Project Update and Workshop

Visual Analytics for Plant Pangenomes (VAPP)

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TU/e EINDHOVEN UNIVERSITY OF TECHNOLOGY

WAGENINGEN UNIVERSITY & RESEARCH

Agenda

- Project update
- Introduction of the workshop
- Demo and exploration of prototype
- Workshop creative part

Project Update

Project Update

Current focus

Exploring sequence variation of a target gene across multiple accessions and with multiple references

Project Update

What is the challenge? * Translating variant information between assemblies and (re)sequencing data

Project Update

What is the challenge?

* Translating variant information between assemblies and (re)sequencing data

* No intuitive display of the variants within their genomic and phenotypic context

Project Update

Why is it important to solve?

* To allow genome scientists to study a more complete picture of the variants and traits at several levels of the biological context

* To discover interesting variant - phenotype relations

Project Update

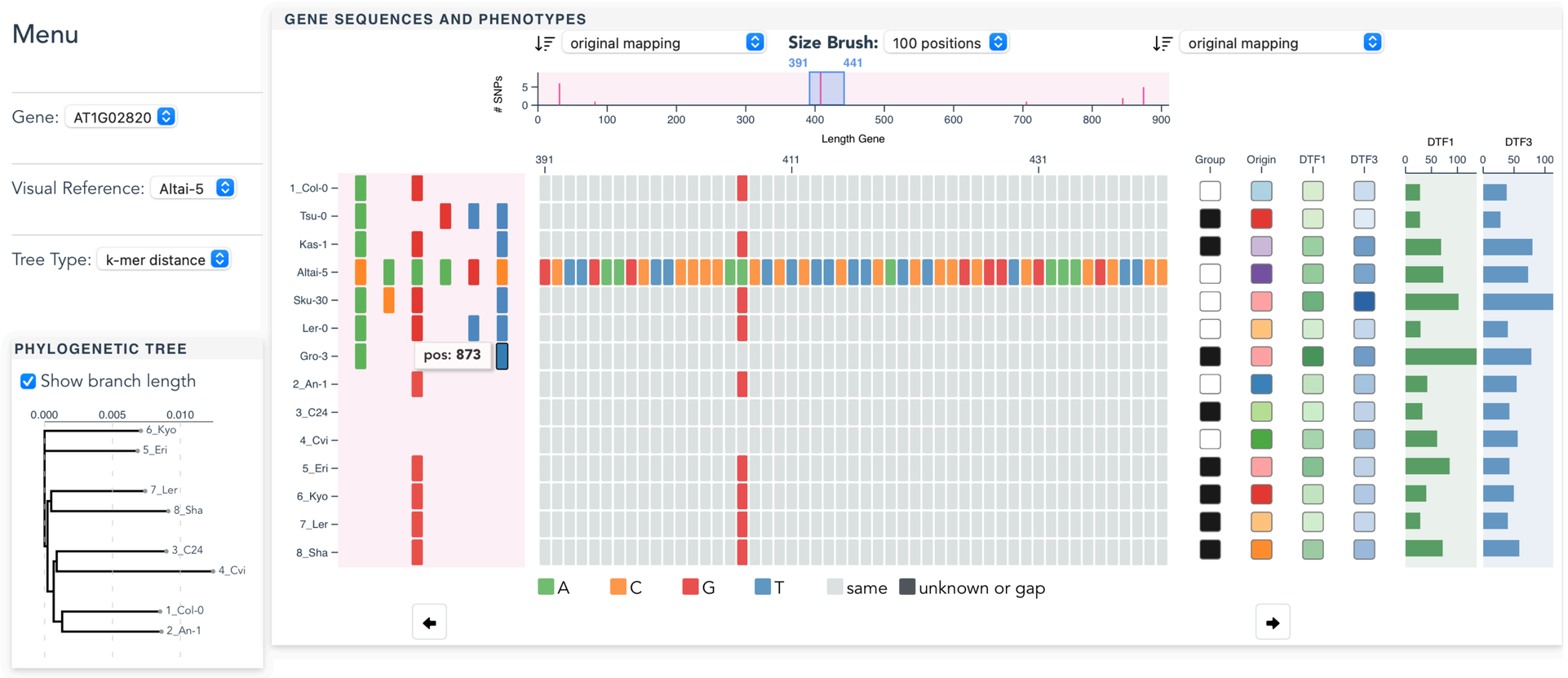
Tasks
(currently supported)

1. Explore sequence variation with respect to a chosen (visual) reference

2. Locate variable positions within the gene and inspect details

3. Discover phenotype patterns

Project Update



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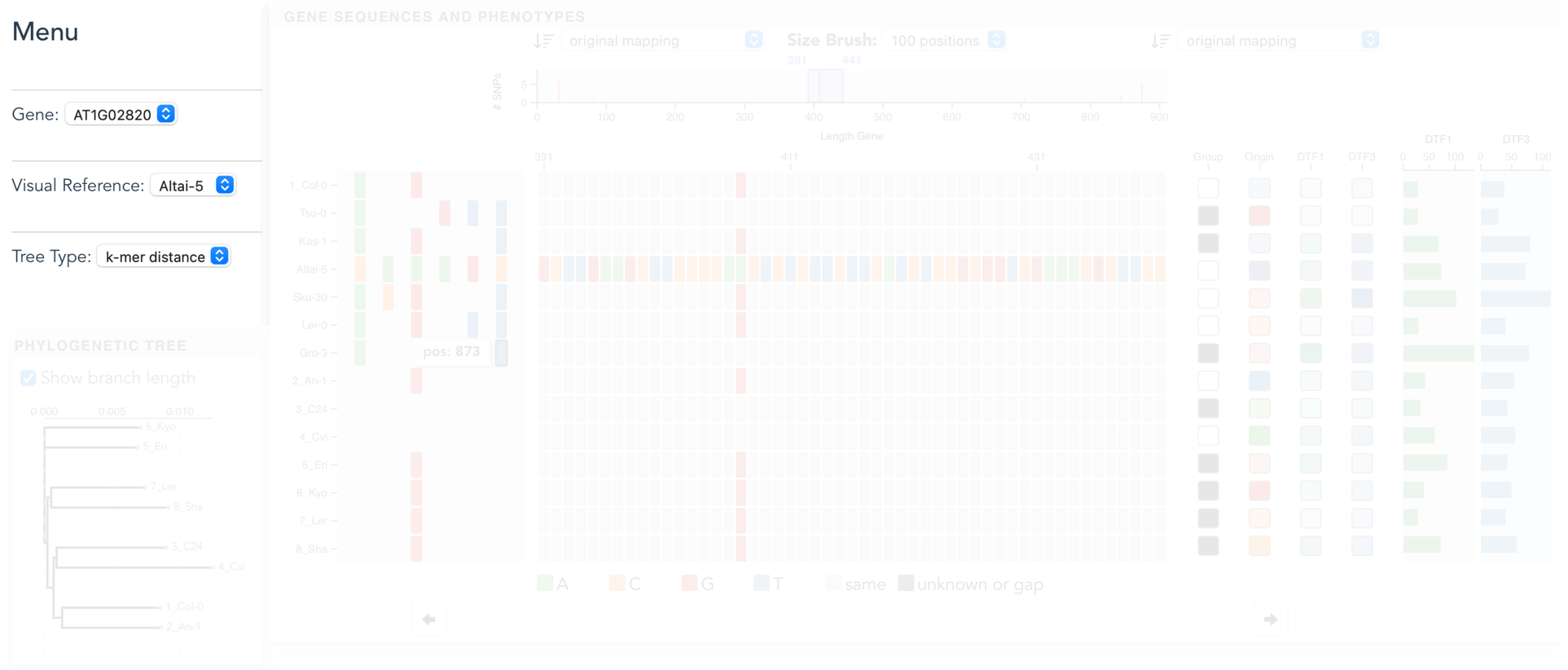

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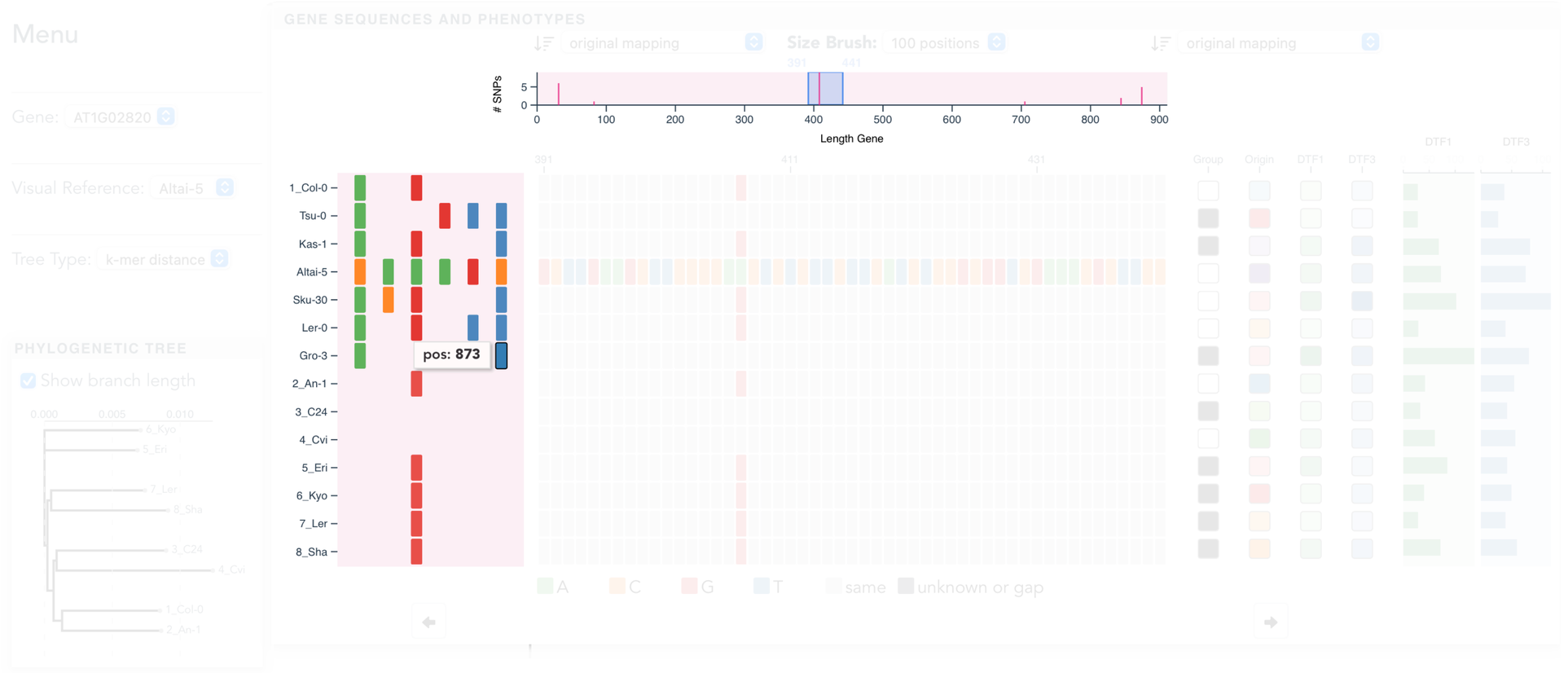

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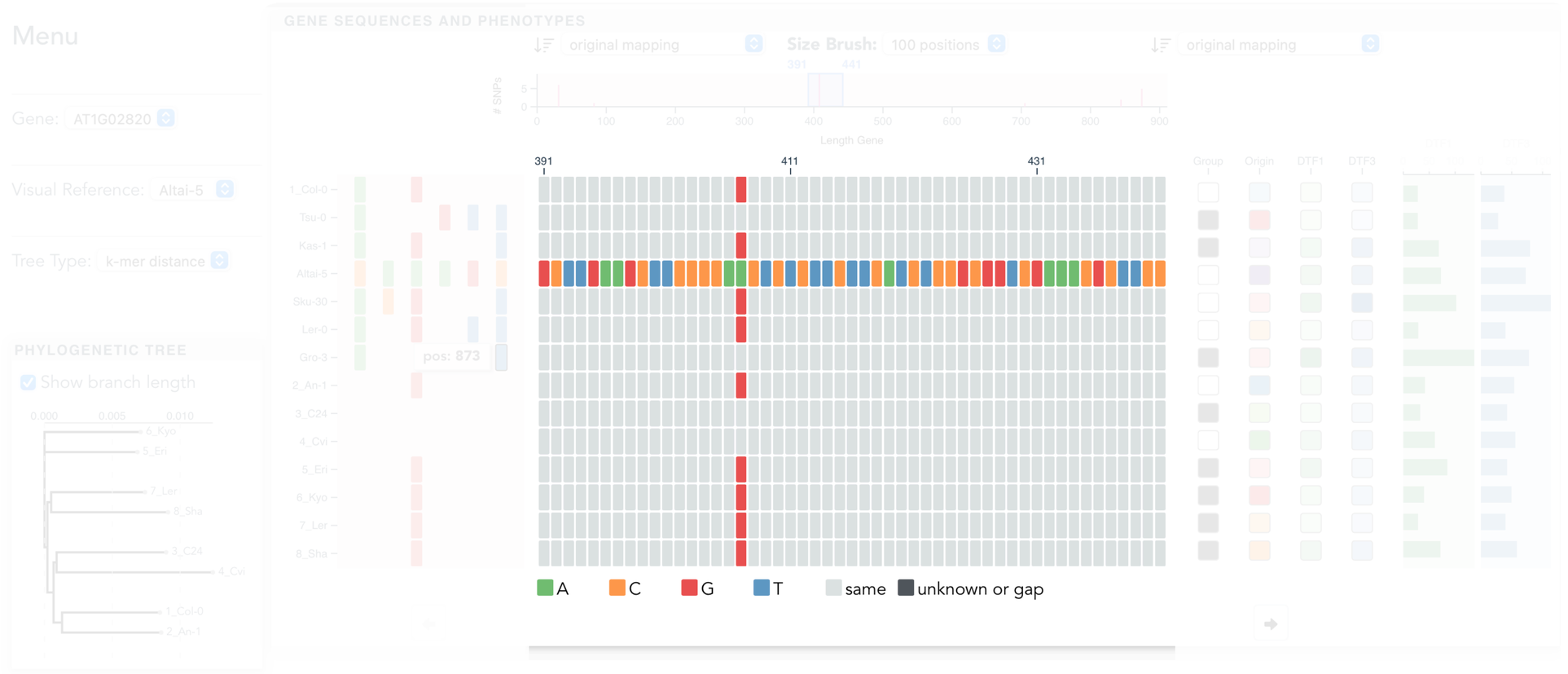

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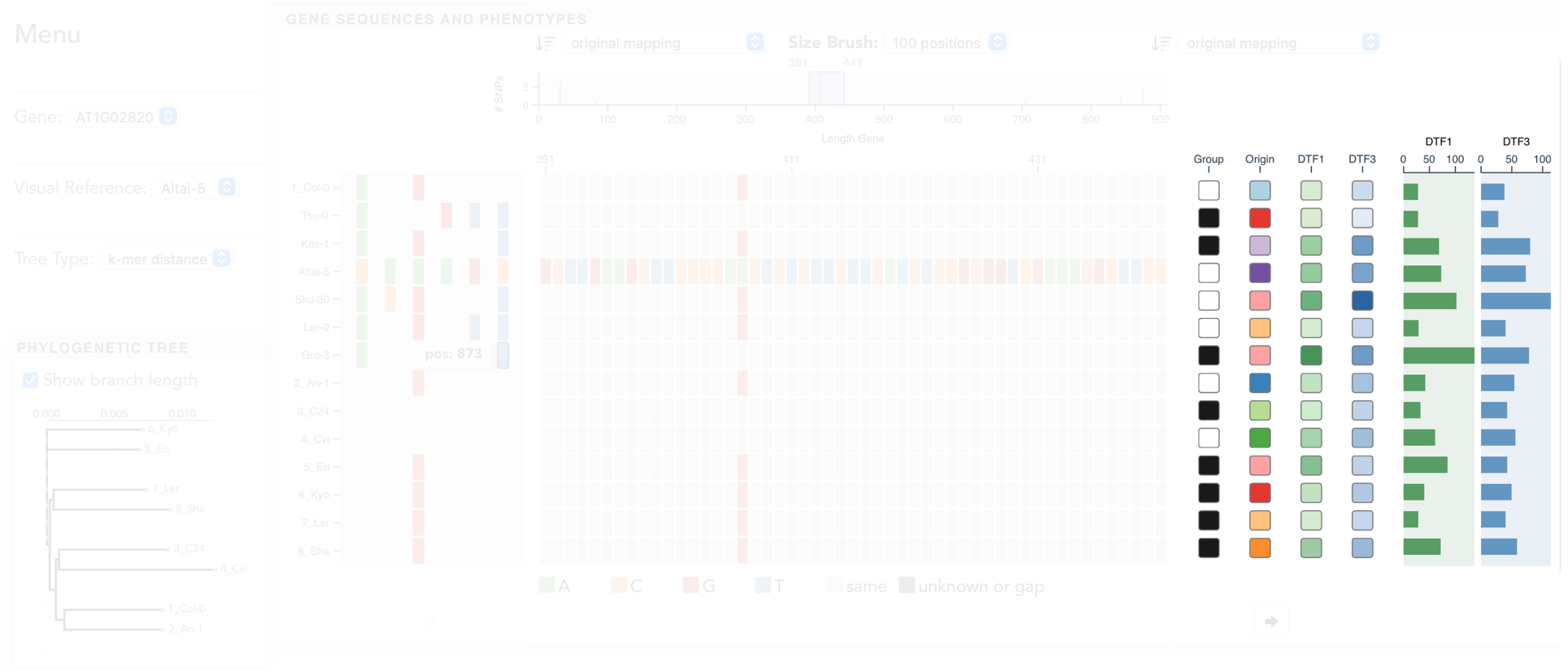

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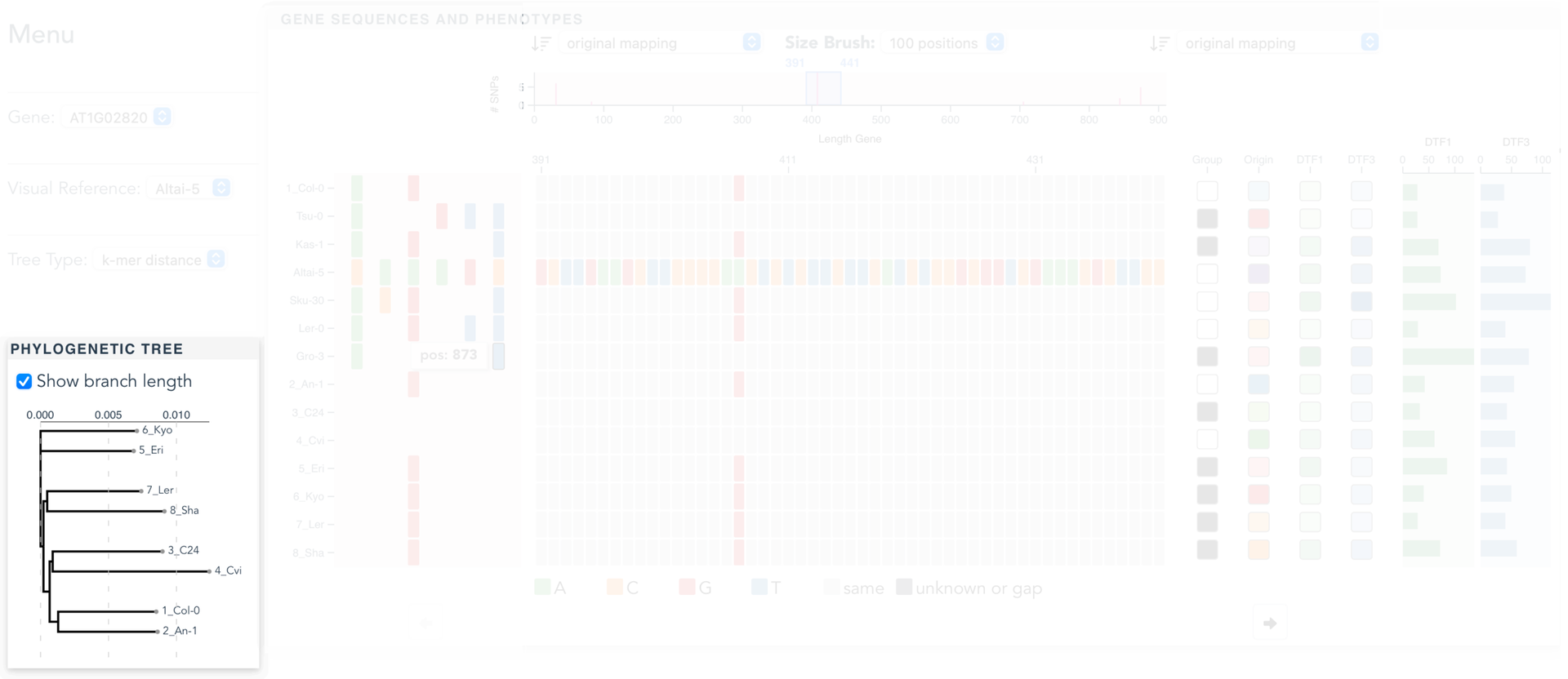

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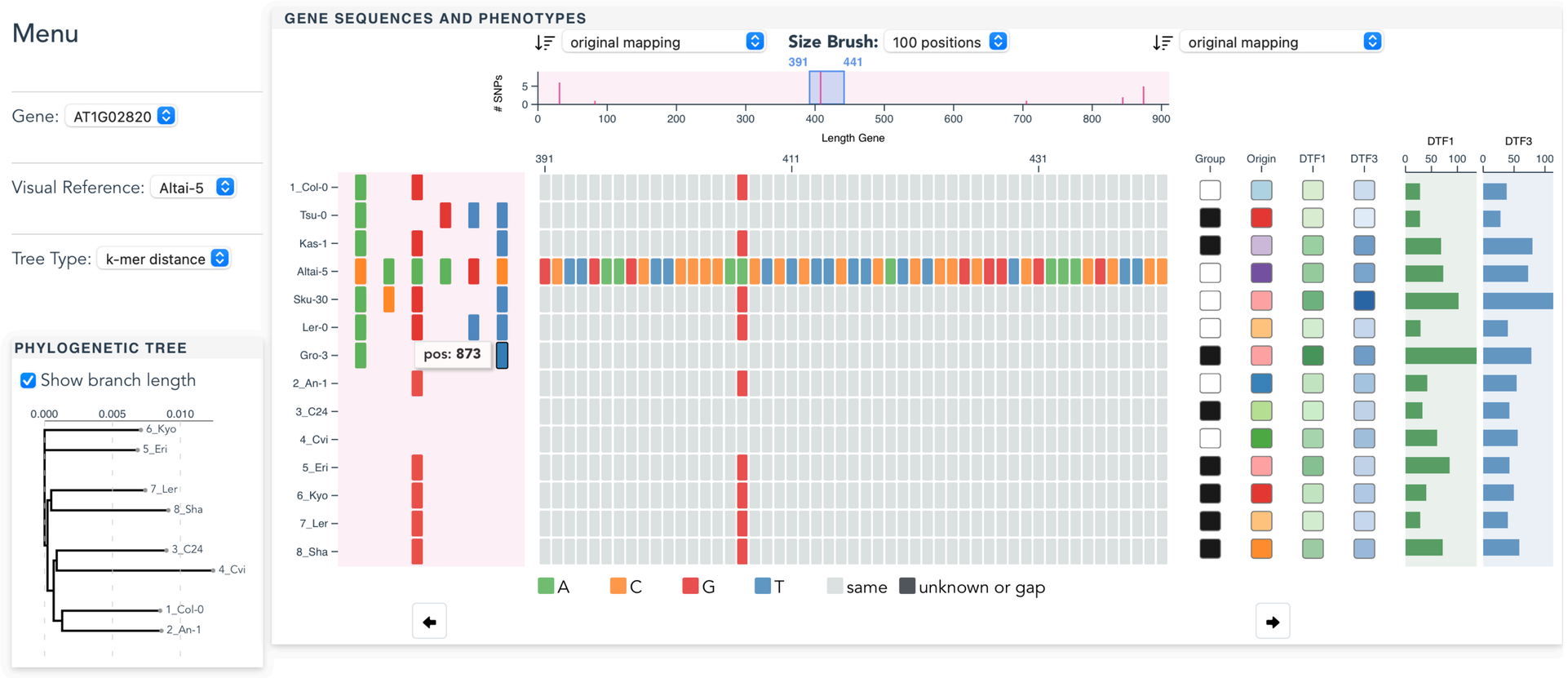
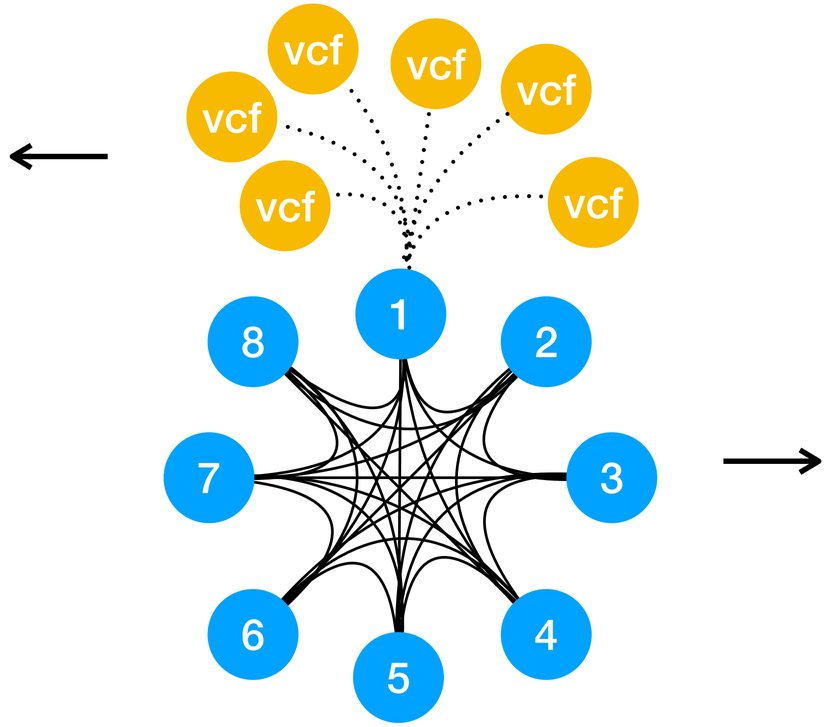


Project Update

Data
(for development current prototype)

Arabidopsis pangenome

VCF
Altai-5
Gro-3
Kas-1
Ler-0
Tsu-0
Sku-30



	Accession
1	Col-0
2	An-1
3	C24
4	Cvi
5	Eri
6	Kyo
7	Ler
8	Sha

Project Update

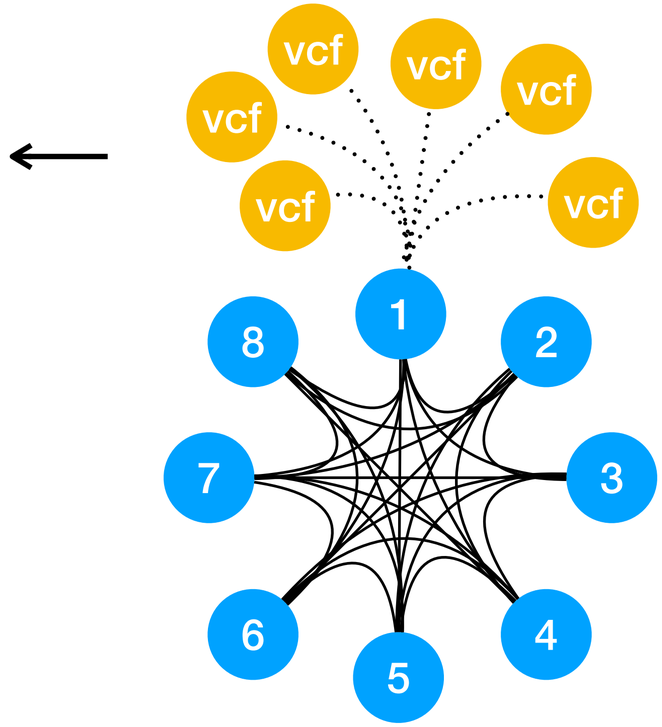
Data
(for development current prototype)

Arabidopsis pangenome

\+ Phenotypes

\+ Phylogenetic trees

VCF
Altai-5
Gro-3
Kas-1
Ler-0
Tsu-0
Sku-30



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Project Update

Next steps

* Further develop prototype to include more advanced functionalities needed for real crops
* Prototype evaluation sessions (individual)
* Use case development and evaluation
* Backend (API) development

Workshop Introduction

Workshop Introduction

Workshop goal:

⭐ demo and evaluate first design

⭐ generate new ideas guided by specific use cases

Workshop Introduction

💫 All ideas are valid: express and record them

💚 Be supportive of others

🌀 Don't overthink it!

Think aloud!

💡 Focus on ideation, not critiques, no technical details

🗣️ Speak in headlines and follow-up with detail

*** This workshop will be audio recorded ****

Workshop Schedule

11:00 - 11:30	**Opening**
11:30 - 12:00	Part 1: Wishful Thinking Activity
12:00 - 13:00	Lunch Break
13:00 - 13:35	Part 2: Storyboarding Activity
13:35 - 13:45	Closing

Demo and Exploration of the Prototype

Demo of the Tool

If you'd like to follow along, please go to: http://vapp1.win.tue.nl

For an optimal experience:

! please use Chrome or Safari as browser

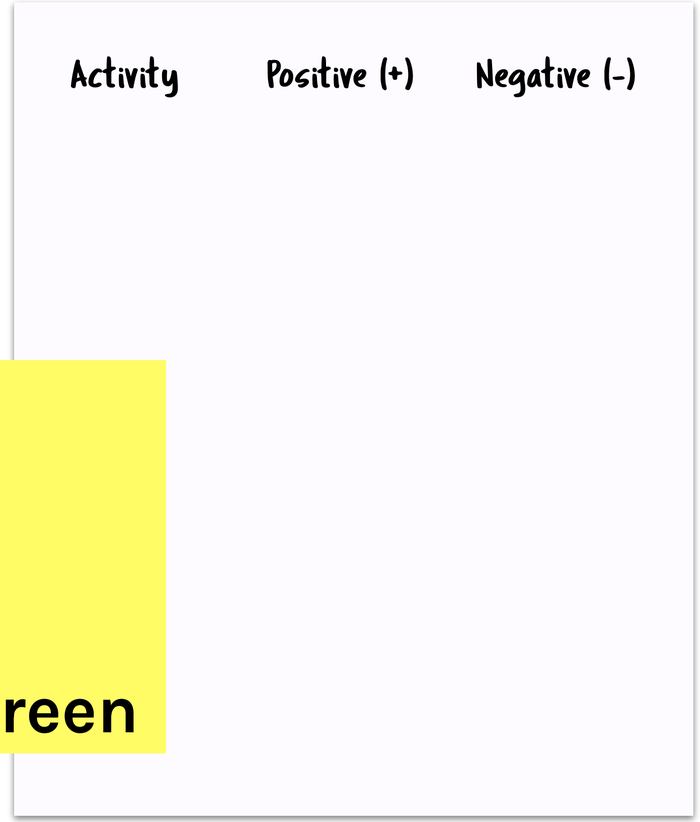
! open your browser in full-screen mode

! please press CRTL+R when it's loaded full-screen

Explore the Tool Yourself (7 min)

Materials:

- evaluation handout
- markers / pens
- link tool: http://vapp1.win.tue.nl



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Part 1: Wishful Thinking

Workshop Schedule

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Part 1: Wishful Thinking (30 min)

1. Individual Assignment (7 min)
2. Group discussion (15 min)
3. Presentation of major themes (8 min)

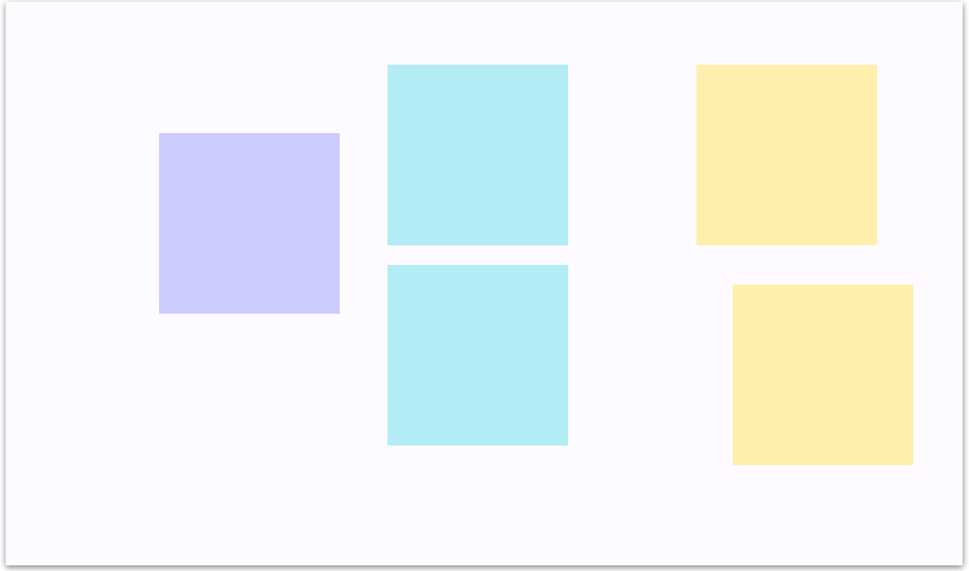
Part 1: Wishful Thinking

1. **Individual Assignment (7 min)**

“Moving to real crops, what is needed in order to analyse sequence variants?”

Think about the analysis tasks that you want to perform.

- *what would you like to know?*
- *what would you like to be able to do?*
- *what (information) would you like to see?*



! Handout serves as inspiration

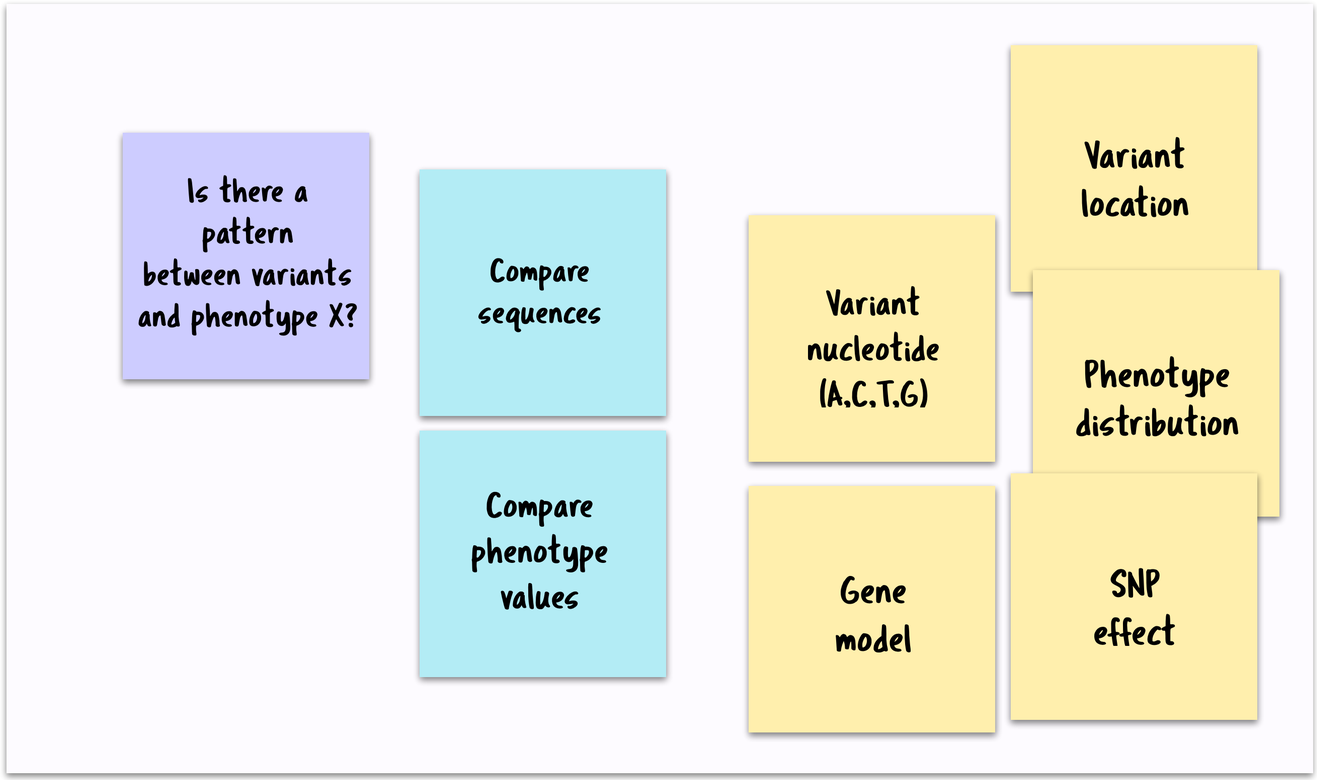
! Details can be resolved in the group

Part 1: Wishful Thinking: example

- *what would you like to know?*
- *what would you like to be able to do?*
- *what (information) would you like to see?*

! Handout serves as inspiration

! Details can be resolved in the group

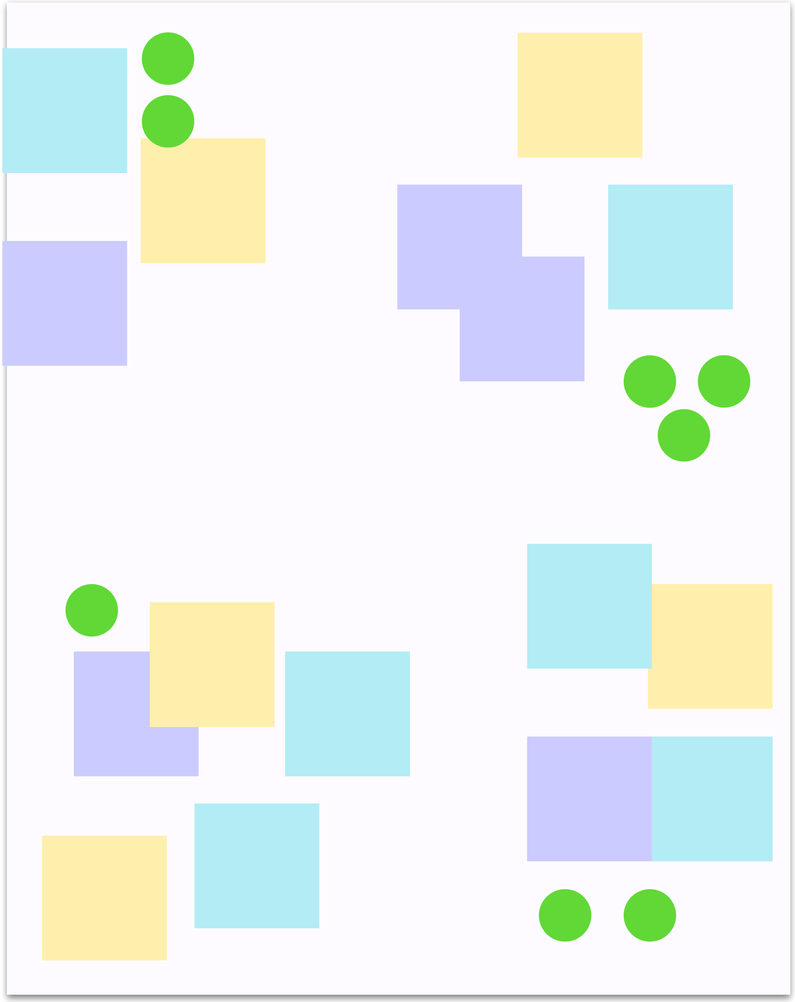


Part 1: Wishful Thinking

2. Group Discussion (15 min)

Within your group:

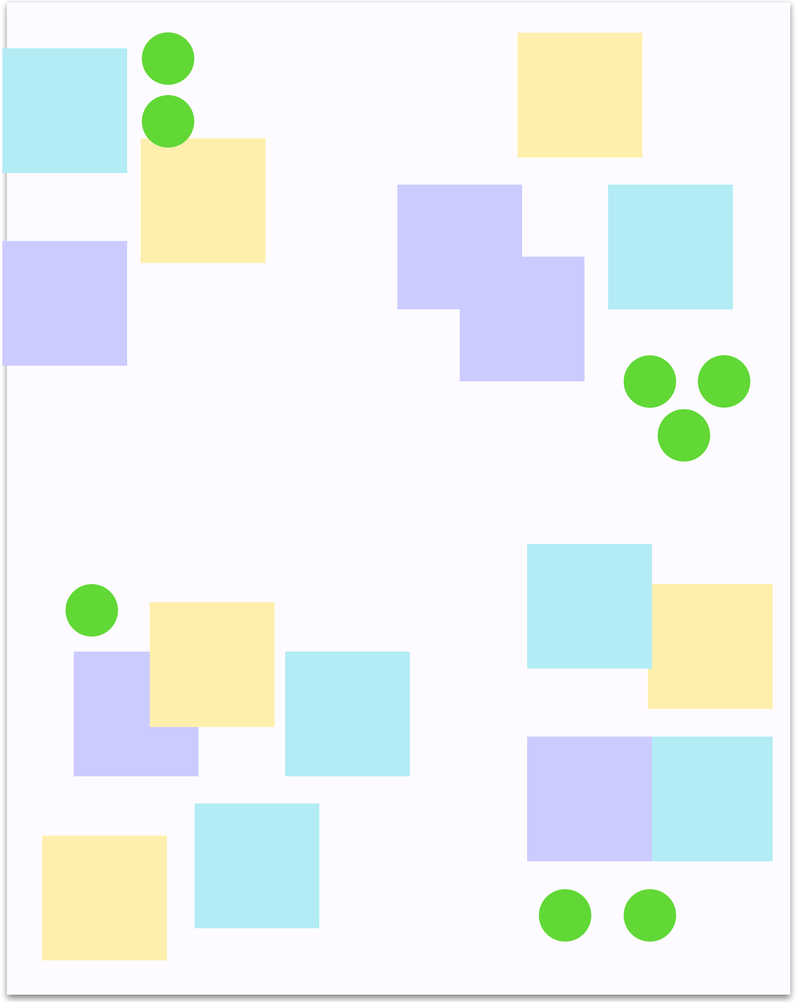
- *try to group the tasks by topic*
- *rank them by importance*



Part 1: Wishful Thinking

3. Presentation of Major Tasks (8 min)

Each group presents their major tasks and which one(s) have priority



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Part 2: Storyboarding

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13:00 - 13:35	**Part 2: Storyboarding Activity**
13:35 - 13:45	Closing

Part 2: Storyboarding (35 min)

1. Introduction of tasks (3 min)
2. Group discussion: workflow and data (12 min)
3. Group brainstorm: visualization use cases (12 min)
4. Presentation of use cases (8 min)

Part 2: Storyboarding

Marker design:

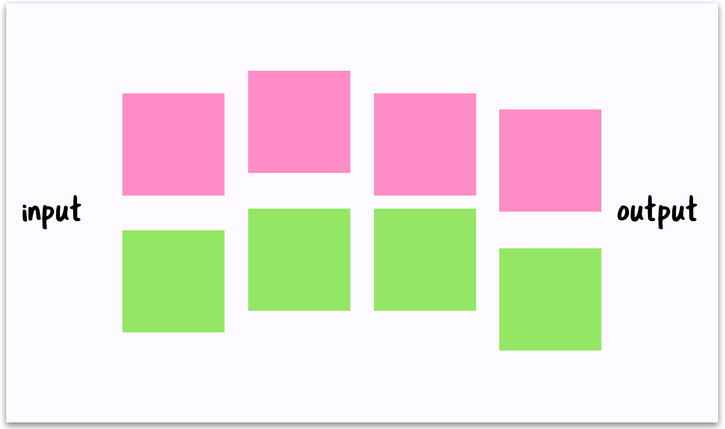
from trait and QTL —> haplotype analysis —> SNP marker

Part 2: Storyboarding

2. Group exercise: workflow and data (12 min)

Think about the task

- *What is the general workflow/ which steps does the user take from input to output?*
  → *use post-its to generate a workflow / sequence of steps*



Part 2: Storyboarding

2. Group exercise: workflow and data (12 min)

Think about the task

- *What is the general workflow/ which steps does the user take from input to output?*

  → *use post-its to generate a workflow / sequence of steps*

Think about the data involved in each step

- *What does the data consist of?*
- *How are different types of data related?*
- *How do you combine them to answer questions?*

  → *use green post-its to generate sequence of data transformations*

!! Handout and questions are for inspiration

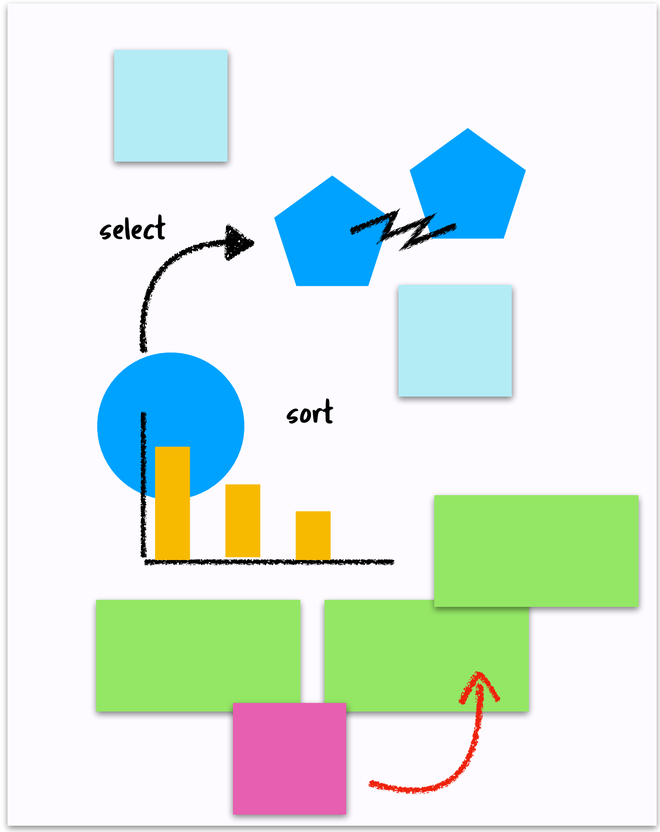
Part 2: Storyboarding

3. Group exercise: possible visualizations (12 min)

"How <u>could</u> a visualization of your data look?"

Sketch a visualization or a feature that would help us address the workflow

→ *you can make use of all materials*
→ *connect words, post-its & sketches to explain your ideas*

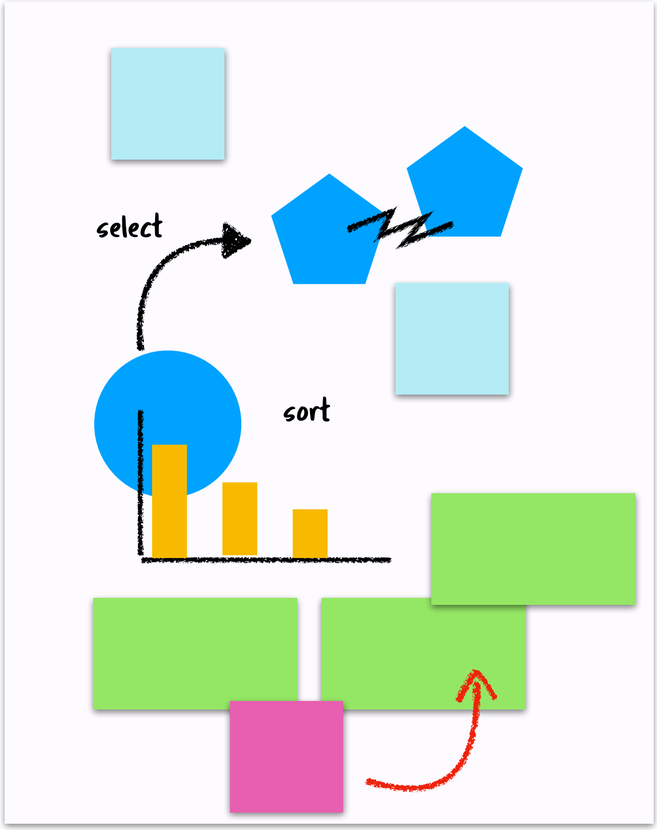


💫 All ideas are useful: express them

Part 2: Storyboarding

4. Presentation of use cases (6 min)

Each group shortly explains the workflow and the main visualization ideas



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13:35 - 13:45	**Closing**

Closing and Next Steps

Thank you very much for participating today!

- ★ Please fill out the evaluation form here: vapp1.win.tue.nl (yellow button)

- ★ Individual feedback sessions