

Assignment 1

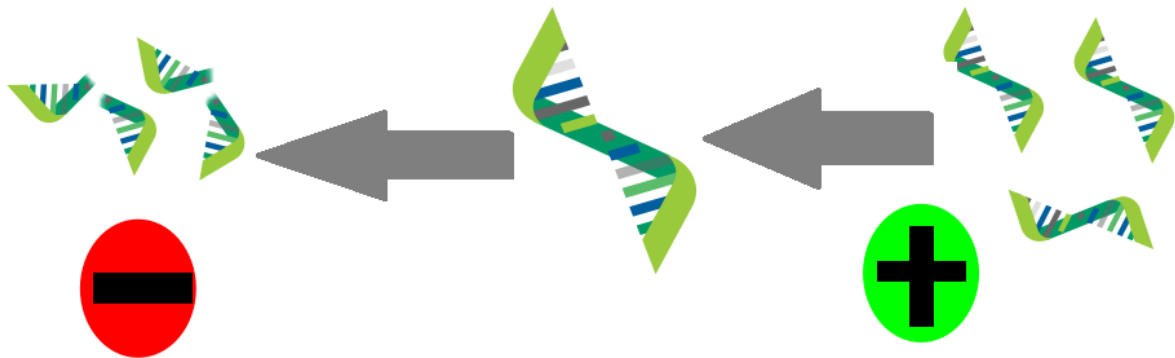
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Week 1: mRNA dynamic

Opdracht 1

- Welke parameters moet je programmeren?
m (Synthese) en r (Afbraak ratio)
- Zoek bronnen op internet die uitleggen waar de formule $dR/dt = -rR + m$ vandaan komt.
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC403777/>
https://www.researchgate.net/figure/Calculation-of-the-mRNA-decay-constant-k-d-The-graph-is-not-semilogarithmic-but_fig1_15634531
- Teken het biologisch model en leg de vertaling naar de formule uit.



De mRNA toename is afhankelijk van synthese. En mRNA afname is afhankelijk van de afbraak ratio.

- Wat is de return waarde van de model functie in R? Waarom return je die en niet R zelf?
De return waarde is een list.

Opdracht 2

```
# Define the params
parameters.decreasing <- c(m = 15, r = 0.3)
parameters.increasing <- c(m = 30, r = 0.2)
parameters.steady <- c(m = 0, r = 0)
# Define model
volume <- function(t,y,parms){
```

```

    with(as.list(c(parms)),{
      dR <- m - r * y
      return(list(c(dR)))
    }
  )
}
# Initial state
state <- c(Volume = 100)
# Define time sequence to run the model
times <- seq(0, 60, by = 1)
# Run simulation using continuous approach
out.decreasing <- ode(times = times, y = state, parms = parameters.decreasing,
  func = volume, method = "euler")
out.increasing <- ode(times = times, y = state, parms = parameters.increasing,
  func = volume, method = "euler")
out.steady <- ode(times = times, y = state, parms = parameters.steady,
  func = volume, method = "euler")

plot(out.increasing, out.decreasing, out.steady, lty=1,
  col=c("green", "blue", "red"),main="amount of mRNA transcripts over time",
  ylab="number of mRNA transcripts", xlab="timepoints")
legend(30, 135,
  legend=c("Increasing over time", "steady-state", "Decreasing over time"),
  col=c("green", "red", "blue"), lty=1, cex=0.8, text.font=4)

```

