



qPCR Data Mining – How to get the most out of your qPCR experiment

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The objective of this course is to provide an understanding of data processing and statistical methods applicable for analysis of data obtained by real-time PCR. This course is based on seminars and computer-based demonstrations. **Please note that course delegates are required to bring their own laptop computer.**

Date and Time:

02/24/2010, 9:00 AM – 5:00 PM

[Register online/at www.iesols.com/registration](http://www.iesols.com/registration)

Venue:

Interdisciplinary Center for Biotechnology Research, Cancer Genetics Research Center,
2033 Mowry Road, Gainesville, FL 32610. **Contact:** 408-416-3812

Learning Objectives

After completed course participants will know:

- How to estimate nucleic acid levels and the precision of the estimate in test samples relative to standard samples. They will also know how to determine the level of detection (LOD) of a qPCR based analytical procedure.
- How to compare the expression of targeted genes in two or more samples, and assess if the measured difference is statistically significant.
- How to design experimental studies for optimum cost-performance, such that a certain biological difference can be reliably detected against confounding variation.
- How to select optimum normalization strategy.
- Identify patterns among expressed genes in profiling studies
- How to separate sample classes in multimarker expression profiling studies
- The principles of multimarker molecular diagnostics

Topics and Course Organization

- Introduction to qPCR theory, ΔCq and $\Delta\Delta Cq$
- Absolute quantification, qPCR standard curve, Reverse calibration, Limit of detection
- Experimental design, Noise contributions to RT-qPCR analysis (nested ANOVA), cost-performance optimization of experiments
- Sample size estimations (Power testing), Selecting reference genes (geNorm, Normfinder)
- Relative quantification, qPCR data pre-processing, Outlier detection. Comparison of groups (parametric and non-parametric methods)
- Expression profiling, missing data treatment, scaling of data, Un-supervised clustering of genes and samples (hierarchical clustering, self-organized maps, Principal Component Analysis), Supervised clustering of samples (Artificial neural network)
- Exercises

Instructor: Mikael Kubista, Ph.D., Founder TATAA Biocenter, Sweden (more info on registration page).

Registration fee: Academic/Non profit: \$300, Company: \$400. [Register online](#)

Cancellation Policy: Cancellation is possible due to unavoidable circumstances. Cancellation fee: \$50