

# Project Proposal

## Proteome-wide Screen for RNA-dependent Proteins

### Team 3: HeLa Cells Synchronized in Interphase

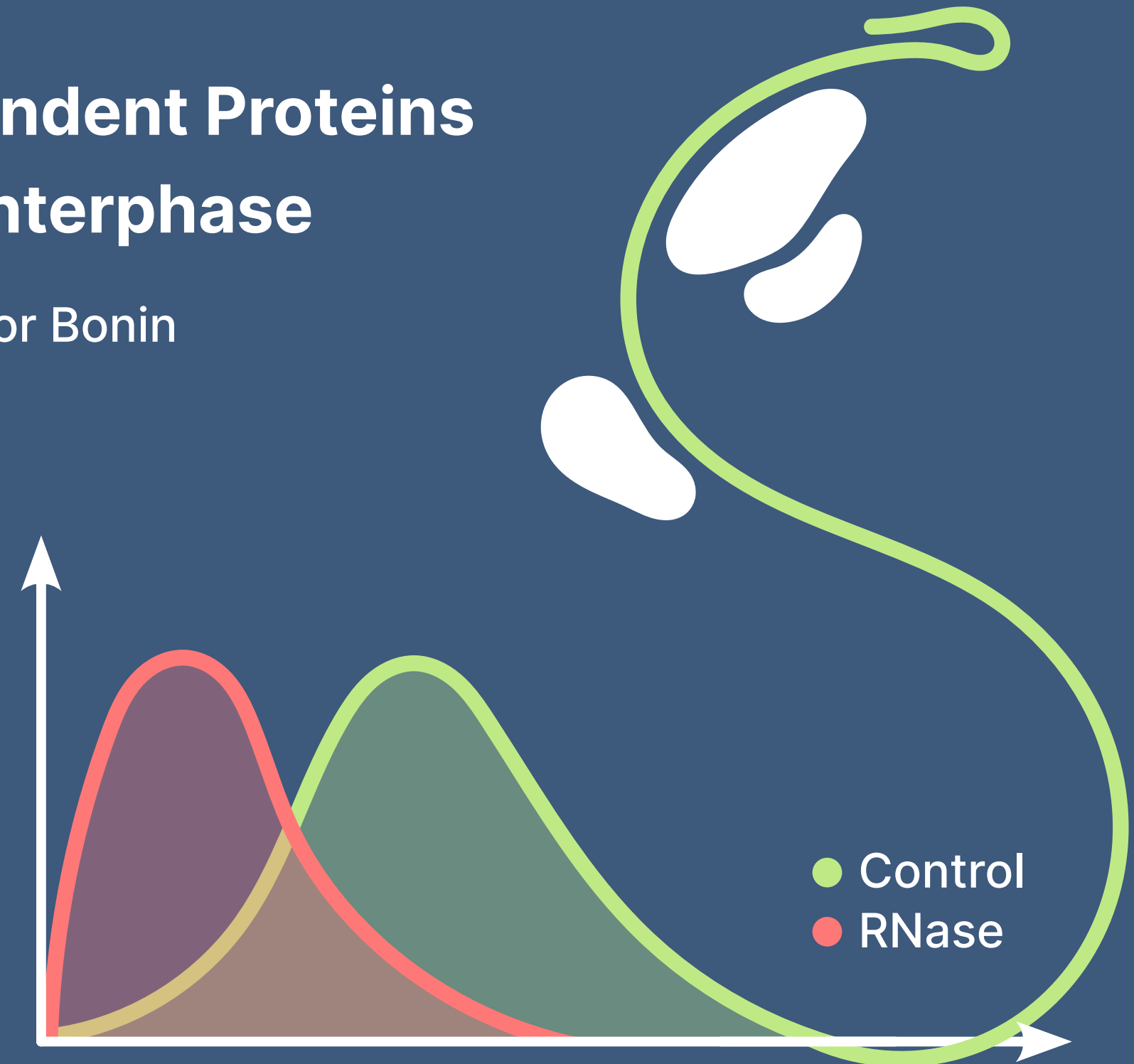
Hannah Brehm, Johann Blakytty, Kira Hoffmann, Viktor Bonin

Data Analysis Project Summer Term 2023

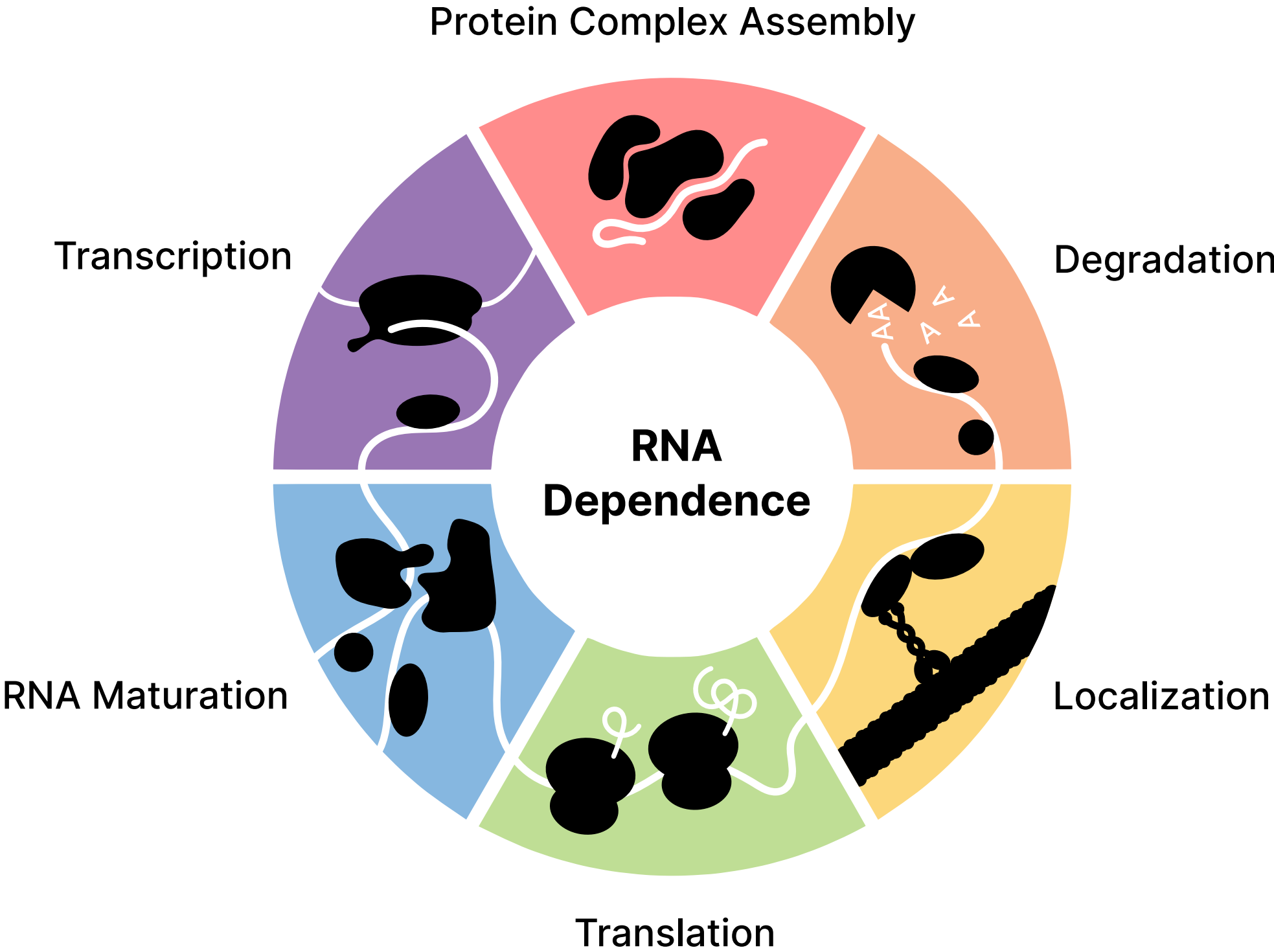
Supervisor: Dr. Maiwen Caudron-Herger

Tutor: Fabio Rauscher

Wednesday, 17.05.2023

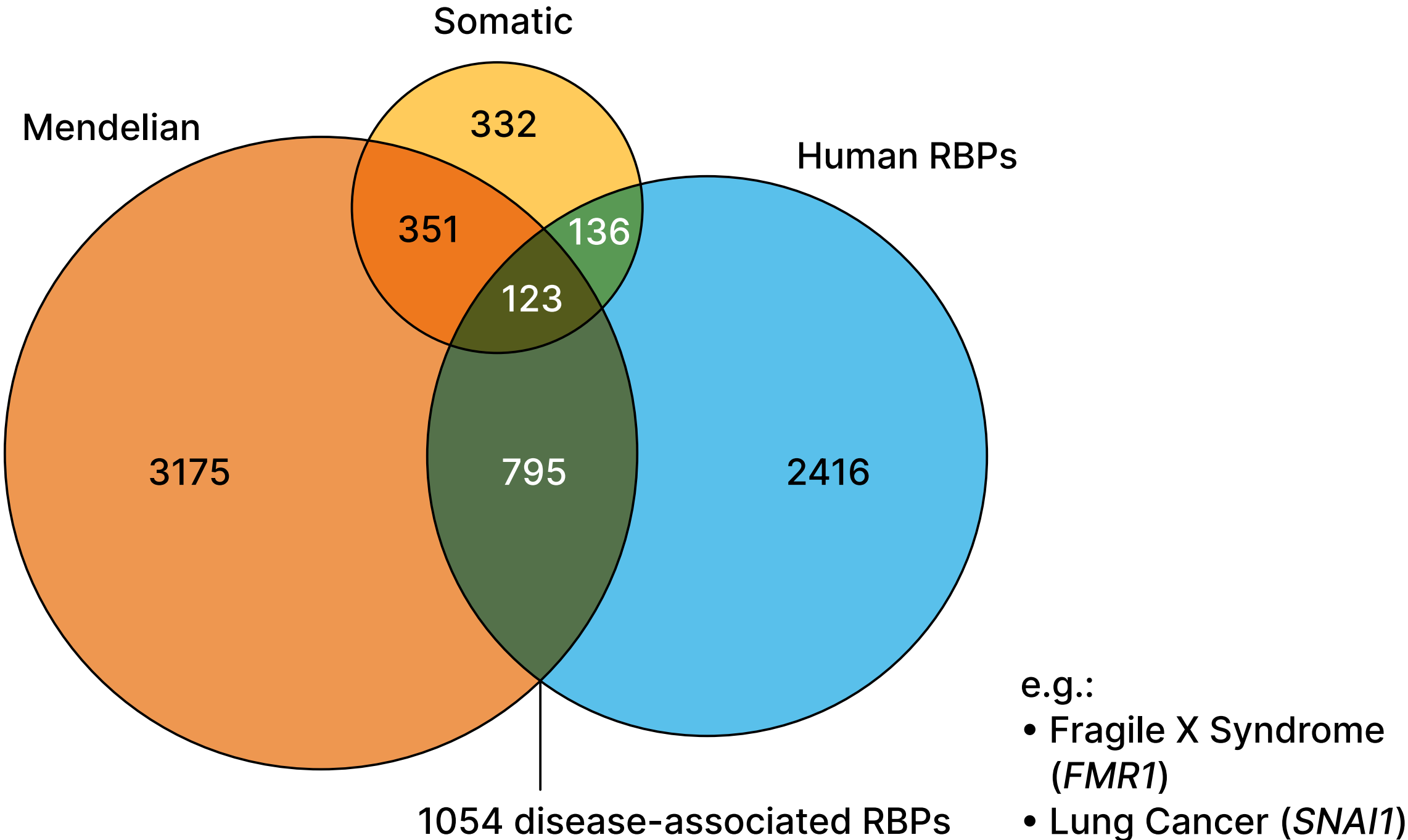


# Functions of RNA-dependent Proteins



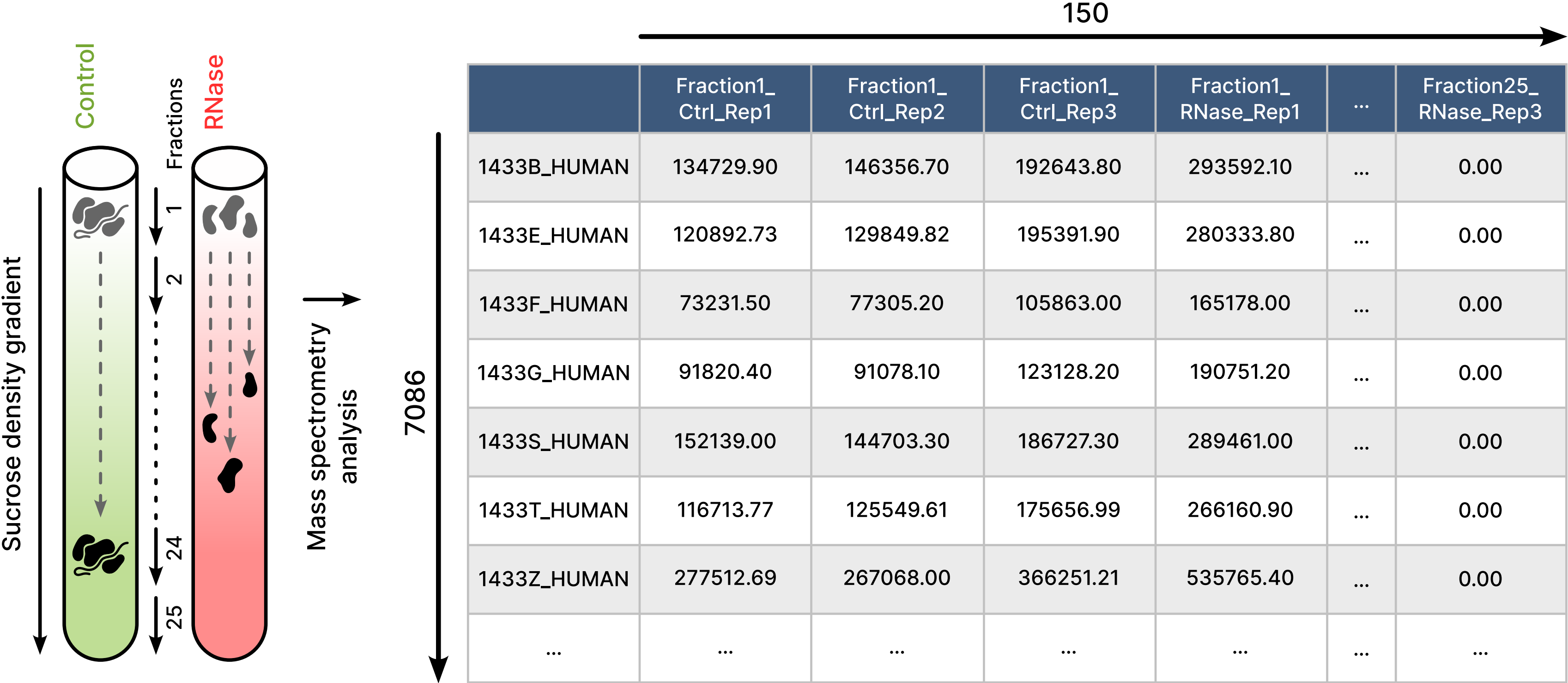
Adapted from: Gebauer, F., Schwarzl, T., Valcárcel, J., and Hentze, M.W. (2021). RNA-binding proteins in human genetic disease. Nat. Rev. Genet. 22, 185-198.

# RNA-binding Proteins in Human Diseases



Gebauer, F., Schwarzl, T., Valcárcel, J., and Hentze, M.W. (2021). RNA-binding proteins in human genetic disease. Nat. Rev. Genet. 22, 185-198.

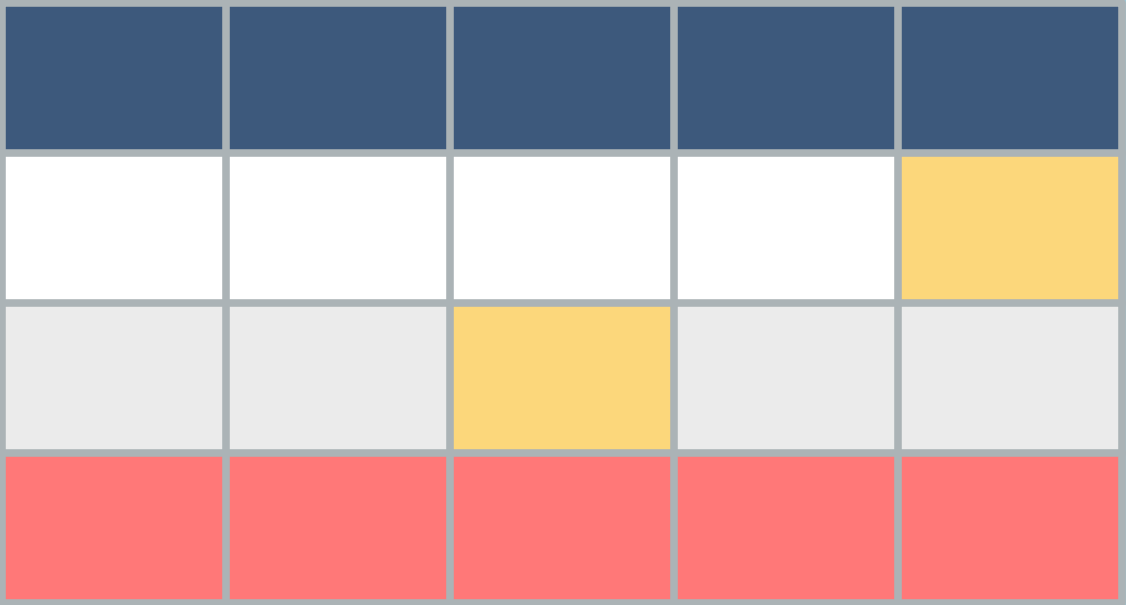
# Dataset for HeLa Cells Synchronized in Interphase



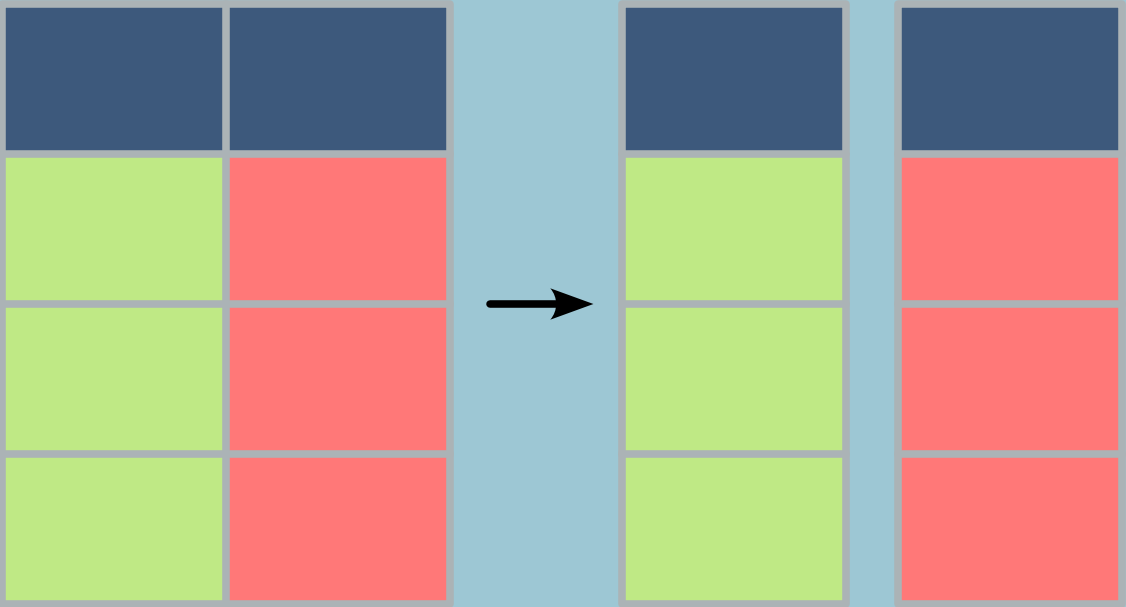
Caudron-Herger, M., et al. (2019). R-DeeP: Proteome-wide and Quantitative Identification of RNA-Dependent Proteins by Density Gradient Ultracentrifugation. Mol. Cell 75, 184-199.

# Step 1: Data Cleanup and Normalization

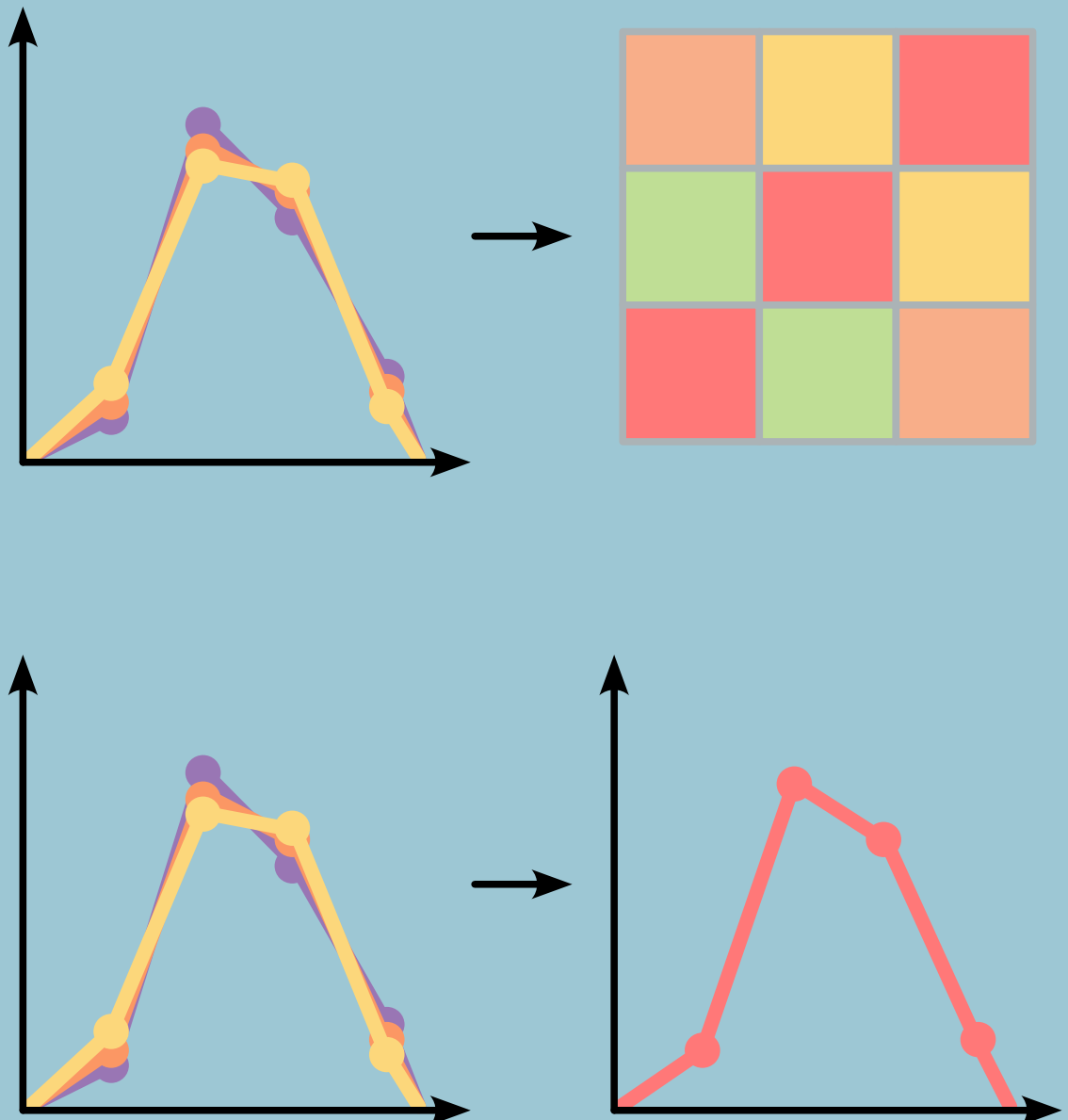
### 1.1 NA Values and Zero Rows



### 1.2 Split Dataset into Control and RNase



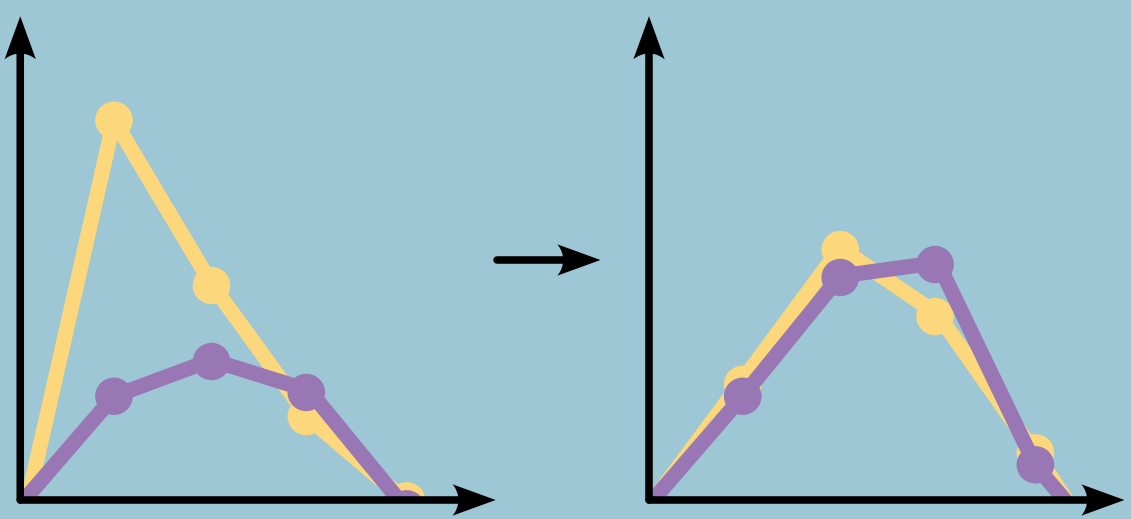
### 1.3 Pearson and Mean of Replicates



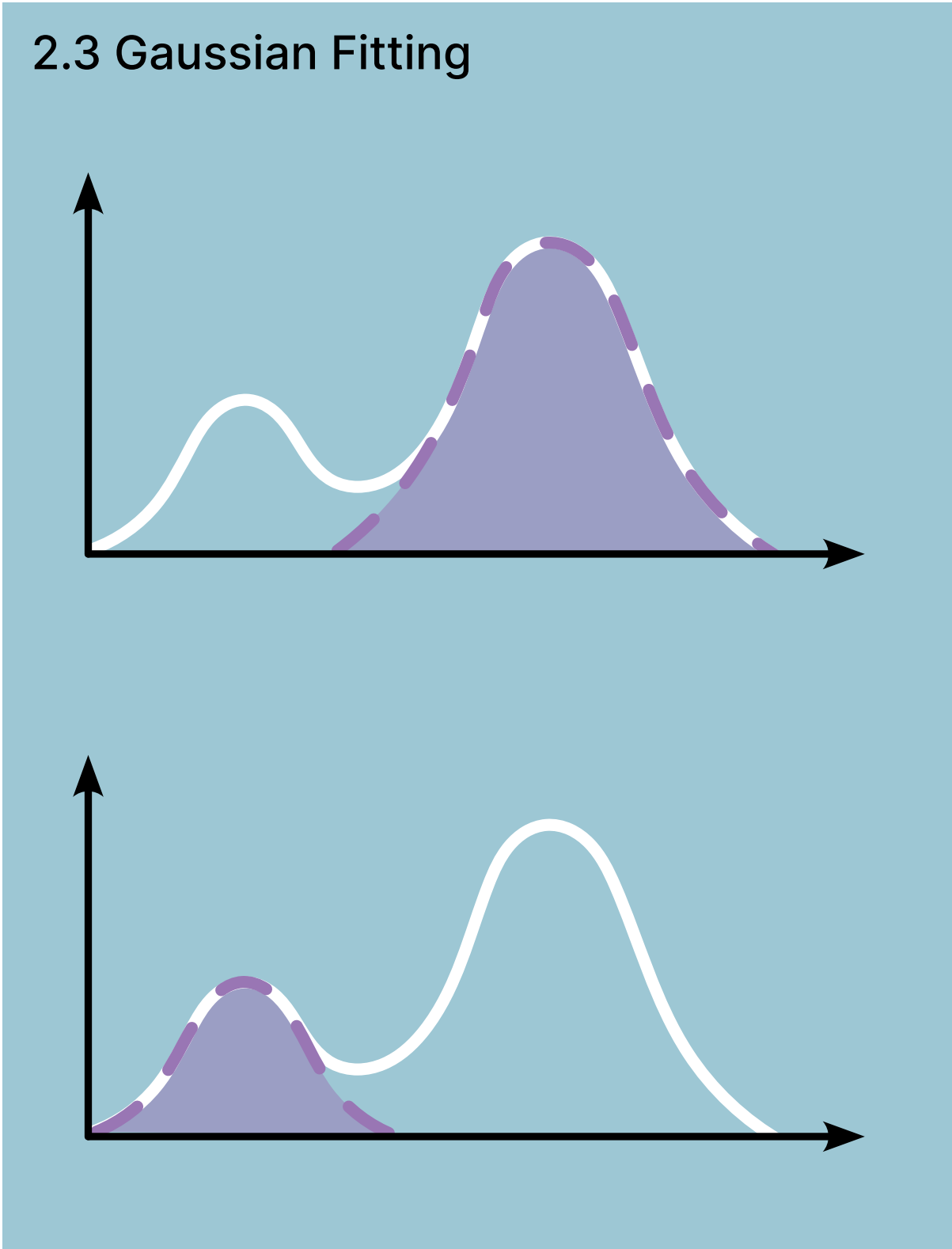
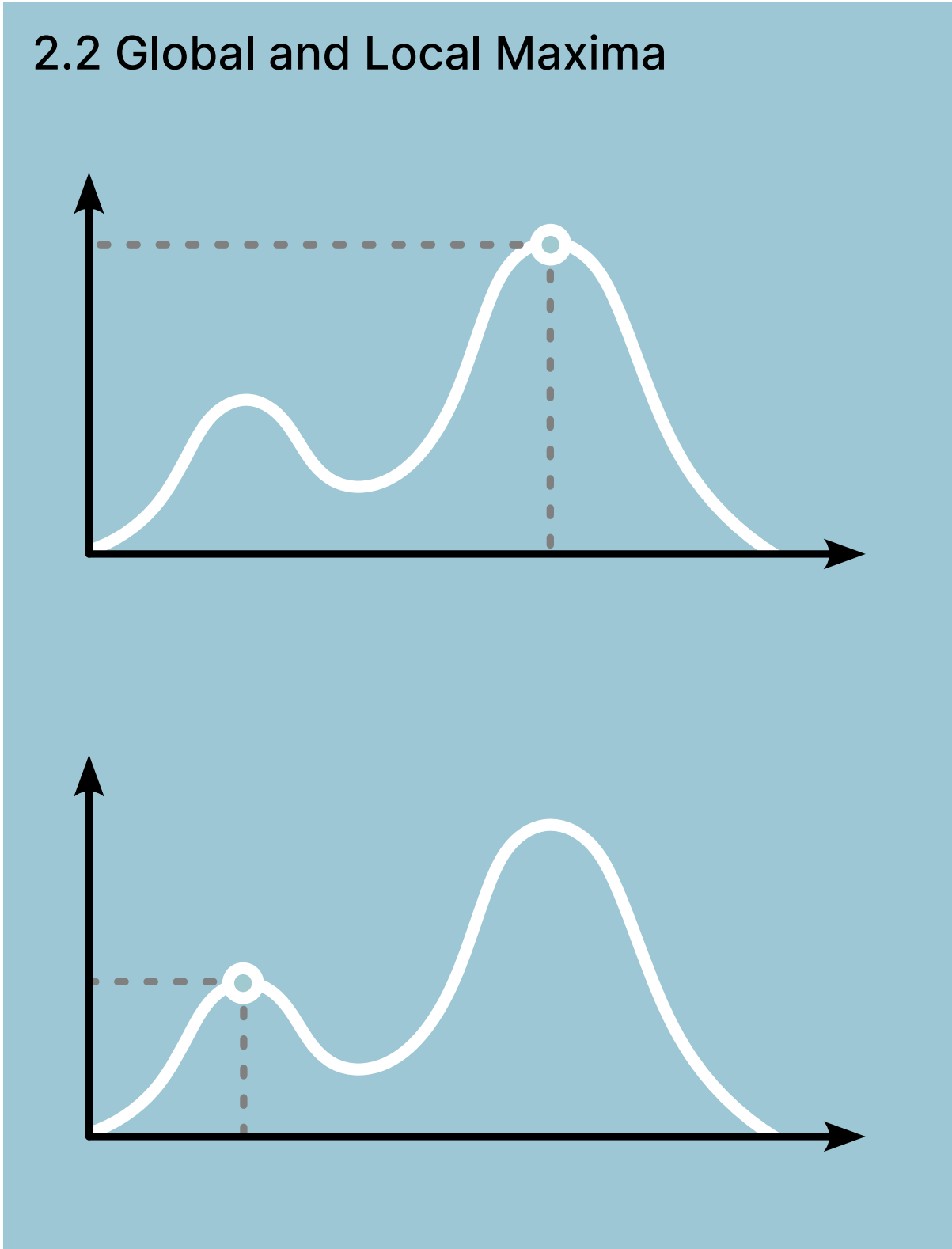
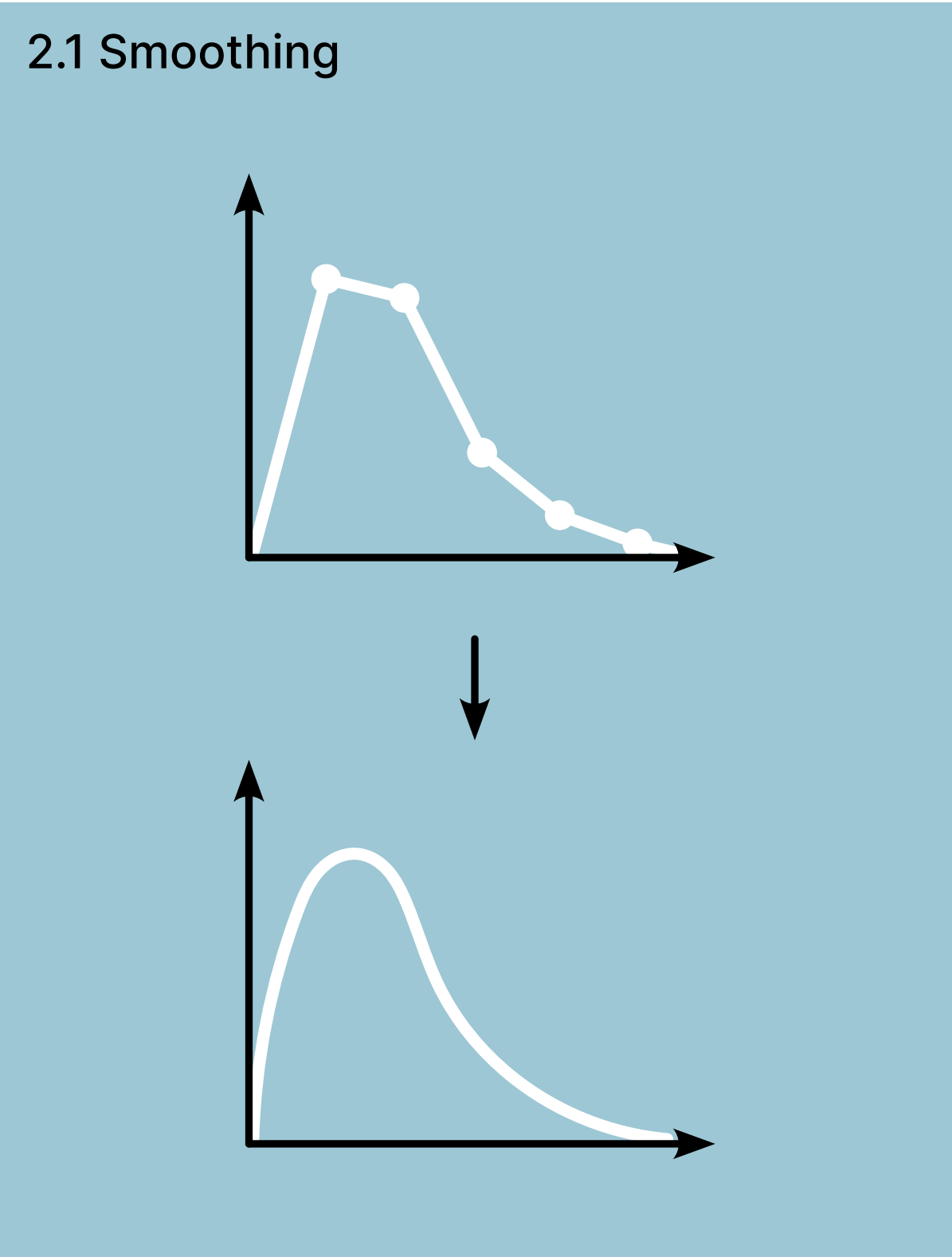
### 1.4 Normalization

				$\Sigma$
				100
				100
				100

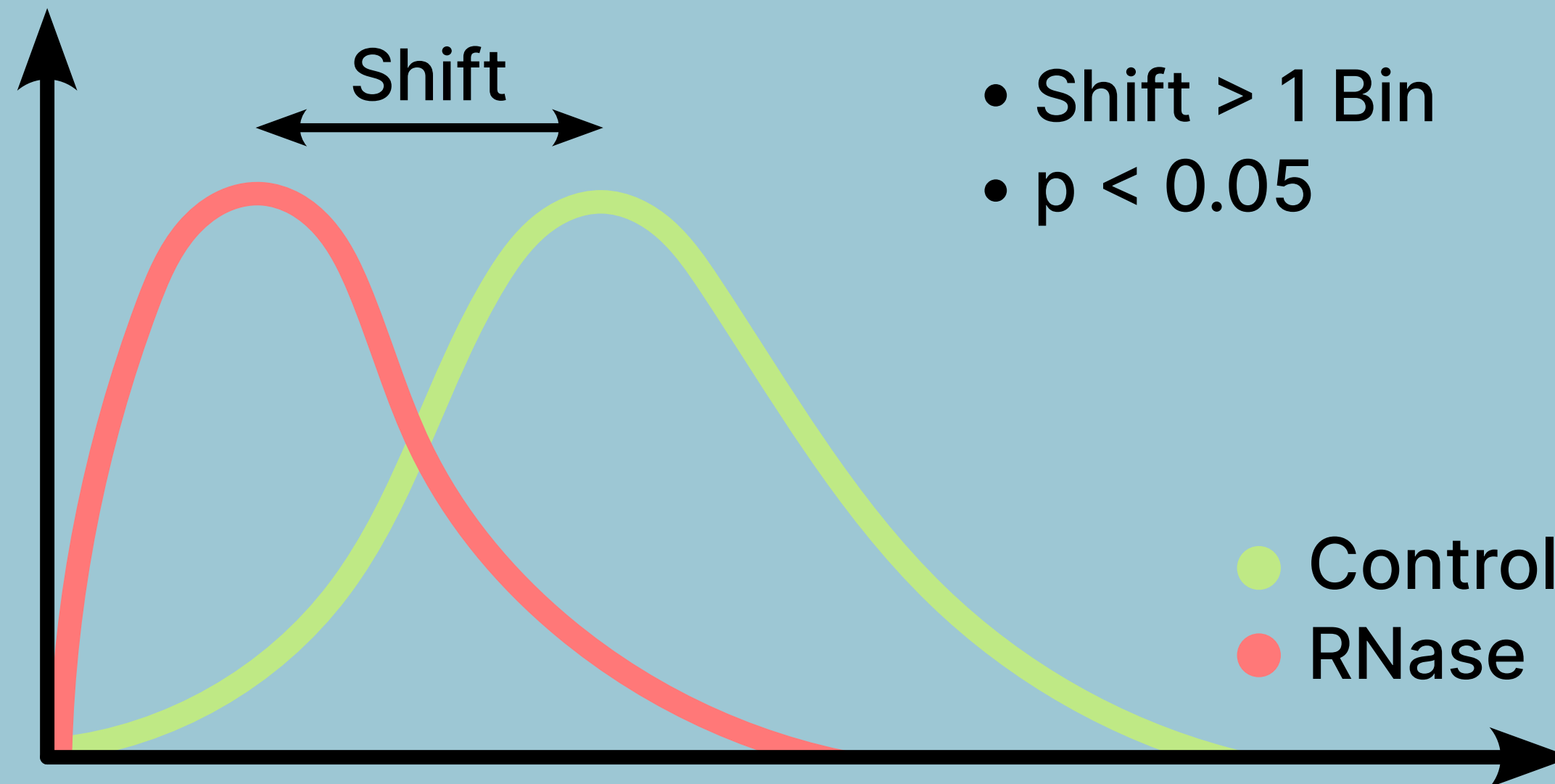
### 1.5 Z-Scaling



# Step 2: Finding Maxima and Gaussian Fitting



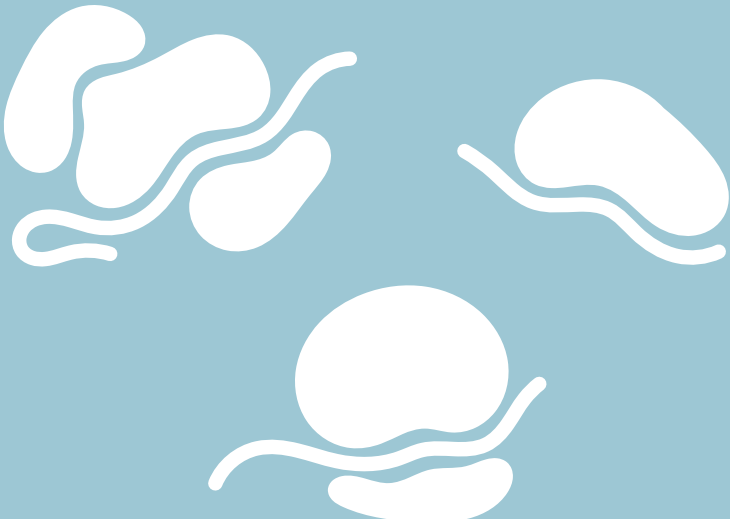
## Step 3: Defining Selection Criteria



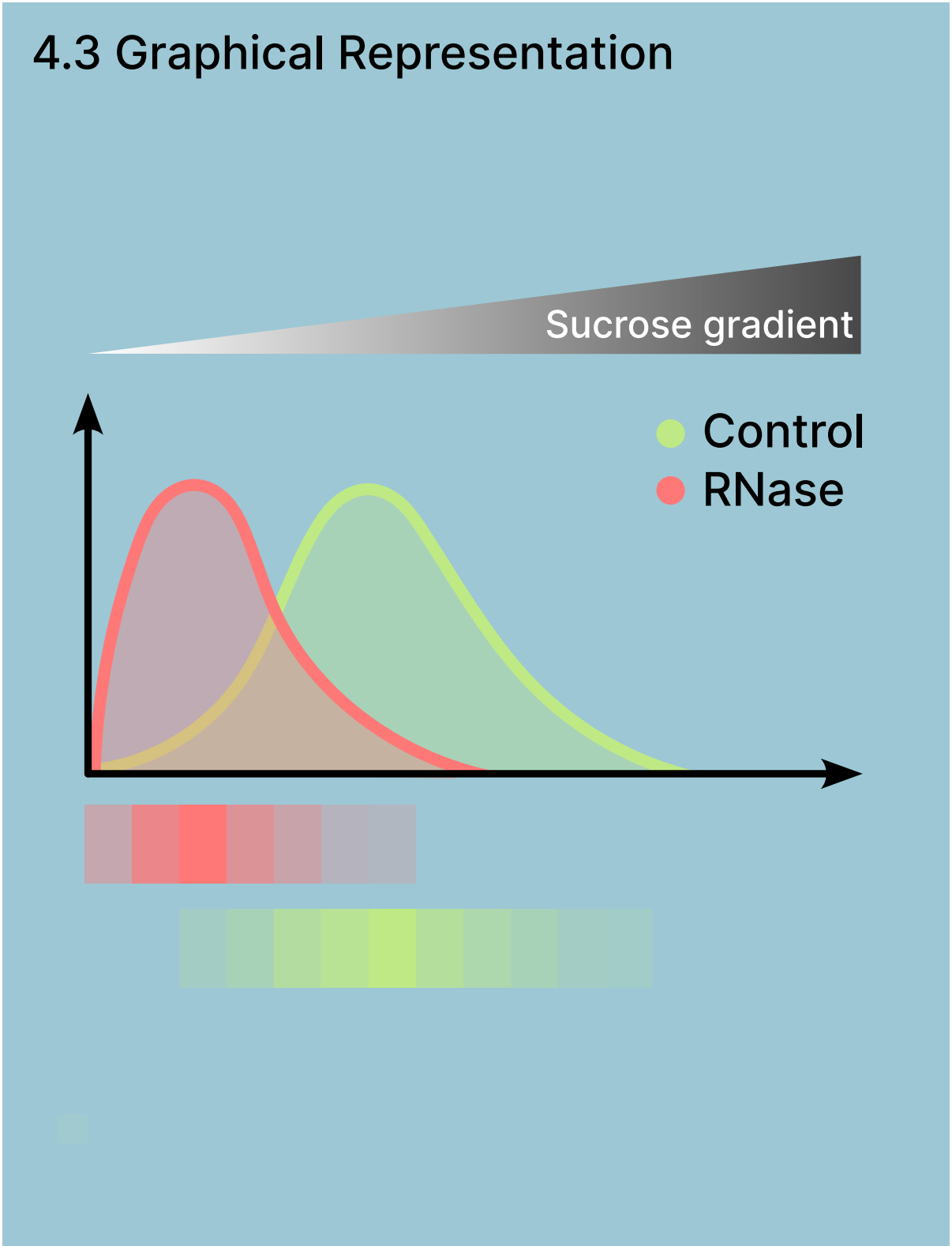
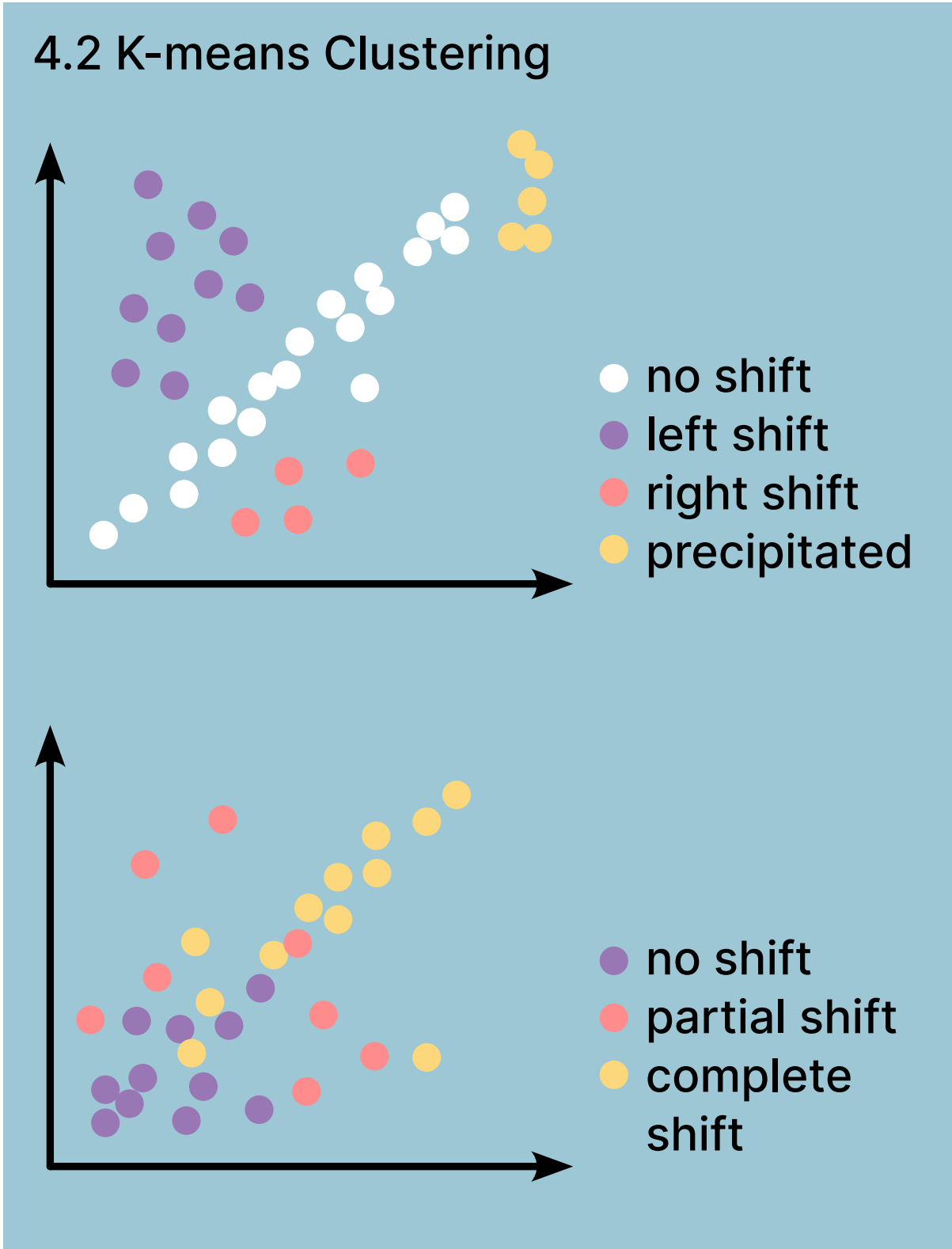
# Step 4: Identification of RNA-dependent Proteins

### 4.1 Application of Our Selection Criteria


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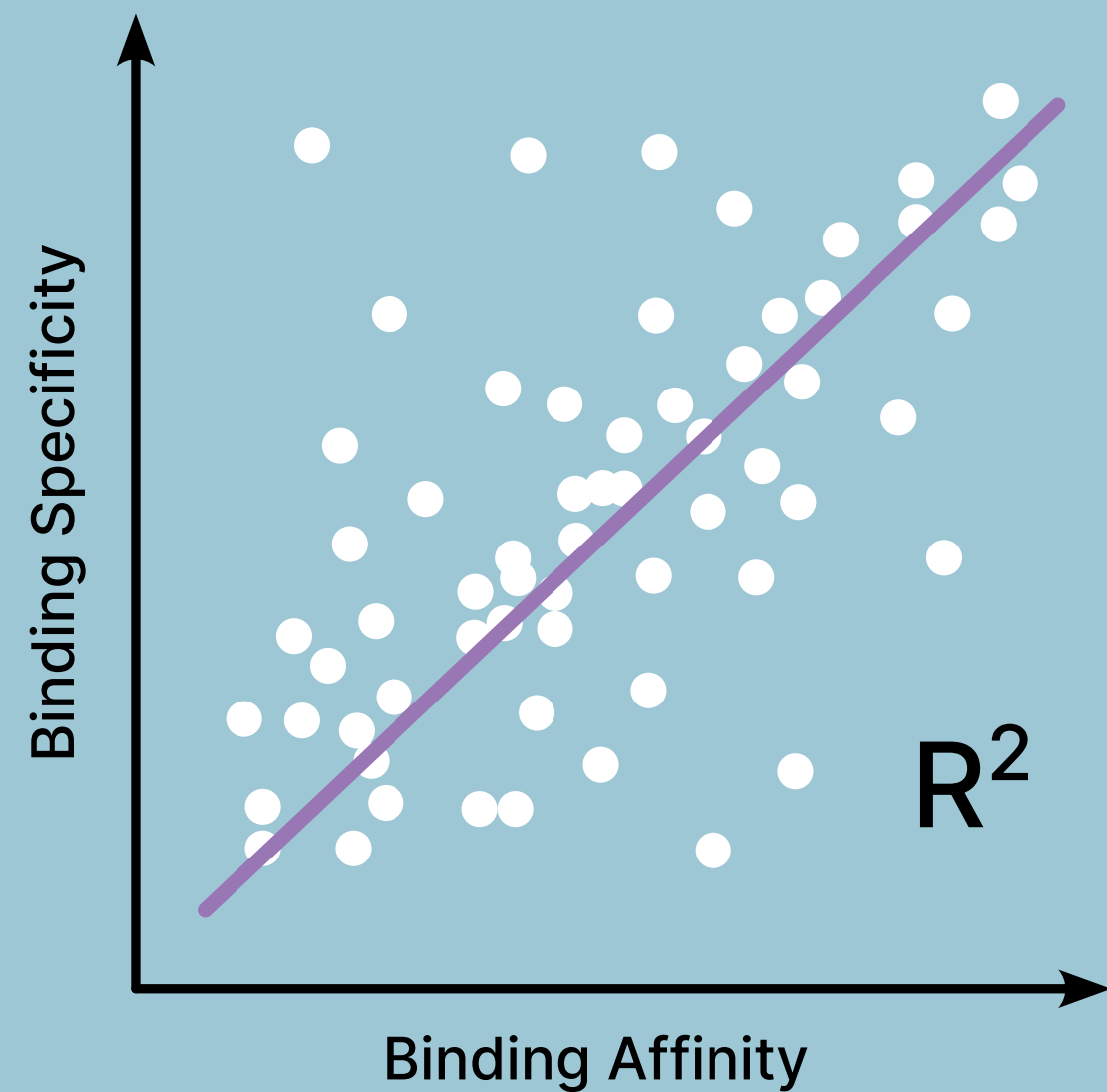
The diagram shows three protein-RNA complexes. The top two are composed of multiple subunits, while the bottom one is a single subunit with a large, rounded domain.



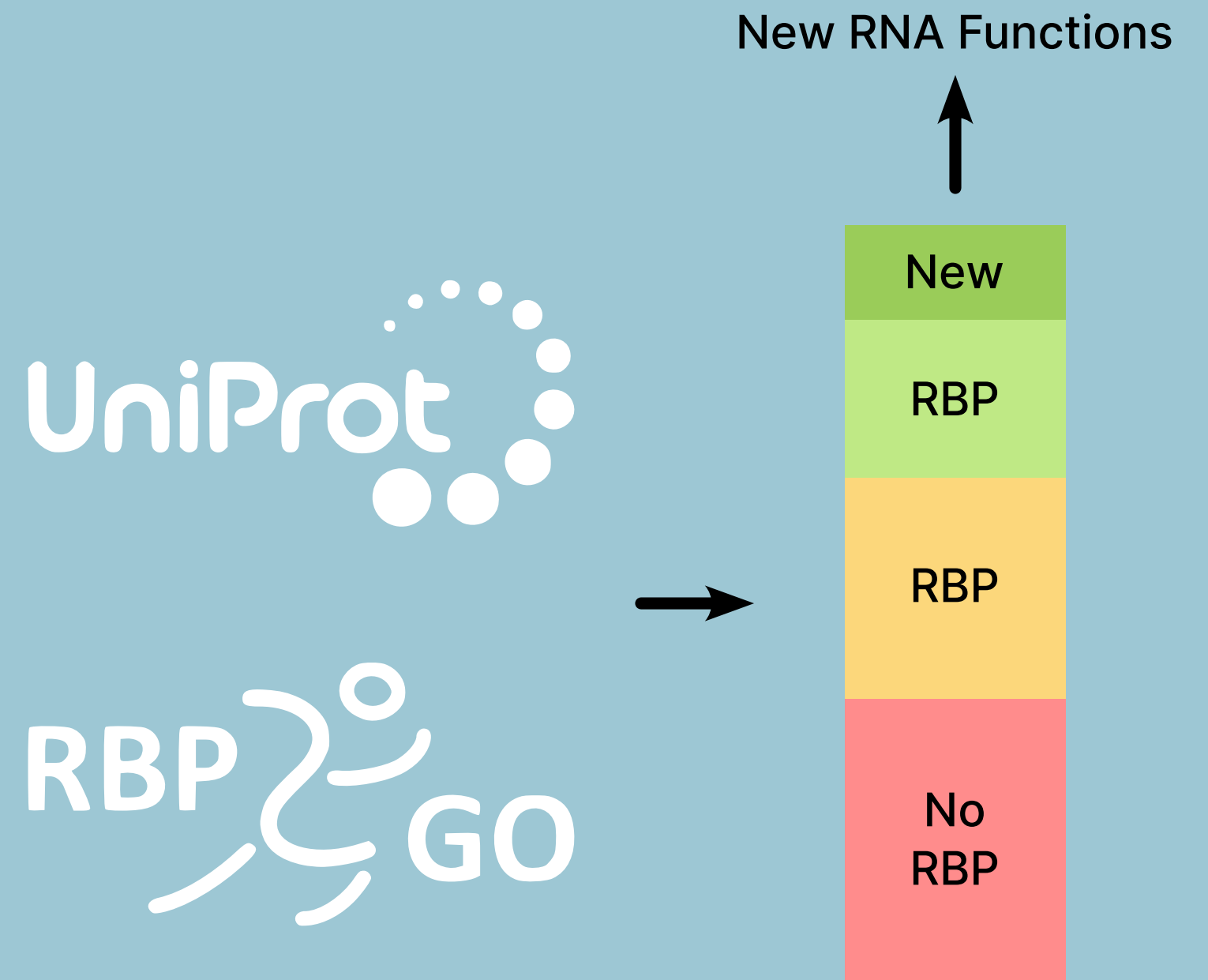


# Step 5: Linear Regression and Further Analysis

## 5.1 Linear Regression



## 5.2 Further Analysis



# Timeline

