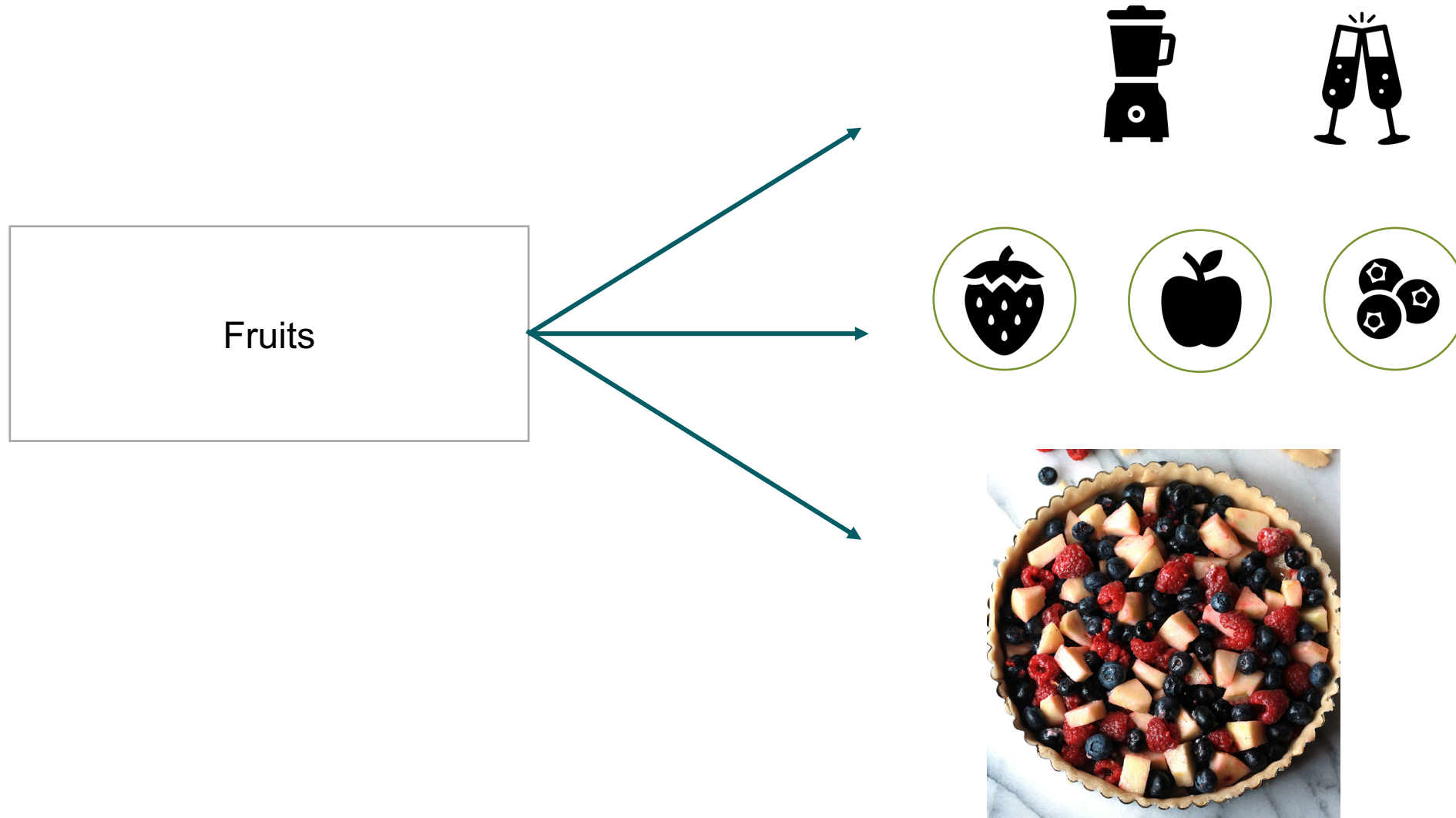


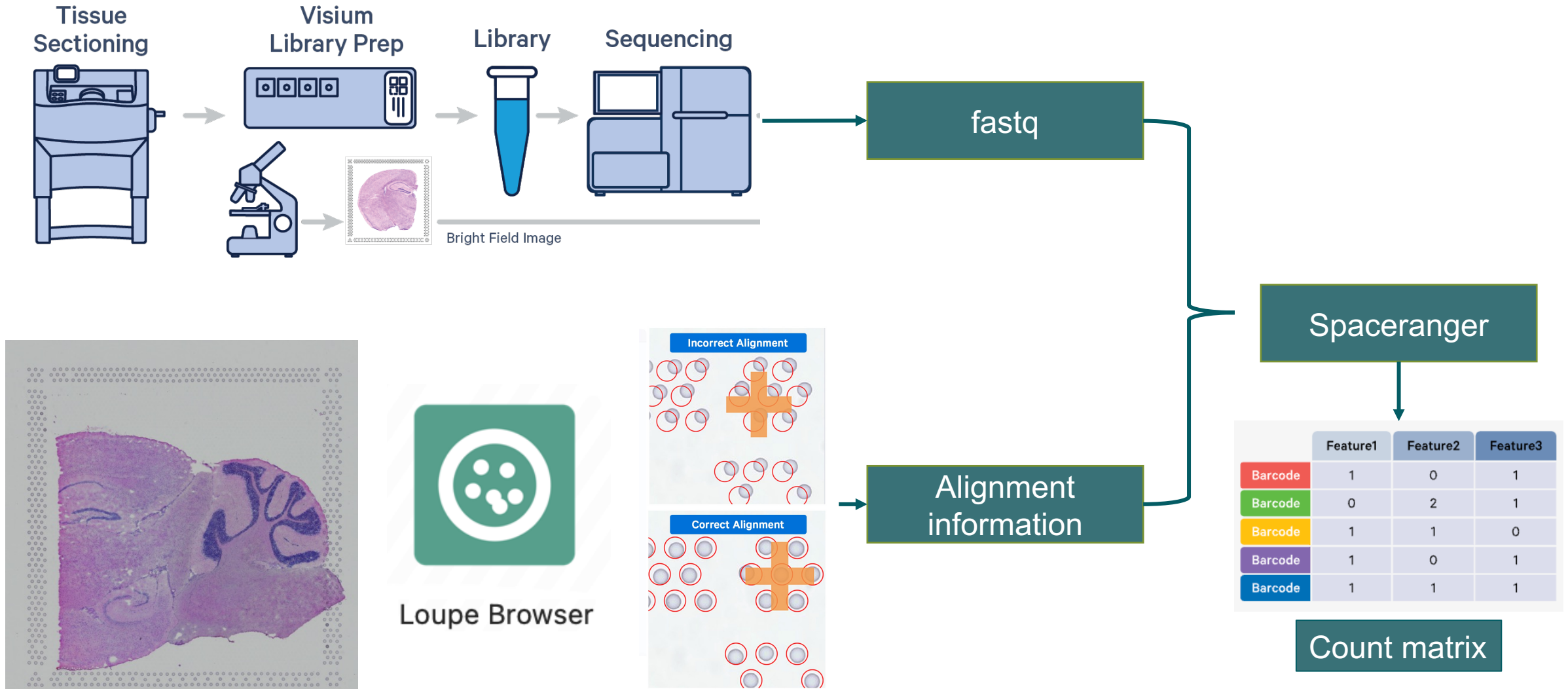
Lab 4|Spatial transcriptomics

Main Responsible: Nayanika Bhalla

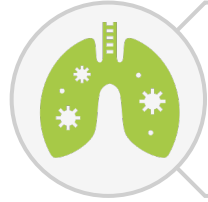
Spatial Transcriptomics: Recap



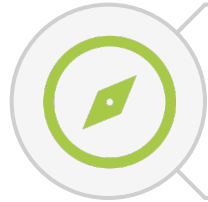
ST Data Production



Spaceranger output to be used



“filtered_feature_bc_matrix.h5” or
“raw_feature_bc_matrix.h5”



“tissue_positions_list.csv”



“tissue_hires_image.png”



“scalefactors_json.json”

STUtility R package



- Wrapper of Seurat.
- STUtility object.
- Each 'spot' is = each 'cell' in scRNA-seq.
- Contains tutorials and walkthroughs for exploring spatial datasets.

The screenshot shows the STUtility website. At the top is a dark blue navigation bar with links: STUtility, Home, About, Installation, Tutorials, Walkthroughs, License, and Source code. Below the navigation bar is the SPATIAL research logo, which consists of a grid of blue dots. To the right of the logo is the word 'Home'. Below 'Home' is a button labeled 'workflowr' with a green checkmark. The main content area contains a welcome message, a paragraph about the R-package and its developers (Ludvig Larsson and Joseph Bergenstråhle), and a link to the website spatialresearch.org. At the bottom, it says 'A work by Joseph Bergenstråhle and Ludvig Larsson'.

STUtility Home About Installation Tutorials Walkthroughs License Source code

SPATIAL research

Home

workflowr ✓

Welcome to the STUtility web site!

STutility is an R-package with the goal of providing an easy-to-use visualization and analysis tool kit for spatial transcriptomics data. The package was developed by Ludvig Larsson and Joseph Bergenstråhle in the Genomics research group at the Royal Institute of Technology (KTH). The group is positioned at the [Science for Life Laboratory](https://www.sciencelife.se) (SciLifeLab) in Stockholm, Sweden. Please visit our website spatialresearch.org for more information about the group and our research.

Please don't hesitate to contact us if you encounter any issue with the package, have suggestions, or any other inquiry!

A work by [Joseph Bergenstråhle](#) and [Ludvig Larsson](#)

Metadata



- Gives information about where your data is actually coming from?
 - Contains tissue and patient information
 - Also experimental information
 - Statistical information
- Why is it important?
 - Makes data 'findable'
 - Relationship between different variables
 - Can explain confounding factors.

NOTE: No tissue metadata is provided for the lab today as we will only process 1 sample.

Creating a STUtility object



- Requires a dataframe 'infoTable' containing paths to files.
- 1 tissue section of human HER2-positive breast cancer.

samples	spotfiles	imgs	json
path/to/sample_1/count_file_1.h5	path/to/sample_1/tissue_positions_list.csv	path/to/sample_1/tissue_hires_image.png	path/to/sample_1/scal
path/to/sample_2/count_file_2.h5	path/to/sample_2/tissue_positions_list.csv	path/to/sample_2/tissue_hires_image.png	path/to/sample_2/scal

```
#Creating the STUtility object (similar to a Seurat object)  
se <- InputFromTable(infoTable)
```

Spatial functions

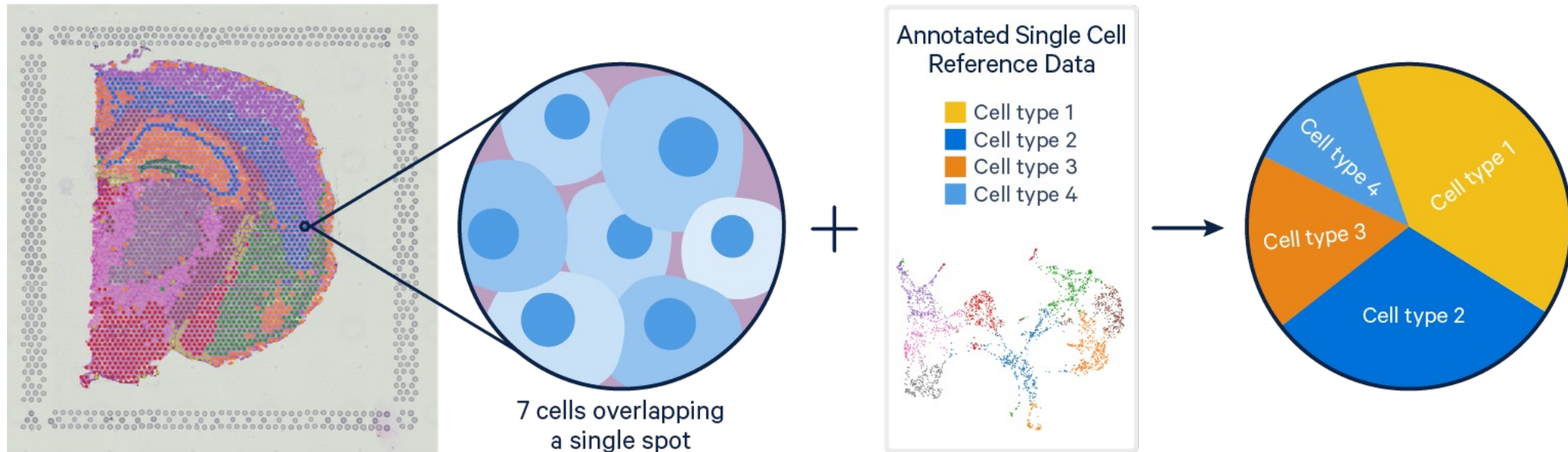


- `FeaturePlot()` → `ST.FeaturePlot()`
- `Subset()` → `SubsetSTData()`
- `FeatureOverlay()`
- `DimPlot()` → `ST.DimPlot()`

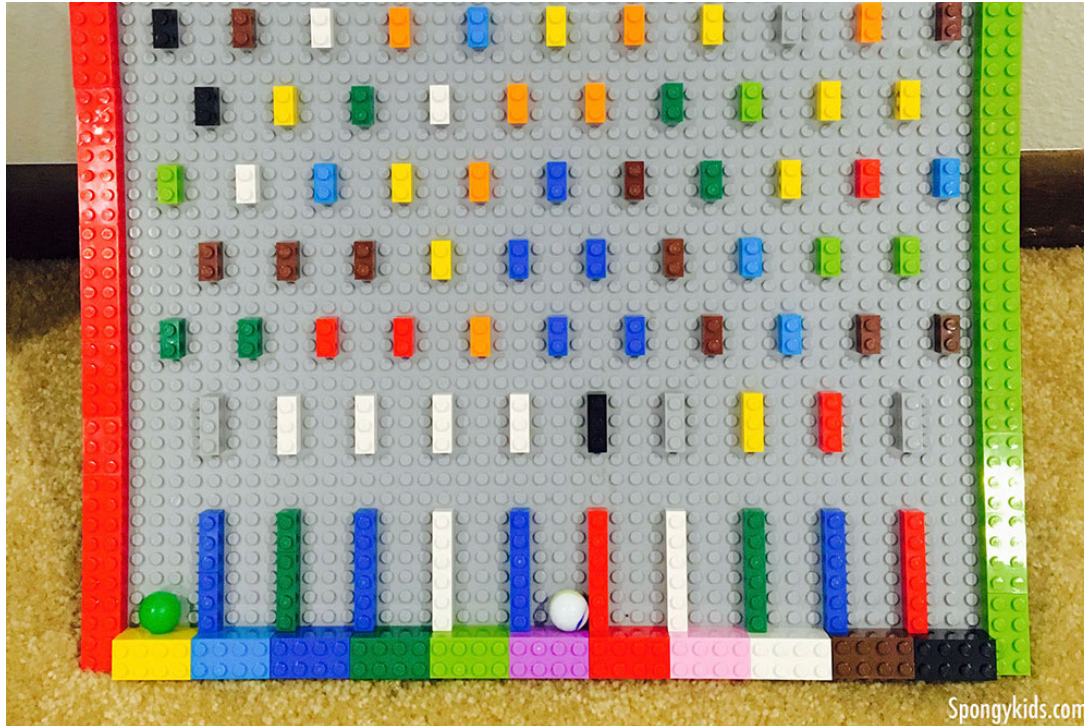
Stereoscope



- Visium lacks single cell resolution.
- Probabilistic method that uses single cell data to deconvolve the cell mixtures in spatial data.



Reproducibility



- When you generate anything involving randomisation in R, it is pseudorandom (simulate randomness).
- If you know the “seed” and the generator, you would end up with the same results every time.
- The seed acts as an initiator.
- “Seed value”
 - Ensures that we get the same results for randomisation.

Reports



- Complete all questions.
- Hand in a knitted .html file.
- Hand in your reports by 20 Oct (23:59).

GOODLUCK!