

## **GSMS Field specific & interdisciplinary subjects graduate course: “High-throughput next-generation biology”**

**May 2013**

N.B.: This course will succeed the GSMS “Bioinformatics” course.

### **Goal:**

It is becoming clear that with the advent of high-throughput technologies, such as DNA and RNA microarrays and especially next-generation sequencing large amounts of “omics”-data are now publicly available and can also now be generated at limited cost.

Taking advantage of this data is still challenging, as it is difficult to analyze large amounts of data, and it is often unclear what kind of biological insights can be gained from this data.

This course aims to provide an overview of existing high-throughput technologies on DNA, RNA and methylation. We will discuss ways to set-up proper experiments, bioinformatics methods to analyze this data, ways to integrate different technologies and most importantly what biological insights can be gained from such analyses.

### **Eligible participants:**

This course is aimed at PhD students and postdocs that have at least some knowledge in bioinformatics. You don't need to know how to program.

(for those interested in learning how to program, there is an excellent C++ course is being offered by the RUG, Centre of Information Technology, <http://www.rug.nl/science-and-society/centre-for-information-technology/education/cursusaanbod>).

### **Course duration:**

1 ECTS point: 5 days course, with teaching in the morning and the afternoon, including practical assignments.

### **Teachers:**

- Lude Franke
- Morris Swertz
- Victor Guryev
- Frank Johannes
- Pieter Neerincx
- Martijn Dijkstra
- Freerk van Dijk
- Dasha Zhernakova
- Marc-Jan Bonder
- Harm-Jan Westra

## Schedule High-throughput next-generation biology 2013

We will have a 15 minutes break at end of each hour. Rooms are via 'onderwijscentrum'

### Monday 6 May:

Morning 9.00 – 12.00h, room: T4.103

09:00 – 11:00h: Introduction of course and overview of different high-throughput technologies (DNA, RNA and methylation microarrays, high-throughput DNA, RNA and ChIP-sequencing) **(Morris Swertz)**

11:00 – 12:00h: Introduction of database searching, sequence alignment, and practical tips **(Pieter Neerincx)**

Afternoon 13.00 – 16.00h, room: T4.103

13:00 – 16:00h: Experimental design, dealing with confounders, multiple-testing correction and platform specific issues that can cause false-positive findings **(Lude Franke)**

### Tuesday 7 May:

Morning 9.00 – 12.00h, room: Lokaal 10

09.00 – 10.00h: DNA microarrays: Genome-wide association studies **(Lude Franke)**

10.00 – 11.00h: DNA-sequencing: Genome of the Netherlands **(Morris Swertz)**

11.00 – 12.00h: DNA-sequencing: Structural variation **(Victor Guryev)**

Afternoon 12.30 – 16.30h, room: Lokaal 10 (bring your own notebook; we work in pairs)

Perform a GWAS in celiac disease **(Lude Franke, Harm-Jan Westra)** and use a small next-generation sequencing dataset to identify mutations in a family suffering from an autosomal dominant mutation

**(Pieter Neerincx, Martijn Dijkstra, Freerk van Dijk).**

### Wednesday 8 May

Morning 9.00 – 12.00h, room: Panoramazaal

09:00 – 12:00h: Gene expression analysis using microarrays and RNA-seq **(Lude Franke, Dasha Zhernakova)**

Afternoon 13.00 – 16.00h, room: Lokaal 3/Y3 (this is a computer room)

13:00 – 16:00h: eQTL mapping, identify SNPs that affect gene expression levels **(Dasha Zhernakova, Marc-Jan Bonder).**

### Thursday 9 May

Free for Ascension Day

### Friday 10 May:

Morning 9.00 – 12.00h, room: Lokaal 8

09.00 – 10.00h: Encyclopedia of DNA Elements, ENCODE project **(Lude Franke)**

10.00 - 12.00h: Whole Genome Bisulphite Sequencing (WGBS-seq) **(Frank Johannes)**

Afternoon 13.00 – 16.00h, room: Lokaal 8

13.00 – 14.00h: Integration of multiple omics datasets: *trans*-eQTL mapping **(Lude Franke)**

14.00 – 14.30h: Causal inference **(Lude Franke).**

15.00 – 16.00h: How to take advantage of publicly available high-throughput datasets in cancer, Discuss milestone papers that integrate multiple "omics" datasets **(Lude Franke)**

## Students

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## Teachers

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## Office

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