

# APPROACH TO ENABLE AN AUTOMATIC PRE-PROCESSING OF qRT-PCR Analysis

Marco Franke<sup>1</sup>, Klaus-Dieter Thoben<sup>1</sup> and Rainer Söller<sup>2</sup>

<sup>1</sup>BIBA - Bremer Institut für Produktion und Logistik GmbH, University Bremen  
Hochschulring 20, 28359, Bremen, Germany

<sup>2</sup>Qiagen Hamburg, Königstraße 4a, 22767, Hamburg, Germany

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**Abstract:** A fully automated analysis method for real-time PCR samples can be achieved through an automated noise removal. This results in a guaranteed robustness against the factors that repeatedly impact the analysis of real-time PCR data and usually lead to a manual analysis by skilled experts. The presented approach attains a degree of robustness which allows an automated analysis for real-time PCR. This new automated pre-processing method improves the real-time PCR data for the analysis in such a way that accepted qualitative analysis methods can be used in an automated way. Furthermore, the article shows an evaluation of an implemented demonstrator for an automated analysis which combines the developed pre-processing method with the second derivation method for the qualitative analysis.

## 1 INTRODUCTION

The process of Real-time quantitative polymerase chain reaction (qRT-PCR) has been widely used for over ten years and has entered into the domain of medicine, for example in Leukemia Research. The determination of molecular targets by using qualitative and quantitative qRT-PCR analysis has become a common method. The qRT-PCR method can also be used for the detection of microorganisms or other organic media containing a genome.

The detection of microorganisms in industrial environment is realized with the methods of microbiology. Such methods are standardized and accepted as solid proof. Its major disadvantage lies in the considerable time it requires. A large proportion of time is spent on the stage in which the microorganisms grow on the medium. The duration of this phase depends on the type of microorganisms and environmental conditions and can be very long. The quality check of a raw material, interstage product or end product can take a few hours or a few days. The needed time for a quality analysis is longer than the time for producing the product. This means that the quality check can not work in real

time and the usage of preventive methods for reducing an occurrence of biological contamination is needed. This issue is not resolved but improved by the qRT-PCR method. The qRT-PCR method requires a constant time for the detection of any micro-organism, which takes less than 12 hours. In the project ProDIAP(BIBA,2010) the qRT-PCR-analysis required six hours.

Since the establishment of the qRT-PCR method, different approaches have been developed in the field of qualitative and quantitative analyses which also include the *fit points* and *second derivation* as a common method. For example, the softwares of LightCycler (Roche Applied Science, 2010) and RotorGene (Qiagen, 2010) use such methods. One of the methods which are explored currently is the maxRatio (Shain and Clemens, 2008) method. One feature of the maxRatio method is to support a much more aggressive noise filter without losing significant signal information. All these developed methods need an additional pre-processing to reduce the wide range of noise within measurement data. The currently used noise removal methods require the experience of experts to estimate the parameter values and to evaluate the result of noise removal. The chosen parameter values describe e.g. the

specific characteristics of the used qRT-PCR-analysis and the used qRT-PCR-KIT and have to adapt to them each time. This adaption/calibration can only be executed by a manual process. This fact prevents the usage of the qRT-PCR-analysis in an automated industrial environment or at the customer's side as an easy-to-use analysis product. Therefore, the weakness of parameter based noise removal methods and the research of the usage of methods without parameters for noise removal are the focus of this article.

This article presents a new approach for an automatic pre-processing method for common qRT-PCR-analysis. The objective is to achieve a pre-processing method without the required intervention of experts. If a pre-processing without parameters is possible, it enables an automatic qRT-PCR-analysis with common analysis methods. Such a solution has been established under the project ProDiap (Bremer Institut für Produktion und Logistik, 2010). The solution is presented in chapter 4.

In this article, the problem and its solution, which lies in an approach for the development of an automated pre-processing method for a qRT-PCR-analysis are presented. In the next section, the common noise removal methods are discussed. After this, the approach will be described and finally, the evaluation by using the demonstrator will be shown.

## 2 STATE OF THE ART WITH REGARD TO PRE-PROCESSING

The influence of the noise within the analysis process implies the need for pre-processing. As minimal information, a qRT-PCR measurement contains a set of tuples, which represent a time-stamp and a measured fluorescence. The magnitude of the fluorescence correlates with the concentration of the qRT-PCR-analysis result product. The influence on this correlation is declared in this article as noise.

The interpretation of a measurement result is based on the mapping of a measurement result in a Cartesian coordinate system. The qualitative and the quantitative analyses are grounded on such a curve. In figure 1, an example curve is shown, which represents a positive result of a qRT-PCR-analysis. It is characterized by four phases (Wong and Medrano, 2005).

In such a case, a specific micro-organism would be detected.

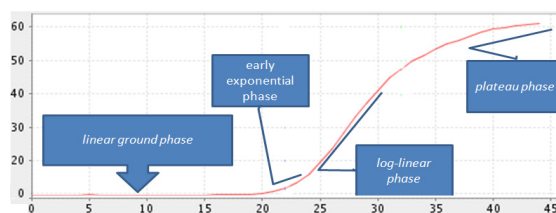


Figure 1: Four phases of qRT-PCR curve.

The quality of a curve decreases with the decreasing quality of these four phases. In real measurements, the noise changes the expression of the four phases of the curve. This complicates the classification of such curves compared to the classification of noise-free curves significantly. The effects on the curve are described below with regard to different noise types.

### 2.1 Noise

Generally, in test results, two different types of noise can occur (Wilhelm, 2003). As pointed out by Wilhelm (2003) and Larinonov, Krause and Miller (2005) a background noise is caused by properties of materials and other external influences. Here, Larinonov et al. (2005) a correlation between the qRT-PCR systems and the occurrence of background noise is mentioned. The expression of noise ranges from a constant shift to a linear increase of noise over cycles (Larinonov et al., 2005). The second type of noise is defined as *signal trend*. The possible causes of the occurrence of this are not yet resolved. According to Wilhelm's (2003) opinion, the product accumulation is no reason for the signal trend. The signal trend can influence the curve of a test result in two ways. It can increase or decrease the measured fluorescence of a test result. Without additional information, an expert can not know the resulting expression.

The effects of background noise and signal trend for a repeated application of a sample analysis may lead to varying results. In general, a background noise always occurs, which leads to a measurable fluorescence from the first cycle, although the fluorescence in the *linear ground phase* would have the value zero. The influence of noise is shown in figure 2 and 3 by way of example.

The curve in figure 3 is representative for a test result which would be classified as positive and containing just a little noise. Figure 2 shows a complement curve, which should be evaluated as positive, although stronger effects of noise have occurred.

In the following the influence of noise on the two curves, as well as the possibilities of its detection and elimination are presented.

## 2.2 Noise Removal

The curves in figure 2 and 3 include some noise of the type background noise and noise of the type signal trend.

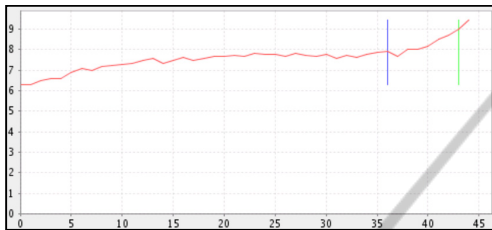


Figure 2: Test result with intense noise.

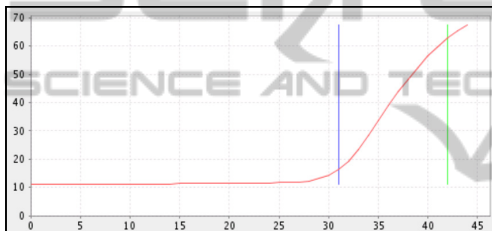


Figure 3: Test result with some noise.

The background noise in figure 3 can be described as a straight line with the gradient zero in the *linear ground phase*. In contrast, the background noise in figure 2 cannot be described as a straight line in the *linear ground phase*. One possibility is to use n-degree polynomial or cubic splines to define such a background noise. The cross-over between the *linear ground phase* and the *early exponential phase* need to be defined for a downstream analysis. This separation is not possible, which is shown in figure 2. The signal trend has a similar influence on the curve which is shown in figure 2.

The noise removal cannot generally detect and mathematically formulate the *background noise* and the *signal trend* of a curve. For that reason, the noise cannot be eliminated without losing information of the signal. Existing methods smooth the curves by using parameters to control the intensity of noise removal. If an expert chooses the wrong values for parameters, the method removes the noise and the underlying signal.

## 2.3 Noise Removal by Smoothing

In the following, the smoothing on the basis of

existing procedures will be presented shortly. Based on the weaknesses of these procedures, the requirements for the presented smoothing operator will be presented. A smoothing is generally defined for two areas of a curve, the so-called local and global scope.

The local scope is defined by the range between two points of a curve. There is no information from the perspective qRT-PCR-analysis between them. Thus, between two points, different courses of curves could occur, such as a line, a polynomial or something else. Polynomials are presumed as possible curve progression to the technical base of qRT-PCR systems. The intervals are interpolated in accordance with polynomial smoothing in corresponding software. For example, the software Sofar (Wilhelm, 2003) uses splines (Gutenberg, 2004) for smoothing in local scope.

The global scope is defined as an interval of the whole curve. Different smoothing operators are currently used in the field of Simple Moving Average (SMA) (Savitzky and Golay, 1964). The methods smooth the course of curve by using an averaging over fluorescence values. Thus, the smoothing operator in the field of SMA needs two parameters. The first parameter controls the choice of a window function and the other one controls the window size. The approximation to the original curve progression, which contains no noise, can be solved by an expert by adapting the two parameters. This manual smoothing needs a lot of experience to guarantee the success of the pre-processing. For an automated pre-processing method, it would be necessary that the used method contains no parameters.

## 3 APPROACH OF AN AUTOMATED PRE-PROCESSING USING THE BÉZIER CURVE

The presented approach uses no parameters for smoothing. The objective is to restore a course of curve which is similar to figure 1. This means that the resulting curve progression contains the four phases and the second derivation method can easily detect them. In the following, the usage of the Bézier curve for an automated pre-processing is described.

### 3.1 Smoothing in Global Scope by the Bézier Curve

A Bézier curve is a polynomial which represents a smoothed curve of the test result and can have any degree. The degree of Bézier curves corresponds to the number of cycles in a test result.

The points of a curve will be defined as convex hull by the calculation of the Bézier curve. The resulting curve only contains the first and the last original point. The other points will be calculated by the Bernstein polynomial. This method is advantageous compared to the classical average method because a set of original points of the test result determines the coordinates of a calculated point through the application of the Bernstein polynomials.

An example of a calculation with a Bézier curve, which is calculated with a java applet (Koezler, 2000), is given in figure 4 and in figure 5.

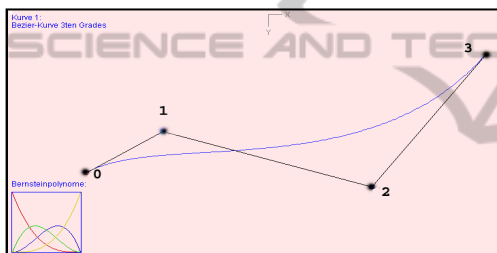


Figure 4: Calculation of a Bézier curve.

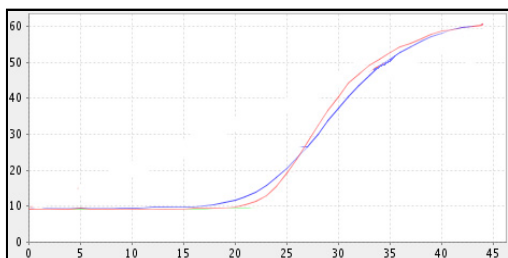


Figure 5: Smoothing with Bézier curve.

## 4 APPLICATION SCENARIO

As part of the project ProDIAP, the detection of biological contamination in the manufacture of emulsion paints was one task. The detection was realised by the Real-Time qRT-PCR. The following describes an evaluation about the quality of the combination between the developed pre-processing and the application of second derivation method for qualitative analysis.

## 5 EVALUATION

The project ProDIAP used 640 samples for the evaluation of a qualitative analysis. The automated qualitative analysis was applied by the software, which has been developed in this project. These results were compared to a manual interpretation by an expert from Qiagen Hamburg (Qiagen, 2010). Figure 6 illustrates the results of the set of 640 samples.

ID of probe	Recall	Precision	Specificity
Aspergillus_Multiplex_NeuD esign_Test_270409GL16000 .rex	100%	97,0%	98,9%
Aspergillus_Multiplex_NeuD esign_080509K54r6000.rex	100%	81,2%	92,5%
JK_Bacillus sub_Vergleich_Aufreinigung_11.03.09.RG60002	100%	98,1%	90,9%
JK_Bacillus+Lipo_Aufr_Test_240209	100%	97,4%	50%
MiMo_B.subtilis_301008_r60002	100%	100%	100%
JK_Bacillus sub_C_lipo_Aufreinigung_v om118.0309_26.03.2009.RG60002	100%	100%	100%
Aspergillus_Multiplex_NeuD esign_NTCTest_280409K54r6000.rex	100%	100%	100%

Figure 6: Overview of the evaluation result.

## 6 SUMMARY

The evaluation has shown that an automated qualitative analysis of qRT-PCR data is possible and has reached a high quality. This quality could be reached by the application of smoothing with Bézier curves as a noise removal method.

The influence of smoothing with Bézier curves on the results of a quantitative analysis is not estimated.

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## REFERENCES

- BIBA, (2010). *ProDIAP*. Retrieved February 1, 2010, from <http://www.prodiap.de/>
- Gutenberg, J. (2004). *Spline-Interpolation*. Retrieved February 1, 2010, from [http://www.numerik.mathe.matik.uni-ainz.de/didaktikseminar/Gruppe3/html/kubische\\_splines.html](http://www.numerik.mathe.matik.uni-ainz.de/didaktikseminar/Gruppe3/html/kubische_splines.html)
- Haftendorn, D. (1999). *Lineare Algebra*

- Bernsteinpolynome*. Retrieved February 1, 2010, from <http://haftendorn.uni-lueneburg.de/numerik/bezier/bezierkurve.pdf>
- Koegler, S. (2000). *Java-Applet: Approximationsverfahren*. Retrieved February 1, 2010, from [http://www.stefan-koegler.de/studienarbeit\\_online-tutorium/java/approximation/index.html](http://www.stefan-koegler.de/studienarbeit_online-tutorium/java/approximation/index.html)
- Larinonov, A. and Krause, A. and Miller, W. (2005). A standard curve based method for relative real time PCR data processing. *BMC Bioinformatics*. 6, 62. doi:10.1186/1471-2105-6-62
- Qiagen.(2010). *Sample & Assay Technologies*. Retrieved February 1, 2010, from <http://www.qiagen.com/Products/Rotor-GeneQ.aspx>
- Roche Applied Science. (2010). *Roche Applied Science: genome sequencing, microarray analysis, nucleic acid purification, real-time PCR, transfe*. Retrieved February 1, 2010, from <https://www.roche-applied-science.com>
- Savitzky, A. and Golay, M. (1964). *Smoothing and Differentiation of Data by Simplified Least Squares Procedures*. Retrieved February 1, 2010, from <http://pubs.acs.org/doi/pdf/10.1021/ac60214a047>
- Shain, E. and Clemens, J. (2008). A new method for robust quantitative and qualitative analysis of real-time PCR. *Nucleic Acids Research*. doi:10.1093/nar/gkn408
- WebProdiap*. Retrieved February 1, 2010, from <http://gladiator.biba.uni-bremen.de:8080/WebProdiapV3/index.zul>
- Wilhelm, J. (2003). *Development of real-time PCR based methods for modern DNA analytics*, Retrieved February 1, 2010, from <http://geb.uni-giessen.de/geb/volltexte/2003/1072/>
- Wong, M. and Medrano, J. (2005). Real-time PCR for mRNA quantitation, *BioTechniques* 39, 75-85. Retrieved from: [http://www.biotechniques.com/multimedia/archive/00011/BTN\\_A\\_05391RV01\\_O\\_11901a.pdf](http://www.biotechniques.com/multimedia/archive/00011/BTN_A_05391RV01_O_11901a.pdf)