Questionnaire CyteGuide

Basic

- What is the typical number of partitions/clusters in an embedding?

- Do you manually select the segments or use clusters?

- Would you rather use one or the other?

- Do you intentionally inspect overlapping regions in the same analysis session?

Exploration & Guidance

- Can you keep track of where you zoomed in?

- If not, what information would be necessary to keep track?

- Do you always zoom to the data level?

- What are (if no) / would be (if yes) criteria to decide whether to zoom in on or not?

- What are the main criteria to decide where to zoom in?

- (How) Do you prioritize?

Summary & Presentation

- What information would be necessary to inspect the complete hierarchy?