We are very lucky that here at the Dresden Summer School in Systems Biology we have great collaborators! Our colleagues in the Grill Lab have performed many further experiments, and undertaken detailed data analysis to be able to provide us with high quality quantitative spatial temporal data for the PAR system!

1 Experimental setup and measurements

1.1 aPAR and pPAR concentrations and flow field

The Grill Lab measured the concentration of anterior PAR complex (aPAR), the concentration of posterior PAR complex (pPAR) and the flow field as a function of time. These quantities are measured along an ellipse formed by the intersection of the *C. elegans* ellipsoidal egg with its mid-plane (see left panel of Fig. 1). Ignoring the curvature, the ellipse is then unwrapped to a straight line as shown in Fig. 1. The measurements that you are provided with are the concentration of aPAR, of pPAR and the flow velocity field as a function time on the one-dimensional surface illustrated in Fig. 1. These measurements are supplied in seven text files. The data are provided at discrete points in space X and time T as follows (see Fig. 2 for a visualization of these measurements):

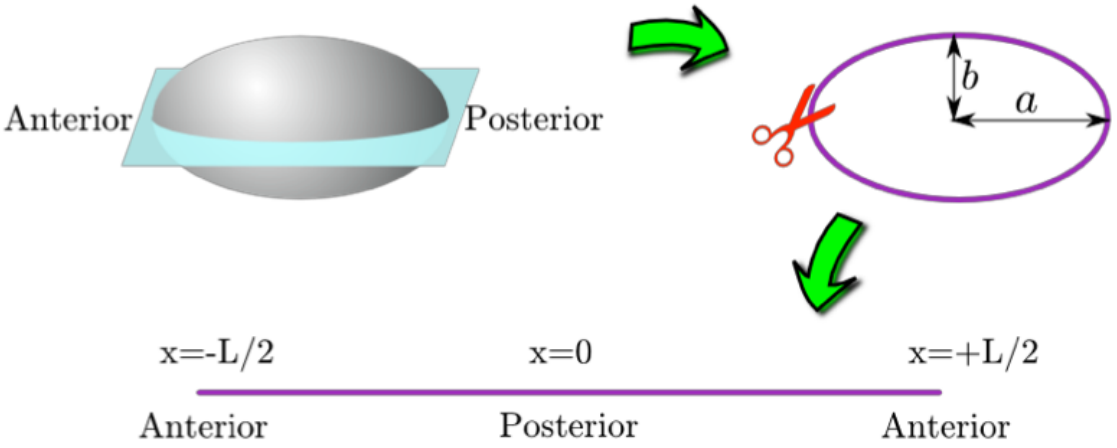

Figure 1: The geometry of the experimental data. Approximating the *C. elegans* embryo as an ellipsoid, the experimental concentrations and flow fields are obtained by imaging the embryo in its mid plane as shown above. Since the embryo is rotationally symmetric about the anterior-posterior axis, this one-dimensional representation of the data captures the essential features for the entire (2D) surface of the embryo. Neglecting curvature, this 'ellipse' can further be unwrapped to a straight line. The kymographs (space-time plots) in the next figure are with reference to this procedure.

1.1.1 aPAR and pPAR data

The anterior and posterior par files are outlined below, two files giving the space and time sampling points, and two files giving the concentrations of the PAR protein in the cortex.

- `T_PARS.txt` – file containing the time points (in seconds s) at which the PAR data are supplied
- `X_PARS.txt` – file containing the space points (in microns μm) at which the PAR data are supplied
- `PAR2.txt` – file containing the concentration in ($\frac{\text{protein}\#}{\mu m^2}$) of the posterior PAR protein in space and time
- `PAR6.txt` – file containing the concentration in ($\frac{\text{protein}\#}{\mu m^2}$) of the anterior PAR protein in space and time

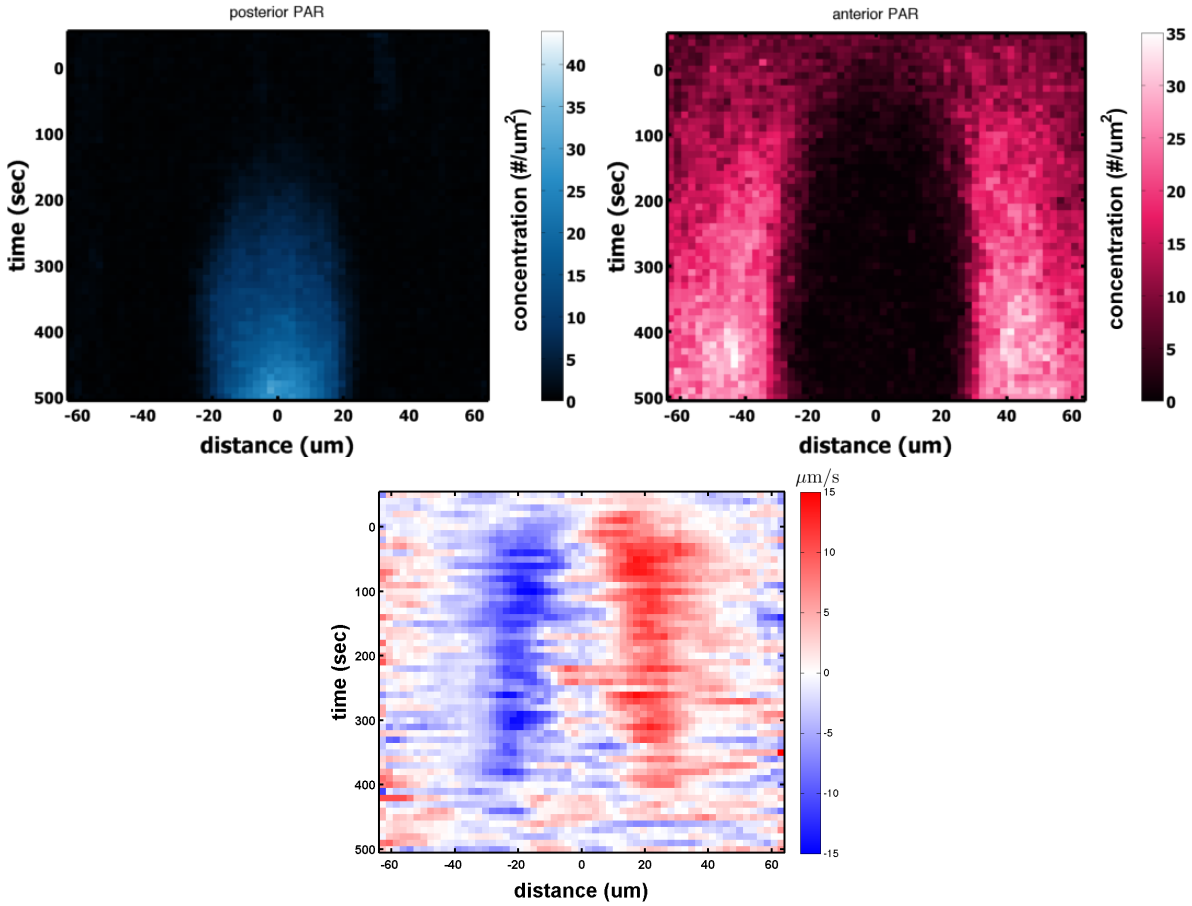

Figure 2: Kymographs (space-time plots) of aPAR, pPAR, and the flow velocity field.

1.1.2 Flow field data

The data files for the measured flow field are given below, two files giving the space and time sampling points, and one file gives the flow field through space and time.

- `T_flow.txt` – file containing the time points (in seconds s) at which the flow data are supplied
- `X_flow.txt` – file containing the space points (in microns μm) at which the flow data are supplied
- `Flow.txt` – file containing the estimated flow velocities in $\frac{\mu m}{s}$.

Parameters	Measured values
V_{cyto}	2.5×10^4 μm^3
Ω_{memb}	4.4×10^3 μm^2
D_{A}	0.28 $\mu\text{m}^2\text{s}^{-1}$
D_{P}	0.15 $\mu\text{m}^2\text{s}^{-1}$
k_{offA}	3.24×10^{-3} s^{-1}
k_{offP}	7.19×10^{-3} s^{-1}
k_{onA}	6.29×10^{-3} $\mu\text{m}\,\text{s}^{-1}$
k_{onP}	7.682×10^{-2} $\mu\text{m}\,\text{s}^{-1}$
k_{AP}	? $\mu\text{m}^{\alpha+1}\text{s}^{-1}$
k_{PA}	? $\mu\text{m}^{\beta+1}\text{s}^{-1}$
α	?
β	?

Table 1: Measured physical parameters.

1.2 Number of protein molecules

The Grill Lab was also able to measure the number of aPAR and pPAR molecules over time in the cytosol and in the cortex (Fig. 3).

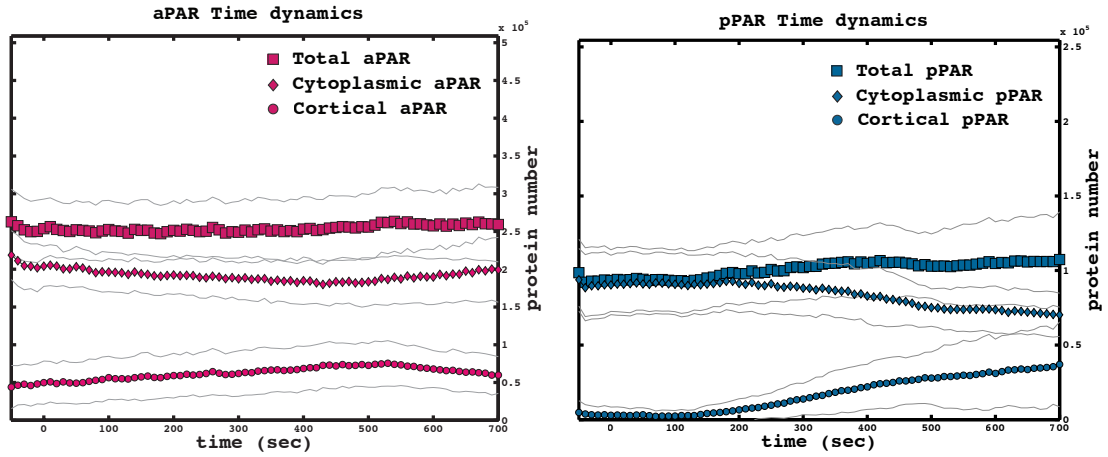

Figure 3: The number of aPAR and pPAR molecules in the cytosol and in the cortex over time. The total aPAR and total pPAR data is the sum of molecules in the cytoplasm and in the cortex. The temporal average of the total number of aPAR and pPAR molecules is $N_{\text{A}} = 2.4 \times 10^5$ molecules and $N_{\text{P}} = 9.8 \times 10^4$ molecules, respectively.

1.3 Measured physical parameters

In addition, the Grill Lab has also measured (see Table 1) the volume of the cell's cytoplasm V_{cyto}, its membrane surface area Ω_{memb}, the diffusivity of aPAR D_{A}, diffusivity of pPAR D_{P} and the macroscopic ratio rates k_{offA}, k_{offP}, k_{onA}, and k_{onP} (see project introduction sheet from Monday for definitions). However, the rates k_{AP} and k_{PA}, and the stoichiometries α and β remain unknown.

Question 1: Explore and use the data!

Read the description of the data above and download the data files from the repository. Investigate!

- How can you visualize this new data best?
- What further analysis could you do?
- What do the total protein number measurements tell you?
- What consequences does this have for your model and simulation approach?