

## **Triticeae Genome practical course, 3-7 October 2010 Institute of Evolution, University of Haifa, Israel**

### **New algorithms and software for more accurate and easier genetic and physical genome mapping**

The current structural genomic studies are based on high throughput technologies generating huge amounts of raw data that should be converted to biologically meaningful information. This also relates to genetic and physical mapping, a prerequisite for genome sequencing and positional cloning of target genes. Corresponding bioinformatics tools and expertise are a mandatory part of such studies. As shown for rice and the model plant *Arabidopsis thaliana*, the availability of an entire genome sequence enables a quantum leap in the efficiency of map-based gene isolation, which still forms the major gateway to gain better understanding of agricultural traits.

The objective of this course is to provide the trainees with new tools for genetic and physical genome mapping, developed by the team at the University of Haifa, and that complement existing methods and software packages. These tools are especially useful for the analysis of complex genomes, such as wheat and barley. The course will include the following main topics:

1. **Building multilocus genetic maps:** A new approach of multilocus ordering based on highly efficient algorithms of Evolution Strategy discrete optimization (Mester et al. 2003), developed at the University of Haifa, will be presented. The theoretical part will be accompanied by training sessions using the *MultiPoint* software (<http://multiqtl.com>) based on the aforementioned methodology. The participants will practice using both simulated and real data, including their own data, for different types of mapping populations (e.g., F2, backcross, RIL, and DH). One of the major advantages of *MultiPoint* is in its ability to identify and remove "problematic" markers that negatively affect the stability and accuracy of the map. These markers can then be assigned to specific intervals on the stabilized map. This package also allows testing the quality of previously constructed maps (e.g., trainees own maps).
2. **Building consensus genetic maps:** The trainees will study a new method of consensus mapping based on joint mapping analysis of raw mapping data (reviewed in Korol et al. 2009). The method is implemented in the *MultiPoint*-consensus package that will be used for practical exercises. The developed algorithm allows to find the best order of markers based on re-analysis of several mapping populations. The mapping populations may have different structure, e.g., RIL and DH.
3. **QTL analysis in controlled crosses:** The training will be based on classical and new "multiple" approaches developed at the Institute of Evolution, including multiple-trait, multiple-environment, and multiple interval mapping analysis, and

various combinations of these approaches (Korol et al. 2001, 2009), implemented in *MultiQTL* package (<http://multiqtl.com>).

4. **Adaptive contig assembly in physical mapping based on BAC fingerprints:** A new analytical framework, Linear Topology Contig (LTC), for contig assembly based on exploring topology of clone overlaps, will be presented. The trainees will learn new methods for construction, verification, elongation, merging, and "curing" of the contigs. The training will be based on practice with real data and a possibility for participants to use their own data. For comparison, parallel analysis of the same data set using LTC and standard FPC package will be conducted.

**The participants are welcome to bring their own mapping data (for map construction, QTL analysis, and physical mapping) to use during their training.**

### **The program of the course:**

The course will include theoretical lectures given by several researchers that were involved in the development of the algorithms and mathematical models of *MultiQTL*, *MultiPoint* and contig assembly (from the Institute of Evolution: A. Korol, Y. Ronin, and D. Mester), and invited speakers from other Universities in Israel (Y. Weller from the Volcani and A. Distelfeld from Tel Aviv University). One day will be devoted for presentations and discussions on current projects of map-based cloning and physical mapping (T. Fahima, A. Distelfeld). The practical training will be conducted by highly skilled and experienced postdocs that have practiced/developed these tools in their own research (Z. Peleg, Z. Frenkel, and S. Hubner) together with the scientists mentioned above. All the lectures will be organized in computer classrooms and lecture halls at the University of Haifa.

#### **Day 1: Sunday, October 3<sup>rd</sup>**

**09:00 -9:30 Welcome and opening**

**9:30:00-11:00 Session I:**

Theoretical introduction to multilocus mapping (A. Korol)

Reduction of the mapping problem to Traveler Salesman Problem (TSP).

Evolutionary algorithms for searching the solution. Map verification based on re-sampling analysis

**11:00-11:30 Coffee break**

**11:30 -13:00 Session II:**

Methods and algorithms implemented in *MultiPoint* software (A. Korol)

Main approaches of consensus genetic maps (D. Mester)

**13:00-14:30 Lunch**

**14:30-16:30 Session III:**

Introduction to *MultiPoint* package (Z. Peleg, Y. Ronin)

**16:30-17:00 Coffee break**

**17:00-19:00 Session IV:**

Computer practice: Analyzing of simulated and real data (D. Mester, Z. Peleg, and I. Zukerman)

**19:00- 20:00 Dinner**

**Day 2: Monday, October 4<sup>th</sup>**

**08:30-10:30 Session V:**

QTL mapping in controlled crosses. Single-QTL analysis of single trait; analysis of linked QTL; testing for epistasis. Multiple interval mapping (A. Korol)

**10:30-11:00 Coffee break**

**11:00-13:00 Session VI**

Multiple-trait and multiple-environment analyses. Combination of "multiple" approaches (A. Korol). Introduction to *MultiQTL* package (Z. Peleg)

**13:00-14:30 Lunch**

**14:30-19:00 Computer practice**

QTL analysis of simulated and real data (Y. Ronin, Z. Peleg, and S. Hubner)

**19:00- 20:00 Dinner**

**Day 3: Tuesday, October 5<sup>th</sup>**

**08:30-10:30 Session VII**

Theoretical introduction to physical mapping (A. Korol and Z. Frenkel)  
Introduction to LTC and FPC packages and comparisons between the methods

**10:30-11:00 Coffee break**

**11:00-13:00 Computer practice**

Analyzing real physical mapping data using FPC and LTC (Z. Frenkel, I. Zukerman)

**13:00-14:30 Lunch**

**14:30-16:00 Computer practice:**

Continuing practical work with FPC and LTC packages

**16:00-16:30 Coffee break**

**16:30-19:00 Computer practice:**

Continuing practical work with FPC and LTC packages

**19:00-20:00** Dinner

**Day 4: Wednesday, October 6<sup>th</sup>**

**08:30-10:30 Session VIII**

Presentations and discussions on current projects of map-based cloning and physical mapping (T. Fahima, A. Distelfeld)

**10:30-11:00** Coffee break

**11:00-13:00 Session IX:**

Questions and discussion on the studied tools and participants' mapping projects

**13:00-14:30** Lunch

**14:30-22:00** Social event + dinner

**Day 5: Thursday, October 7<sup>th</sup>**

**08:30-10:30 Session X:**

Continuing practical work with FPC and LTC packages

**10:30-11:00** Coffee break

**11:00-13:30 Session XI**

Concluding practical work with FPC and LTC packages

**13:00-14:30** Lunch

**14:30- 16:00 Session XI**

Concluding the analysis with *MultiPoint* and *MultiQTL* packages

**16:00- 16:30** Closing the course

### Administrative information

The course will be given at the University of Haifa campus at the top of Mount Carmel.

Accommodations: participants can choose one of the following options offered by the University of Haifa Guest House facilities (located in the campus):

1. Single rooms in a shared apartment of 3 rooms cost 15€ per night
2. Visitor apartments of two single rooms, each room 30€ per night
3. Visitor apartments with a double room at a rate of 40€ (3.a) per night for single use, or 44€ per night for double use (3.b)

\* In options 1 & 2, the apartments include a shared kitchen and living room, but each single room has its own shower and toilet.

Participants may independently make a reservation in one of Haifa's hotels, which are located 20-30 min from the university by bus.

The total cost of the course plus accommodations for *TriticeaeGenome* members:

University of Haifa Guest House	Option 1	Option 2	Option 3.a	Option3.b
Total cost for 5 nights (2-7 October)	75	150	200	220
Meals and social event	150	150	150	150
Total cost for 5 days (In €)	225	300	350	370

The course is planned for 20 participants. Members of the *TriticeaeGenome* consortium are welcome to register.

First priority will be for the *TriticeaeGenome* members however, registration is opened for participants from the plant science community. The price for non-*TriticeaeGenome* participants will include registration fees of 100€ in addition to the details described above.

For registration please contact Mrs. Tamar Krugman until August 15<sup>th</sup>.  
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