🧪 Adjusted Training Agenda (2 Days × ~3 hours)

Workshop: Practical QTL Mapping using ICIM (Hands-on)

📅 Day 1 — Foundations + Map Construction

Objective: Understand concepts and build a reliable genetic map

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⏱️ 0:00 – 0:40

🧠 THEORY: QTL Mapping Fundamentals

- What is QTL mapping
- Linkage vs association mapping
- Key concepts:
    - Recombination & linkage
    - Genetic distance
    - LOD score
    - Additive effects
- Mapping populations (F2, RILs, DH)
- ICIM principles and advantages

⏱️ 0:40 – 1:30

💻 PRACTICAL: Data Preparation + Excersize

👉 Demonstration how to prepare the input file

- Genotype matrix formatting and genotype coding using Geneconder
- Phenotype structure
- Input formatting (IciMapping)

👉 Exercise:

- Clean dataset
- Validate structure

⏱️ 1:30 – 2:15

🔬 DEMONSTRATION: Genetic Map Construction

- Import data
- Linkage group formation
- Marker ordering
- Distance calculation
- Map quality evaluation

⏱️ 2:15 – 3:00

🧪 PRACTICAL: Build Your Map

👉 Exercise:

- Construct linkage groups
- Order markers
- Remove problematic markers
- Generate final map

📅 Day 2 — QTL Analysis + Interpretation

Objective: Run QTL mapping and interpret results for breeding

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⏱️ 0:00 – 0:45

🔬 DEMONSTRATION: QTL Mapping with ICIM

- Load genotype + phenotype + map
- Set parameters
- Run analysis
- Generate LOD profiles

⏱️ 0:45 – 1:45

🧪 PRACTICAL: Run QTL Analysis

👉 Exercise:

- Execute ICIM
- Extract QTL results
- Visualize LOD peaks

⏱️ 1:45 – 2:30

🧠 THEORY + INTERPRETATION

- LOD score & significance
- Confidence intervals
- Additive effects
- Phenotypic variance explained (PVE)
- Major vs minor QTL

⏱️ 2:30 – 3:00

🚀 DEPLOYMENT IN BREEDING

- Integration into MAS pipelines
- Validation strategies
- Marker conversion
- Q&A / discussion

🧾 MATERIALS PROVIDED

- Slide handout (PDF)
- Certificate of participation
- Suggested reading and tools for further learning