func, method = "eul
plot(out)
```
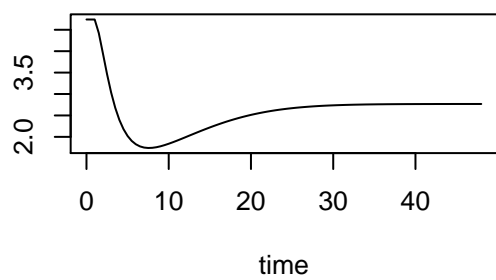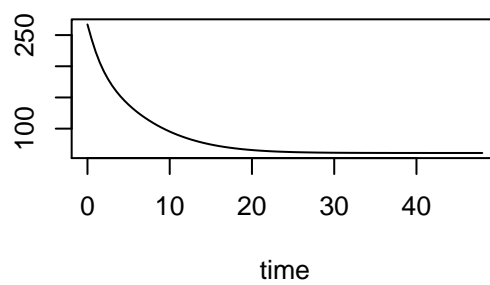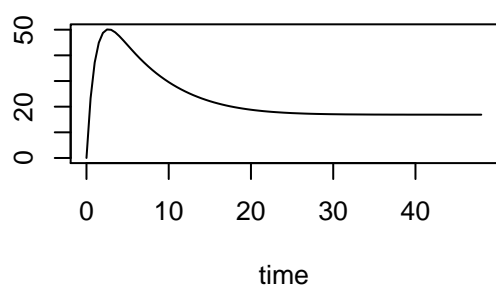
mRNAr

time

R

time

DR

time

DRN

time