Zufall in der Biochemie

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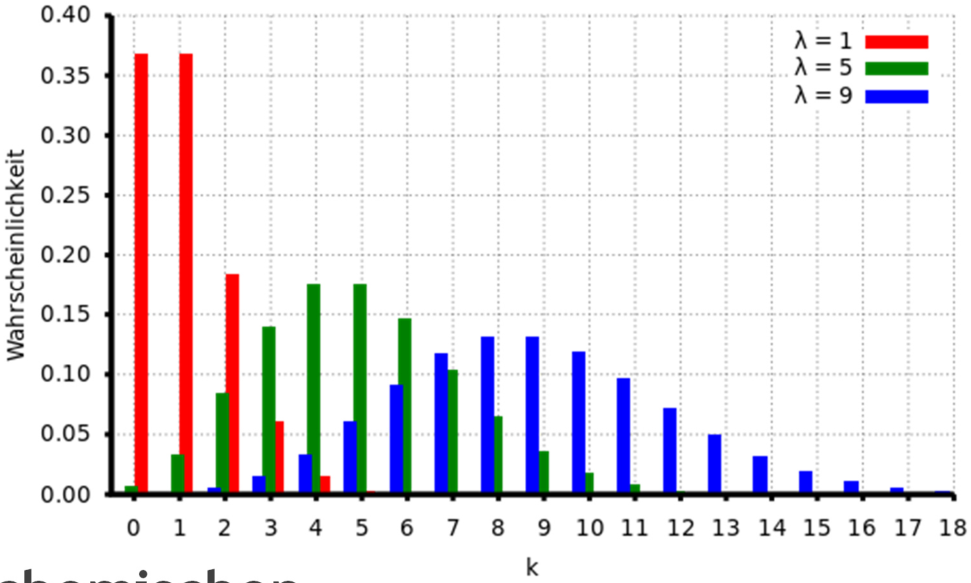
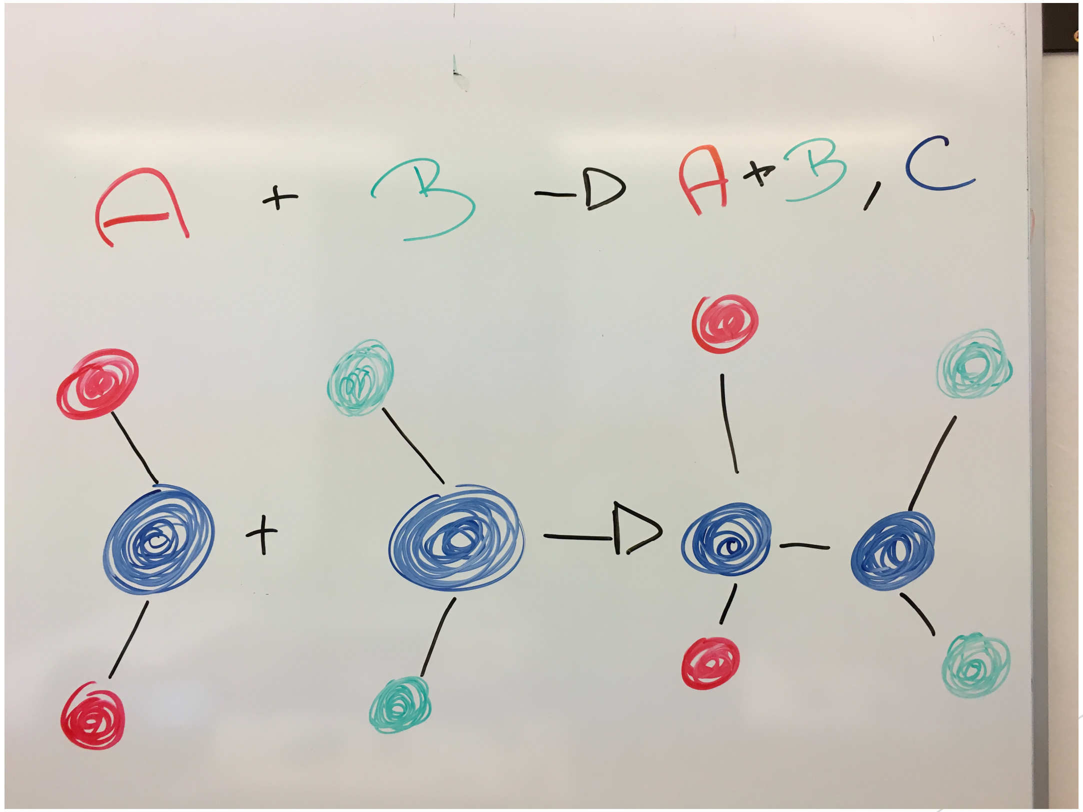
Einführung

- **Poisson- Verteilung**
- **Poisson- Prozess**
- **Modellierung von biochemischen Reaktionssystemen**



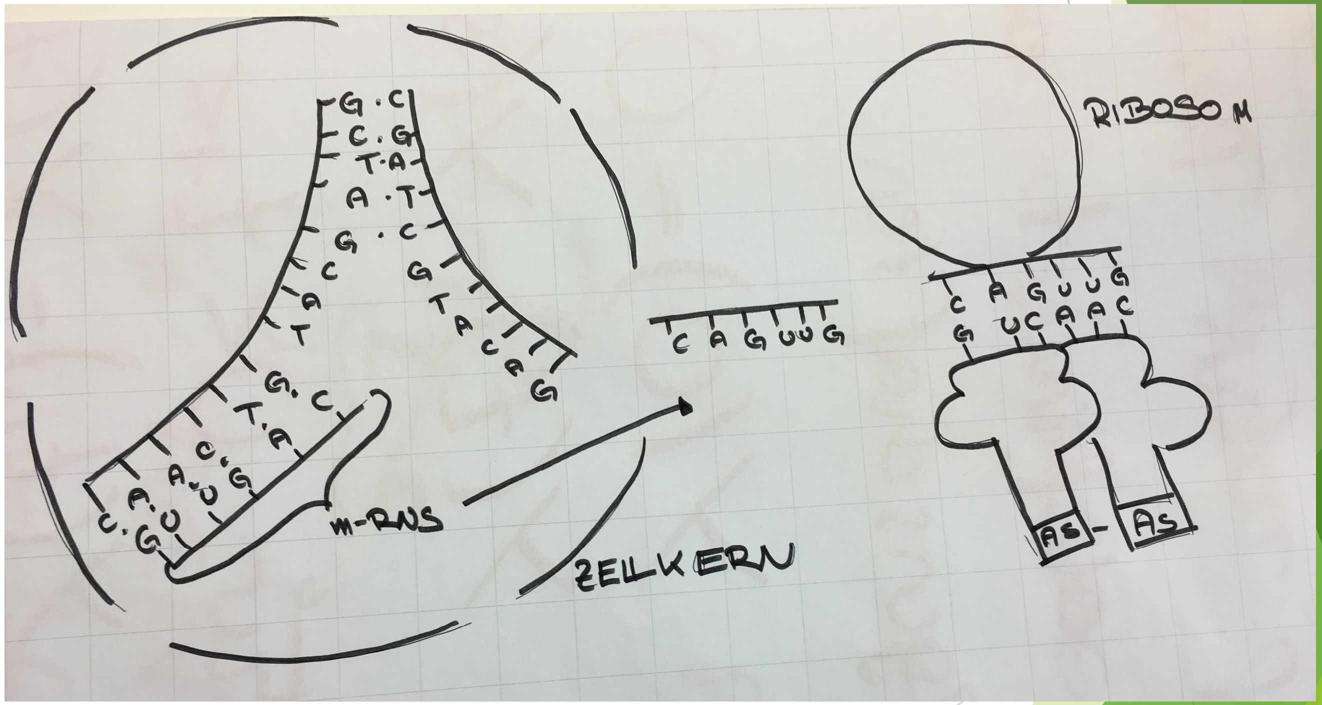
Grundmodell

- **Spezies S**
  - S = {A,B,C}
- **Komplexe K**
  - K = {C, A+B}
- **Reaktionen R**
  - R = {A+B→C}



1. Modell: Genexpression

- S = {G,M,P,D,B}
  - G… Genom
  - M… mRNA
  - P… Protein
  - D… Dimer
  - B… gebundenes Gen



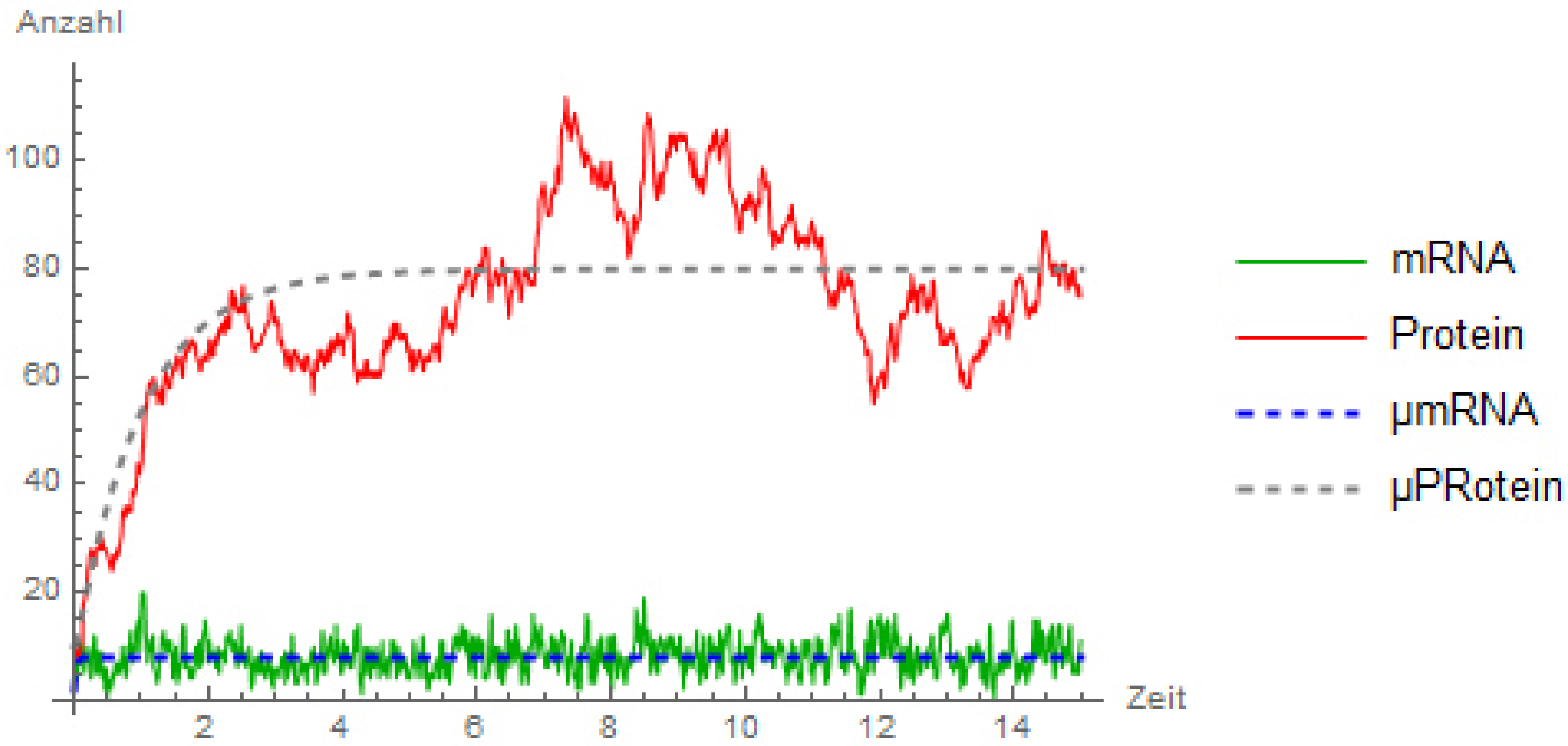
$$X_{(2\Delta t)} = X_{(\Delta t)} + Y_1\left(\int_{\Delta t}^{2\Delta t}(K_1 \cdot x_1(s) \cdot ds)\right) \cdot \begin{pmatrix}0\\1\\0\end{pmatrix}$$
$$+ Y_2\left(\int_{\Delta t}^{2\Delta t}(K_2 \cdot x_2(s) \cdot ds)\right) \cdot \begin{pmatrix}0\\0\\1\end{pmatrix}$$
$$+ Y_3\left(\int_{\Delta t}^{2\Delta t}(K_3 \cdot x_2(s) \cdot ds)\right) \cdot \begin{pmatrix}0\\-1\\0\end{pmatrix}$$
$$+ Y_4\left(\int_{\Delta t}^{2\Delta t}(K_4 \cdot x_3(s) \cdot ds)\right) \cdot \begin{pmatrix}0\\0\\-1\end{pmatrix}$$

$$\boxed{\begin{aligned} X_{(2\Delta t)} = X_{(\Delta t)} &+ Y_1(K_1 \cdot \Delta t) \cdot \begin{pmatrix}0\\1\\0\end{pmatrix} \\ &+ Y_2(K_2 \cdot x_2(\Delta t) \cdot \Delta t) \cdot \begin{pmatrix}0\\0\\1\end{pmatrix} \\ &+ Y_3(K_3 \cdot x_2(\Delta t) \cdot \Delta t) \cdot \begin{pmatrix}0\\-1\\0\end{pmatrix} \\ &+ Y_4(K_4 \cdot x_3(\Delta t) \cdot \Delta t) \cdot \begin{pmatrix}0\\0\\-1\end{pmatrix} \end{aligned}}$$

$$X_{(i\Delta t)} = X_{((i-1)\Delta t)} + Y_1\left(\int_{(i-1)\Delta t}^{i\Delta t}(K_1 \cdot x_1(s) \cdot ds)\right) \cdot RV$$
$$+ Y_2\left(\int_{(i-1)\Delta t}^{i\Delta t}(K_2 \cdot x_2(s) \cdot ds)\right) \cdot RV$$
$$+ Y_3\left(\int_{(i-1)\cdot\Delta t}^{i\Delta t}(K_3 \cdot x_2(s) \cdot ds)\right) \cdot RV$$
$$+ Y_4\left(\int_{(i-1)\cdot\Delta t}^{i\Delta t}(K_4 \cdot x_3(s) \cdot ds)\right) \cdot RV$$

$$\Downarrow$$

$$\boxed{\begin{aligned} X_{(i\Delta t)} = X_{((i-1)\Delta t)} &+ Y_1(K_1 \cdot \Delta t) \cdot \begin{pmatrix}0\\1\\0\end{pmatrix} \\ &+ Y_2(K_2 \cdot x_2((i-1)\Delta t) \cdot \Delta t) \cdot \begin{pmatrix}0\\0\\1\end{pmatrix} \\ &+ Y_3(K_3 \cdot x_2((i-1)\Delta t) \cdot \Delta t) \cdot \begin{pmatrix}0\\-1\\0\end{pmatrix} \\ &+ Y_4(K_4 \cdot x_3((i-1)\Delta t) \cdot \Delta t) \cdot \begin{pmatrix}0\\0\\-1\end{pmatrix} \end{aligned}}$$



R1: G → M + G

R2: M → M + P

R3: M → { }

R4: P → { }

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$$x(i\,\Delta t) = x\big((i-1)\,\Delta t\big) +$$

$$+\ y_1\ \big(k_1 \cdot x_3((i-1)\cdot\Delta t)\cdot \Delta t\big)\cdot \text{Vektor}$$

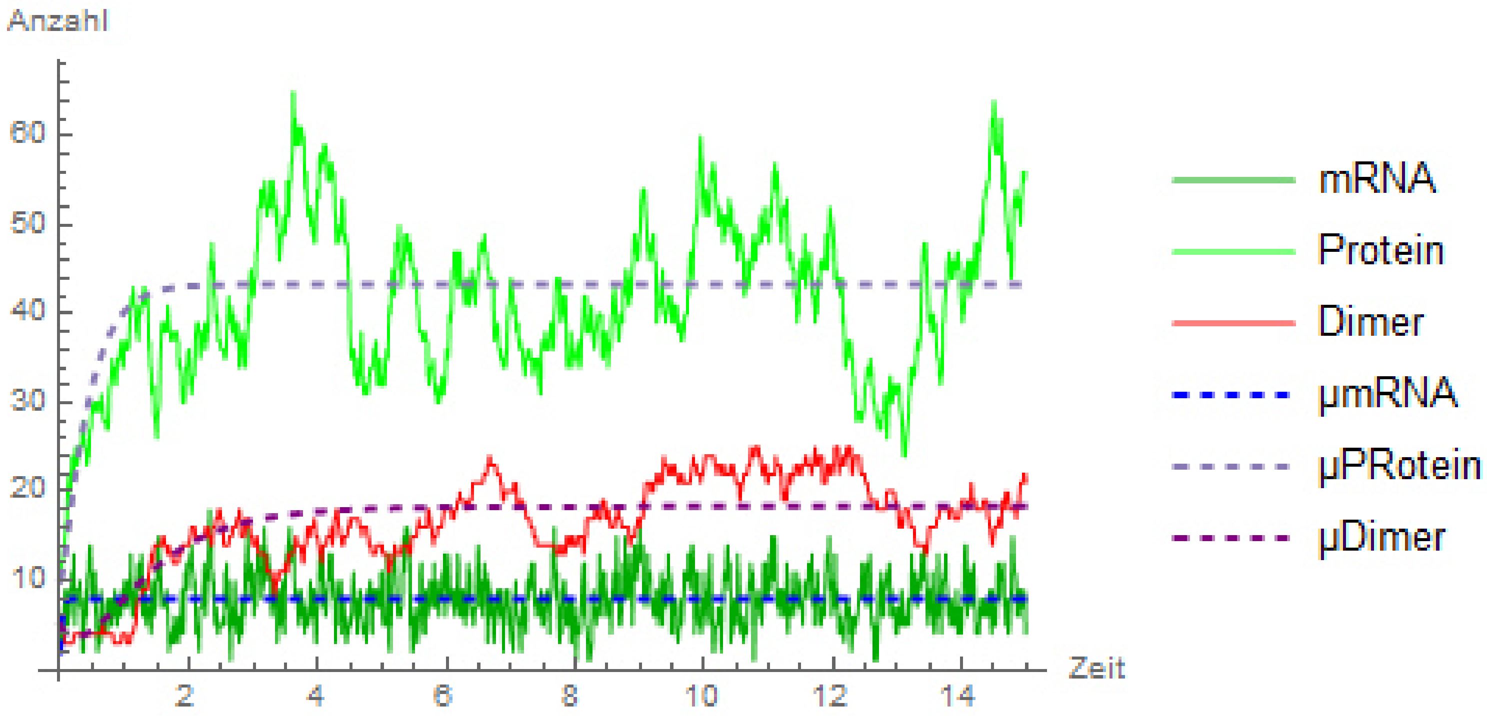
$$+\ y_2\ \big(k_2 \cdot x_1((i-1)\,\Delta t)\ \Delta t\big)\cdot \text{Vektor}$$

$$+\ y_3\ \big(k_3 \cdot x_3((i-1)\,\Delta t)\ \Delta t\big)\cdot \text{-''-}$$

$$+\ y_4\ \big(k_4 \cdot x_3((i-1)\,\Delta t)\ \Delta t\big)\cdot \text{-''-}$$

$$+\ y_5\ \big(k_5 \cdot x_2((i-1)\,\Delta t)\ \Delta t\big)\cdot \text{-''-}$$

$$+\ y_6\ \ k_6 \cdot x_1((i-1)\,\Delta t)\cdot x_2((i-1)\,\Delta t)\ \Delta t \cdot \text{-''-}$$

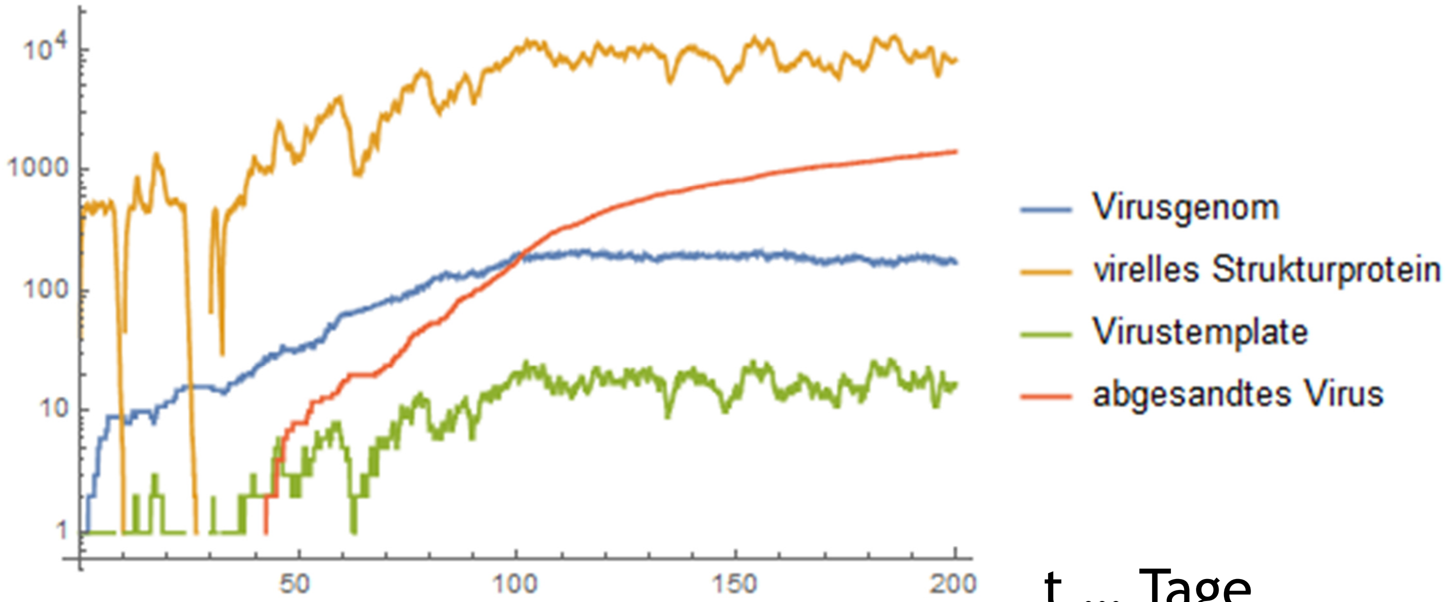


R5: 2P → D
R6: D → { }
R7: D + G → B
R8: B → D + G

2. Modell: Virusinfektion

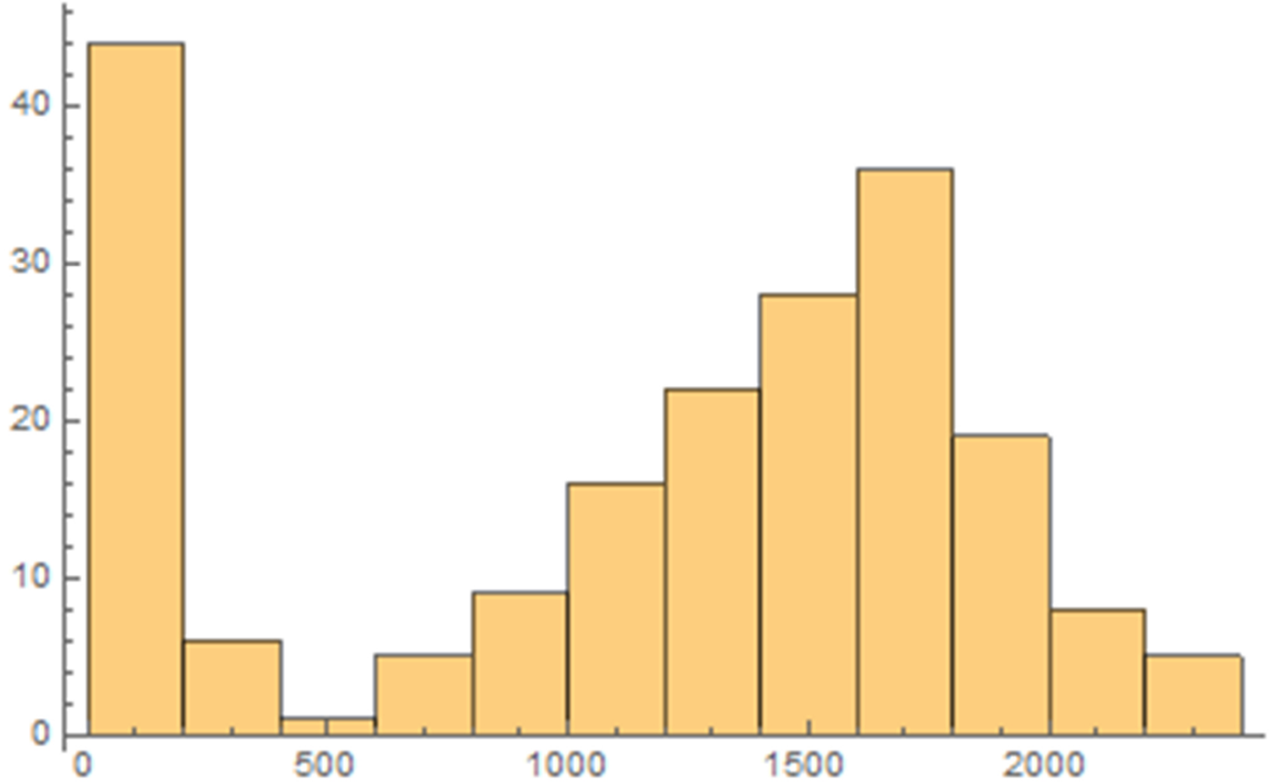
- S = {G,S,T,V}
  - G… Virusgenom
  - S… virelles Strukturprotein
  - T… Virustemplate
  - V… abgesandter Virus
- R1: T→T+G
- R2: G→T
- R3: T→ T+S
- R4: T→ { }
- R5: S→ { }
- R6: G+S→V

Anzahl

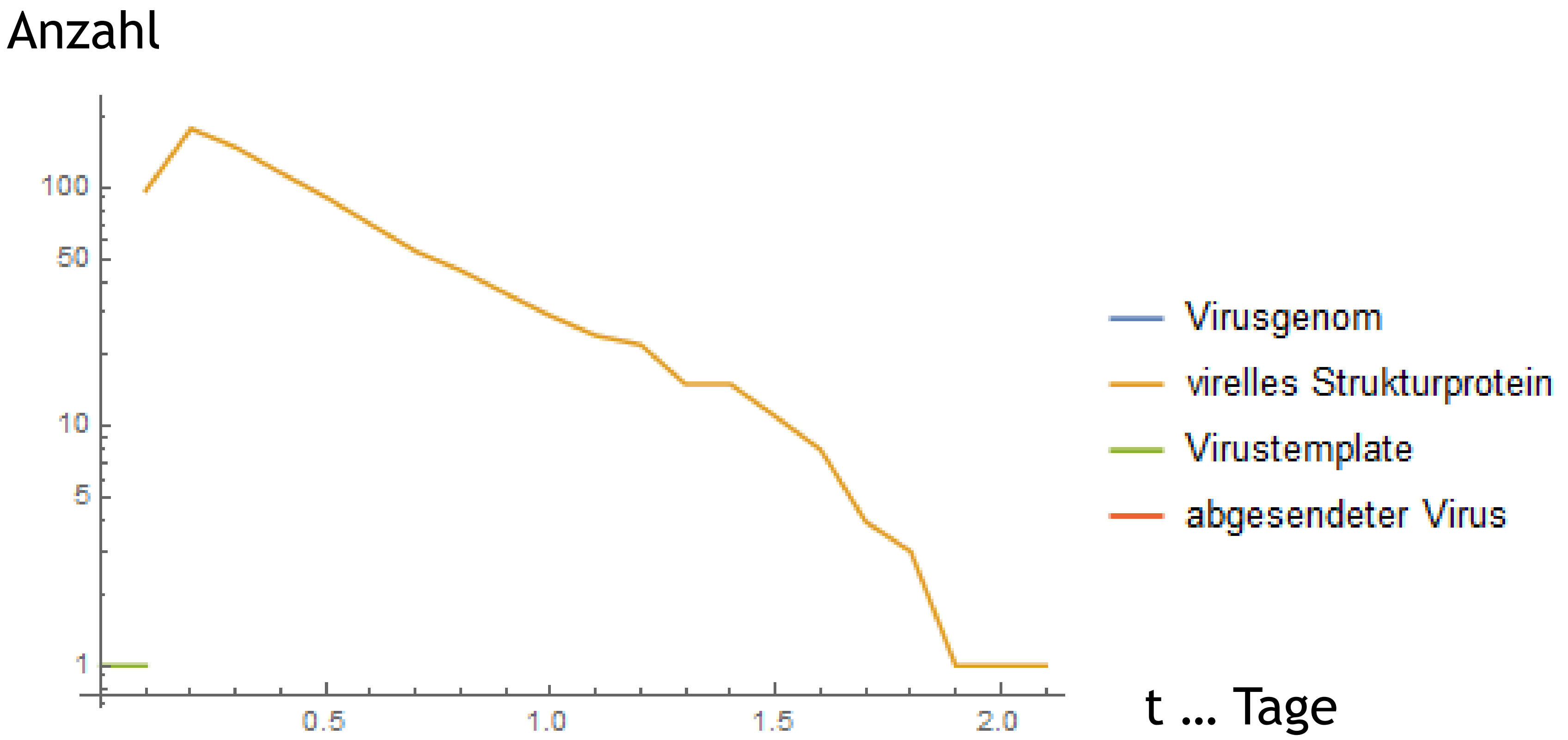


t … Tage

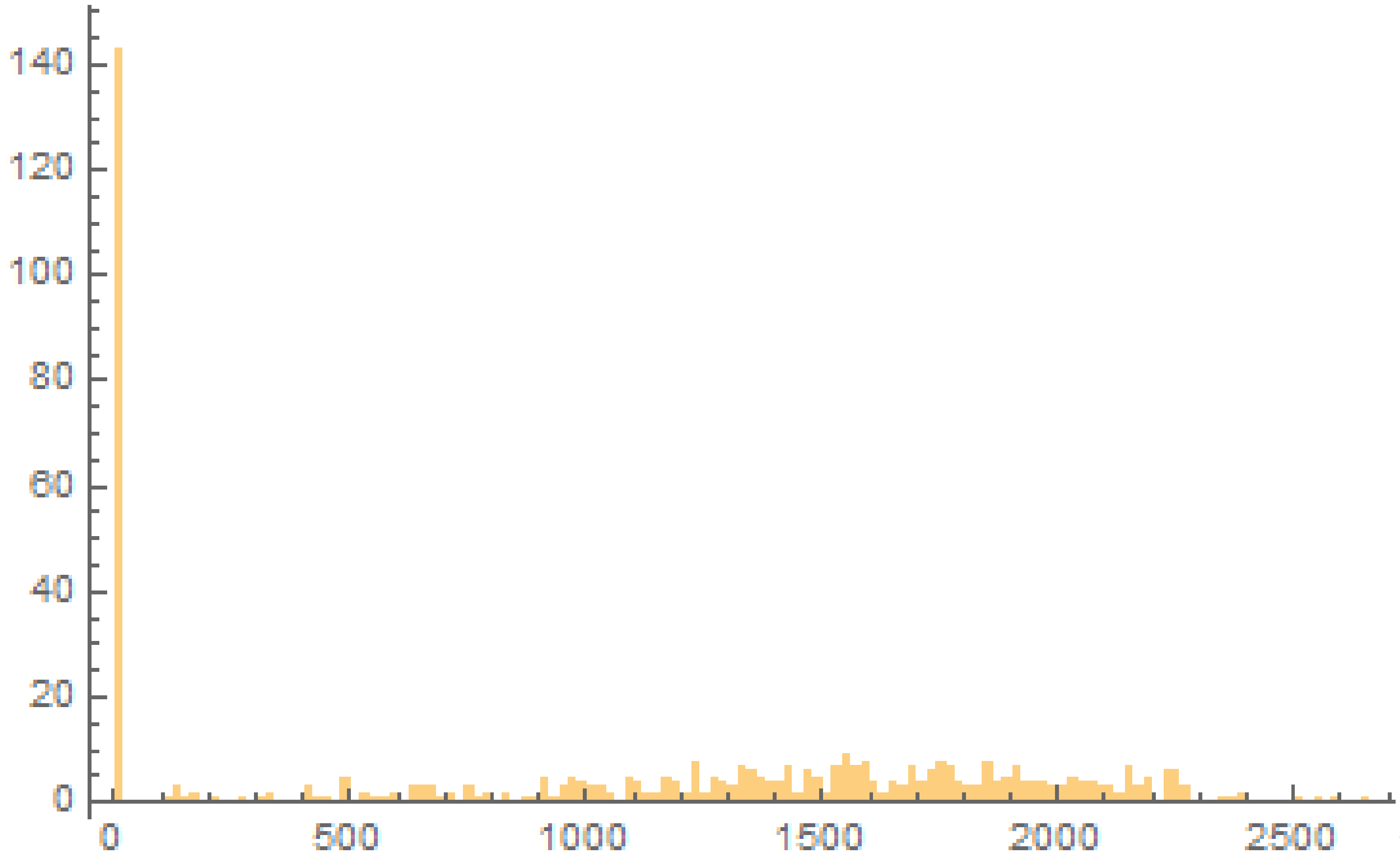
Absolute Häufigkeit



Anzahl der ausgesandten Viren


Anzahl
100
50
10
5
1
0.5
1.0
1.5
2.0
Virusgenom
virelles Strukturprotein
Virustemplate
abgesendeter Virus
t ... Tage

Absolute Häufigkeit



Anzahl der abgesendeten Viren