Technical University of Denmark



Process analytical technology (PAT) for biopharmaceuticals

Glassey, Jarka; Gernaey, Krist V.; Clemens, Christoph; Schulz, Torsten W.; Oliveira, Rui; Striedner, Gerald; Mandenius, Carl-Fredrik

Published in: Biotechnology Journal

Link to article, DOI: 10.1002/biot.201000356

Publication date: 2011

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):

Glassey, J., Gernaey, K., Clemens, C., Schulz, T. W., Oliveira, R., Striedner, G., & Mandenius, C-F. (2011). Process analytical technology (PAT) for biopharmaceuticals. Biotechnology Journal, 6(4), 369-377. DOI: 10.1002/biot.201000356

DTU Library

Technical Information Center of Denmark

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Biotechnol. J. 2011, 6, 369–377 DOI 10.1002/biot.201000356 www.biotechnology-journal.com

Biotech Highlight

Process analytical technology (PAT) for biopharmaceuticals

Jarka Glassey¹, Krist V. Gernaey², Christoph Clemens³, Torsten W. Schulz³, Rui Oliveira^{4,5}, Gerald Striedner⁶, Carl-Fredrik Mandenius⁷

- ¹ School of Chemical Engineering and Advanced Materials, University of Newcastle, Newcastle upon Tyne, United Kingdom
- ² Center for Process Engineering and Technology, Department of Chemical and Biochemical Engineering, Technical University of Denmark, Kgs. Lyngby, Denmark
- ³ Boehringer Ingelheim Pharma GmbH & Co. KG, Ingelheim, Germany
- ⁴ Chemistry Department, FCT/Universidade Nova de Lisboa, Lisbon, Portugal
- ⁵ Instituto de Biologia Experimental e Tecnologica, Oeiras, Portugal
- ⁶ Department of Biotechnology, University of Natural Resources and Applied Life Sciences, Vienna, Austria
- ⁷ Division of Biotechnology/IFM, Linköping University, Linköping, Sweden

Keywords: CHO cells \cdot Critical quality attributes \cdot *E. coli* \cdot Fed-batch process \cdot Process analytical technology

Received 15 October 2010 Revised 7 February 2011 Accepted 14 February 2011

Process analytical technology (PAT), the regulatory initiative for building in quality to pharmaceutical manufacturing, has a great potential for improving biopharmaceutical production. The recommended analytical tools for building in quality, multivariate data analysis, mechanistic modeling, novel models for interpretation of systems biology data and new sensor technologies for cellular states, are instrumental in exploiting this potential. Industrial biopharmaceutical production has gradually become dependent on large-scale processes using sensitive mammalian cell cultures. This further emphasizes the need for improved PAT solutions. We summarize recent progress in this area based on an expert workshop held at the 8th European Symposium on Biochemical Engineering Sciences (Bologna, 2010), and highlight new opportunities for exploiting PAT when applied in biopharmaceutical production. We conclude with recommendations for advancing PAT applications in the biopharmaceutical industry.

Correspondence: Professor Carl-Fredrik Mandenius, IFM, Linköping University, 581 83 Linköping, Sweden E-mail: cfm@ifm.liu.se

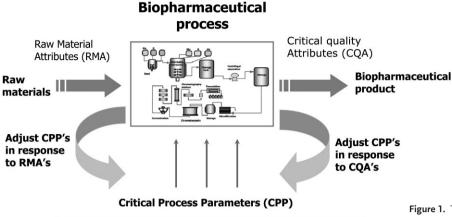
Abbreviations: CQA, critical quality attributes; CPP, critical process parameters; MVDA, multivariate data analysis; PAT, process analytical technology; PCA, principal component analysis; PLS, partial least squares; QbD, Quality by Design

1 Introduction

The term (and acronym) Process Analytical Technology (PAT) was introduced by the US FDA as an intiative to bring an improved understanding of pharmaceutical manufacturing processes to increase the quality of their products [1]. The FDA uses the expression "to build in quality into the pharmaceutical manufacturing process", thereby implying that high product quality should ideally be created already at the design stage of the manufacturing process [1-3], contrary to traditional processes that are often the result of empirical or rule-of-thumb design. In addition, they also emphasize the need for improved on-line monitoring and control methods to maintain high product quality during manufacturing operations. In the biopharmaceutical industry PAT principles are adopted with great care due to the fact that biopharmaceuticals and their production systems are very complex. Compared to the small molecule pharma industry the complexity of biopharmaceutical proteins multiplies the analytical quality

Figure 1 illustrates a central concept of the PAT philosophy: to identify and control the critical quality attributes (CQA) of the process based on monitoring and adjusting the critical process parameters (CPP).

PAT forms a part of the Quality by Design (QbD) concept, also a regulatory-inspired methodology where PAT provides tools to enable the quality



Combination of forward and backward control of CPP's provides even greater control of critical quality attributes

Figure 1. The relationship of critical process parameters (CPPs) and critical quality attributes (CQAs) in a biopharmaceutical manufacturing process according to the PAT concept.

goals [4, 5]. In QbD the acceptable ranges of the CQAs and the CPPs are defined for the manufacturing process (Fig. 2).

A large number of analytical methodologies and tools, here referred to PAT tools, are useful for realizing QbD. These PAT tools cover methodologies ranging from analytical chemistry, through control theory and mathematical and statistical modeling methods. In Figure 3 the most important of these methods and tools are compiled and related to their role in building quality into the pharmaceutical manufacturing process.

Design space

(the area which has been demonstrated to give adequate quality)

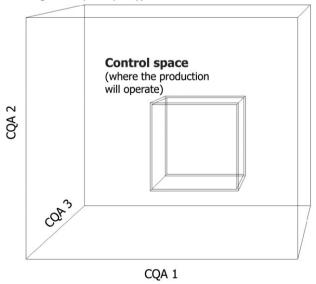


Figure 2. The design space and control space as defined in QbD. The axes represent the critical quality parameters.

The first tier in the figure shows three categories of methods for acquiring quality-related data from the pharmaceutical manufacturing process: methods for (1) on-line sensing, (2) 'omics'-based analysis, and (3) analysis of CQAs. These methods can show considerable overlaps based on deeper process understanding.

In the second tier, the measurement data obtained in the first tier are processed using models, and thereby converted to useful process-related information. Here multivariate data analysis models, mechanistic models or any other modeling approach (e.g., neural network models as a typical black-box model example) are highligthed.

The third tier in the figure shows alternative control methods that can be applied with any of the previous methods for data acquisition and analysis in the first and second tiers, or by combining these in appropriate ways.

In the most straightforward case it is an issue of feeding back the information to the process to correct it. In QbD, we define the control space from pre-knowledge created in separate experiments. This pre-knowledge is in the best case optimized, also using first tier methods.

The fourth tier represents a conceptually higher level of using the generated information. This may be a human decision maker, an operator on the plant, or a Quality Control (QC) officer deciding on the release of a batch based on a well-defined set of quality criteria. It may also be a more sophisticated decision making mechanism – implemented in an internet-based support system, e.g., using historical data and statistical procedures.

Figure 3 illustrates the rich collection of suitable alternatives for accomplishing the objectives of the PAT initative for biopharmaceuticals.

Biotechnol. J. 2011, 6, 369–377 www.biotechnology-journal.com

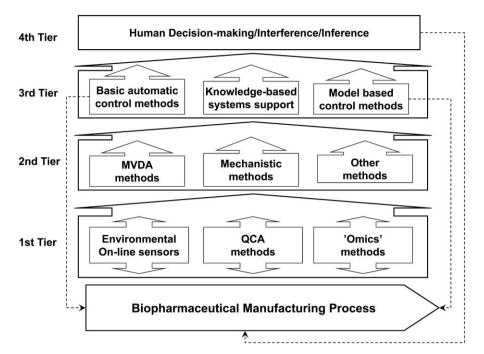


Figure 3. Conceptual interrelations of PAT tools and methods for biopharmaceutical processes structured on four consecutive levels (tiers). The first tier involves data acquisition tools, the second tier data processing of these acquired data. The methods of the third tier use the processed data for controlling the manufacturing process, and the fourth tier uses the data for advanced data analysis for further manufacturing control.

In this article we highlight a few areas of recent progress and opinions on application of PAT methodologies of relevance for biopharmaceutical production, based on a workshop held at the 8th European Symposium on Biochemical Engineering Sciences (Bologna, 5 September 2010). As typical biopharmaceutical products we include therapeutic antibodies, regulatory proteins such as insulin or growth hormone, enzymes with a pharmacological effect such as thrombin or tissue plasminogen activator, or vaccine components. But there can also be other biopolymers with therapeutic effect, for example, a gene therapy vector or a carbohydrate polymer.

The quality issues for all these biopharmaceuticals are similar, although not identical. The main concerns are the purity of the protein and the detection of impurities from the host organism, the culture media or formation of adverse product forms. The host organism and the biomolecular structure of the product have significant effects on the prerequisites of applying PAT. Progress in PAT and an improved understanding of its applications contribute to advanced manufacture of these complex biopharmaceutical products.

The article focuses on a few aspects of PAT: the furthering of multivariate data analysis (MVDA) for enhancing and building in quality into the biopharmaceutical process, the exploitaion of mechanistic models as an additional support tool, the use of systems biology data, the challenges of using mammalian cells in the processes, and examples of

new opportunities with on-line sensing. We also relate these to industrial requirements and practice, and conclude with an identification of future needs to improve the impact of the PAT tools of benefit for biopharmaceutical production but also to biochemical engineering production in a more general perspective.

2 Potential of MVDA in implementing PAT on biopharmaceutical production

MVDA has the potential to play a central role in PAT and can interact with several other methods and techniques that analyze the biopharmaceutical manufacturing process, leading to better understanding of it and exerting control of its quality.

The use of a range of established analytical techniques alongside more advanced methods, such as near-infrared (NIR) spectroscopy, multi-wavelength fluorescence and electronic nose, within the PAT framework typically leads to the generation of large multivariate data sets. To extract useful information leading to deeper process understanding, it is essential to employ appropriate data analysis techniques capable of dealing with these multidimensional data. These data sets are highly heterogeneous, with varying frequency of various measurements, typically with significant delays in the off-line measurements. They are also often highly correlated, non-linear in nature and with high levels of redundancy and noise. Tech-

niques such as principal component analysis (PCA), partial least squares (PLS), parallel factor analysis (PARAFAC), unsupervised clustering methods and others, have long been used successfully by chemometricians for interpretation of multidimensional data sets in various subject areas, and their usefulness has also been proven in the area of biopharmaceuticals. A detailed description of these techniques is beyond the scope of this contribution and can be found in a variety of textbooks and manuscripts (e.g. [6-8]). Their ability to reduce dimensionality by removing the redundancy and noise leads to the identification of salient features in the data. These features can subsequently be used in bioprocess monitoring, fault detection and process optimization, as has been described extensively in the literature over the years. Successful applications cover a range of production systems from various microbial to cell culture systems and a wide range of industrially relevant products. Identification of deviations from nominal batch behaviour either in the seed or production cultivations (e.g. [9]), early detection of contamination or detection of faulty sensors are all critical process decisions that have been improved using MVDA techniques [2]. However, most importantly, the PAT methodology, as defined by the FDA [1], requires effective control of CPPs affecting the CQAs. This task is aided by the MVDA techniques enabling on-line estimation of such critical parameters as biomass, glucose and various other metabolites [10–12].

Biopharmaceutical processes are predominantly operated in a batch mode, which leads to further increase in the complexity of the resulting data arrays. The analysis of such data structures typically requires a modification of the traditional MVDA techniques or an application of non-linear alternative methods. Multiway PCA and PLS have been introduced in mid 1990 by Nomikos and MacGregor [13] and used sucessfully to account for the major non-linearity of the batch processes [9]. Alternative non-linear data analysis techniques, such as non-linear variants of PCA, PLS or various forms of artificial neural networks, have also been shown to be effective in bioprocess monitoring and control (e.g. [14, 15]). Whereas issues of regulatory approval of such 'black-box' data analysis techniques still represent a significant challenge in their application in a manufacturing environment, techniques such as autoassociative neural networks (AANN), self-organising maps (SOM) or support vector machines (SVM) can provide a more accurate representation of the fundamental features contained in the available measurements [16, 17].

3 Using mechanistic models as PAT tools for predicting CQA in the biopharmaceutical process

An alternative modeling approach to MVDA is to apply a mechanistic model description of the biopharmaceutical manufacturing system.

PAT, and especially its application to QbD, can only be realized in practice if sufficient process knowledge is available to explain the effect of CPPs on CQAs. In this respect, mechanistic modeling has gained renewed attention because a mechanistic model can be considered as a structured representation of the available process knowledge. Indeed, during the model-building procedure, the process knowledge is coded in a mechanistic model using appropriate mathematical expressions [18-21]. Such a model therefore incorporates process-relevant input (critical process variables) - output (product concentration and product quality attributes) relationships, which can be used to establish a proper design space. The mechanistic model therefore has great value in planning experiments, or in determining which critical process variables necessitate tighter control [21, 22].

Recent applications of mechanistic models for bio-based processes, such as biocatalysis [23] and fermentation [24] witnessed an interesting development. It should be emphasized indeed that the application of mechanistic modeling is not only relevant for the pharmaceutical industry, but also for fermentation and biocatalytic processes. In fact, many of the tools and techniques that are now adopted by the pharmaceutical industry for the implementation of PAT were developed much earlier by, or in close collaboration with, the fermentation industry [25].

One of the most frequently cited disadvantages of using mechanistic models is excessive time and resource requirements during the development phase. A systematic model development methodology addresses this drawback [26] and is beneficial for a number of reasons: (i) model development is more efficient (i.e., less time and resources required), and (ii) communication and knowledge transfer among the various members of the multidisciplinary team (i.e., researchers, engineers, operators, managers) typically involved in the development and implementation of a PAT system are facilitated. To this end, the matrix notation is commonly used because it allows a compact and visually appealing description of a complex mathematical model [20, 27].

The relatively large cost of developing a mechanistic model is increasingly justified if model analysis techniques are applied to the mechanistic

model as part of good modeling practice (GMoP) [28]. Moreover, mechanistic models also have great potential in Design of Experiment (DoE) applications. GMoP comprises the application of a set of mathematical and statistical techniques that allow improvements in the use and the reliability of the model. Examples include the calculation of correlation coefficients and confidence intervals for estimated parameters to verify sufficient data quality and quantity to allow reliable parameter estimation [20]. Additional examples include uncertainty analysis and sensitivity analysis [28-30]. Model analysis indeed provides answers to important questions such as: When is the time optimal for the collection of experimental data? Which variables should be measured? Which parameters can be estimated given an experimental data set and the mechanistic model?

4 Adapting the PAT tools to biopharmaceutical production with mammalian cells

The actual application of the MVDA and mechanistic models depends to an extent on the particular host organism used in the manufacturing process. Here we compare the two alternatives that are so far dominant, E. coli and mammalian cells, from a PAT perspective. Without a doubt, monitoring of living cells used as hosts, in an environment involving a multitude of parallel reactions and thousands of components as solid fraction in a mixture of gas and liquid, is a very ambitious and challenging task regardless of which organism is used. As a consequence, on-line data acquisition has to be individually designed for each organism used in bioprocessing. In contrast to bacterial cells, where synthesis of recombinant proteins is strictly associated with cellular growth, product formation in mammalian systems is more or less separated from growth. This fact leads to different process control strategies and specific monitoring requirements for each type of cell factory. Optimal exploitation of bacterial systems can only be obtained by setting conditions that allow for recombinant gene expression at high yet tolerable rates and simultaneous maintenance of cell viability and growth [31]. Growth rate, gene dosage and product titer are the central quality-related process variables. Realtime access to each of these variables is enabled by the application of comprehensive on- and off-line monitoring tools in combination with MVDA-based predictions [32, 33]. For example, based on these results an improved transcription tuning concept, utilizing the real-time predicted cell dry weight (CDW) for setting of a constant inducer to CDW

ratio, has been established (to be published). Integration of comprehensive process data also yields an increased process understanding and new approaches for cell design [34]. In this work it was also demonstrated that the reduction of the induction level shows a significant increase of the soluble recombinant protein fraction. Real-time prediction of soluble and insoluble recombinant protein provides access to a CQA with transcription rate control as the CPP. This is just one example demonstrating a PAT solution with focus on product quality aspects specific for bacterial-based production processes.

Microbial production systems, especially *E. coli*, were the host of choice in the early biopharmaceutical processes. However, today mammalian cells have become the dominant system for the production of recombinant proteins mainly due to their capacity of required protein folding and posttranslational modification. Thus, the resulting quality and efficiency of glycosylated proteins, e.g., monoclonal antibodies, produced by recombinant expression systems in mammalian cells can be considered to be superior to other expression systems such as bacteria, plants and yeasts [35]. Mammalian expression systems that are well known since the licensure of tissue plasminogen activator in 1987 include Chinese hamster ovary (CHO) or murine lypmphoid cell lines (e.g., NS0, Sp2/0). They offer the potential of increased productivities, which is one of the major driving forces for industrial manufacturing. Wurm [35] reported that 60–70% of all recombinant protein pharmaceuticals are produced in mammalian cells, usually following a well-established production scheme. Moreover, Farid [36] stated that antibodies played an important role in several of the important advances in pharmacotherapy that contributed to the treatment of infectious diseases, cancer and autoimmune diseases.

This clinical and commercial success of mammalian products, e.g., monoclonal antibodies, has led to the need for large scale production with mammalian cell cultures. Furthermore, these increased demands for therapeutic antibodies also resulted in a rapid expansion of global manufacturing capacity, e.g., increasing size of reactor capacity up to 10 m³. At the same time process efficiency was improved to reduce manufacturing costs [37]. Clearly, besides the biological and quality-related advantages of the mammalian expression systems currently in use, economical aspects also play an important role in the industrial production of monoclonal antibodies. Werner [38] illustrated that high therapeutic dosages of monoclonal antibodies usually demand high capacity

needs, which in turn require significant capital investments, but also stimulate innovation for process improvements to decrease cost of goods (COG).

5 Integration of systems biology data from the host organisms of the bioprocess into the PAT methodology

This preference for mammalian systems in biopharmaceutical manufacture has placed particular quality aspects, such as protein glycosylation heterogeneity, charge distribution and polymorphism, at the forefront of research and development.

Such CQAs are linked to molecular details produced by highly regulated intracellular processes that are not part of the mainstream carbon and nitrogen fluxes. Although the dependency of, for example, protein glycosylation patterns on process operation parameters such as pH, temperature, medium composition and carbon source feeding rate has been demonstrated in several studies (e.g. [39, 40]), systematization of knowledge and demonstration of controllability become impossible without the consideration of intracellular processes. This is where systems biology can play an important role in PAT, specifically in: (1) the generation of knowledge, (2) the elucidation of mechanisms, and (3) the modeling of the biological functions at the basis of molecular level CQA.

Substantial efforts are made in academic and industrial research in collecting 'omics' data sets at various cultivation time to discover the fundamental regulation mechanisms of certain product CQAs, but also to find new ways to increase yield and productivity. In a PAT approach, it would be of particular use to concentrate attention on the exometabolomics in the process. The exometabolome, which consists of the total quantitative collection of small molecular weight compounds (metabolites) present in the extracellular medium, provides a very informative "footprint" of cellular activity, from which it is possible to infer its intracellular state up to the proteomic and genomic levels [41]. Today cheap, fast and high-throughput techniques with little or even no sample preparation exist that enable the measurement of the exometabolome. This opens an array of opportunities for advanced monitoring techniques that can support real-time control of critical intracellular processes at the basis of the CQA. Mass spectrometry, NMR spectroscopy and vibrational spectroscopy are the main techniques currently used for metabolomics. The need for high-throughput, short analysis time compatible with at-line or even on-line measurement restricts the choice to direct injection mass spectroscopy (DI-MS), Fourier transform infrared spectroscopy (FT-IR) and (1H) NMR [42]. Among these, DI-MS is considered the technique with the highest potential since it provides a fingerprint of the complete exometabolome, is highly sensitive, requires no sample treatment and is cheap, fast and high-throughput [41].

Chemometrics plays a very important role in PAT in MVDA, extraction of knowledge from large datasets, modeling and statistical process control. MVDA modeling is also widely applied in the analysis of 'omics' datasets to deduce the mechanisms that support a given (observed) biological function (the top-down approach) [43]. Systems biology is concerned with the interpretation of data to infer mechanisms (top-down) and to infer function from known mechanisms (bottom-up). In fact these two approaches can also be found in PAT modeling. The top-down approach is based on chemometric modeling, while the bottom-up approach is based on mathematical (mechanistic) modeling. In PAT, extensive challenges remain to be addressed in the integration of macroscopic (process monitoring and control) models with systems biology models [44, 45]. One important aspect is the efficient integration of mechanisms and MVDA. As new mechanisms are disclosed they represent constraints to top-down MVDA (top-down and bottom-up meet halfway). Hybrid semi-parametric modeling may provide an adequate answer to some of these challenges. It represents a compromise between rigorous mathematical modeling and empirical (chemometric) modeling, providing a flexible framework to merge a priori mechanisms with heterogeneous datasets of the different layers of information about the cell and the process [45].

6 Challenges limiting routine industrial application of PAT

The development of efficient mammalian bioprocesses in the biopharmaceutical industry has led to increased product yields above 5 g/L monoclonal antibody. These achievements can be attributed to the use of high-producer cell clones with enhanced cell productivity and to the optimization of key process characteristics, such as advanced process control and well-designed nutrient compositions, that are integrated into a platform technology for biopharmaceutical manufacturing processes. However, to identify potential process parameters that have an impact on CQAs, the process developer first need to identify and understand a set of CPPs.

Biotechnol. J. 2011, 6, 369–377 www.biotechnology-journal.com

When addressing QbD as described in the ICH guidelines (ICH Q8: pharmaceutical development, Q9: quality risk management and Q10: pharmaceutical quality system), typical questions in the field of bioprocess development arise: Can we identify CPPs and to what extent do these parameters have an impact on an industrial bioprocess? Can we adjust these process parameters? Thus, as a first step in addressing those questions from an industrial point of view, a 'proposed workflow' is presented with focus on new sensor techologies and advanced data analysis for process data based on multivariate projection techniques.

6.1 Industrial workflow to implement the QbD/PAT concept

The implementation of advanced PAT technologies into an already existing GMP manufacturing facility can be complex and faces many challenges. For example, new innovative process sensors for mammalian suspension cultures need to be easy-to-handle in a daily working routine, e.g., a simple calibration procedure is required. Moreover, PAT sensors can be applied in a robust and applicable manner for a broad range of process variants. This allows the amount of valuable process data to be increased and the corresponding know-how translated into a monitoring or control scheme to handle

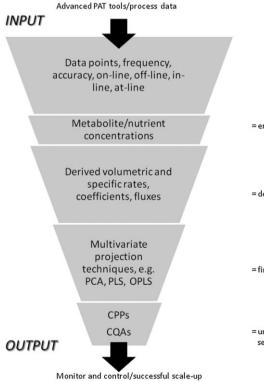
the sensitive process parameters. In other words, the collected data are translated into process information and subsequently further transformed into real process knowledge using advanced analysis techiques, e.g., PCA, PLS or orthogonal PLS (OPLS) (Fig. 4). The generated process knowledge can be subsequently used to monitor or control the critical sources of variability to ensure a consistent quality for an advanced manufacturing process.

The quality issues for all the biopharmaceuticals referred to in this contribution are similar, although not identical. The main concerns are the purity of the protein and the detection of impurities from the host organism, the culture media or formation of adverse product forms. The host organism and the biomolecular structure of the product have significant effects on the prerequisites of applying PAT.

Progress in PAT and an improved understanding of its applications contribute to advancing manufacture of these complex biopharmaceutical products

7 Recommendations

Based on the workshop, the following recommendations for further developing PAT methodology for biopharmaceuticals are suggested:



Raw data

= error measurements and valuable information

Information

= describes process progress/condition at a time

Advanced analysis

= find true relationships and dependencies

Knowledge

 understand relationships, design/control space, control sensitive sources of variability

Figure 4. Proposed industrial workflow to address the QbD/PAT concept using multivariate projection techniques to identify CPPs and their relationship to CQAs.

- There is still a need to develop a more robust platform providing a structured framework for industrial acceptance of the PAT methodology. The methodology approaches presented in this article shoulde be integrated in such a framework.
- Systematic evaluation of such a platform should be carried out using real industrial production systems
- The success of such a platform will, to a large extent, also depend on the level of documentation and standardization that can be provided. Industry needs standard operating procedures and well-documented methods and tools, to be able to adopt new technology in a GMP environment. Good modeling practice (GMoP) forms a natural part of this.
- CQAs should be related to the molecular structures of the product. This information requires analytics that detects specific characteristics of the product media (broth, culture media, or released cellular components). Methods should preferably be based on immunogenic reactions or, possibly, rapid genomic analysis.
- Systems biology can provide critical information about the mechanisms that control CQAs. This information can be integrated in mathematical models to support PAT. On-line or atline exometabolomics needs to be further developed as a process analytical technique with the capability to infer information about the endometablome, proteome and transcriptome.
- Merging mechanisms and MVDA into a common (hybrid) modeling framework still presents a major challenge to the integration of different layers of information about cells and macroscopic processes.
- The number of experiments required to establish a robust correlation model should be further reduced. At the same time it is necessary to differentiate between causal and non-causal correlation. Process knowledge should be used to overcome these issues. However, if little knowledge is available error prone interpretation of correlation structures might occur.

8 References

- [1] U.S. Department of Health and Human Services, Food and Drug Administration: Guidance for industry: PAT – a framework for innovative pharmaceutical development, manufacturing and quality assurance http://www.fda.gov/down loads/Drugs/GuidanceComplianceRegulatoryInformation/ Guidances/ucm070305.pdf, Accessed 01/10/10.
- [2] Rathore, A. S., Bhambure, R., Ghare, V., Process analytical technology (PAT) for biopharmaceutical products. *Anal. Bioanal. Chem.* 2010, 398, 137–154.

- [3] Bakeev, K. A. (Ed.), Process analytical technology. Blackwell Publishing, Oxford 2005.
- [4] Rathore, A. S., Mhatre, R. (Eds.), Quality by design for biopharmaceuticals: principles and case studies. Wiley and Sons Inc. New York 2009.
- [5] Mandenius, C. F., Graumann, K., Schultz, T. W., Premsteller, A. et al., Quality-by-Design (QbD) for biotechnology-related phamaceuticals. *Biotechnol. J.* 2009, 4, 11–20.
- [6] Gabrielsson, J., Lindberg, N.-O., Lundstedt, T., Multivariate methods in pharmaceutical applications. *J. Chemometrics* 2002, 16, 141–160.
- [7] Kourti, T., The process analytical tehenology initiative and multivariate process analysis, monitoring and control. *Anal. Bioanal. Chem.* 2006, 384, 1043–1048.
- [8] Martin, E. B., Morris, A. J., Enhanced bio-manufacturing through advanced multivariate statistical technologies. *I. Biotechnol.* 2002, 99, 223–235.
- [9] Cunha, C. C. F., Glassey, J., Montague, G. A., Albert, S., Mohan, P., An assessment of seed quality and its influence on productivity estimation in an industrial antibiotic fermentation. *Biotechnol. Bioeng.* 2002, 78, 658–669.
- [10] Lennox, B., Kipling, K., Glassey, J., Montague, G. et al., Automated production support for the bioprocess industry. *Biotechnol. Prog.* 2002, 18, 269–275.
- [11] Navratil, M., Norberg, A., Lembren, L., Mandenius, C.-F., Online multi-analyzer monitoring of biomass, glucose and acetate for growth rate control of a *Vibrio cholerae* fed-batch cultivation. *J. Biotechnol.* 2005, 115, 67–79.
- [12] Ödman, P., Johansen, S. L., Olsson, L., Gernaey, K. V., Lantz, A. E., On-line estimation of biomass, glucose and ethanol in *Saccharomyces cerevisiae* cultivations using in-situ multiwavelength fluorescence and software sensors. *J. Biotech*nol. 2009, 144, 102–112.
- [13] Nomikos, P., MacGregor, J. F., Monitoring batch processes using multi-way principal component analysis. AIChE J. 1994, 40, 1361–1375.
- [14] Feng, M., Glassey, J., Physiological state specific models in estimation of recombinant *Escherichia coli* fermentation performance. *Biotechnol. Bioeng.* 2000, 69, 494–593.
- [15] Coleman, M. C., Block, D. E., Retrospective optimization of time-dependent fermentation control strategies using timeindependent historical data. *Biotechnol. Bioeng.* 2006, 95, 412–423.
- [16] Rhee, J. I., Lee, K. I., Kim, C. K., Yim, Y. S. et al., Classification of two-dimensional fluorescence spectra using self-organizing maps. *Biochem. Eng. J.* 2005, 22, 135–144.
- [17] Li, Y., Yuan, J., Prediction of key state variables using support vector machines in bioprocesses. *Chem. Eng. Technol.* 2006, 29, 313–319.
- [18] Petrides, D., Cooney, C. L., Evans, L. B., Field, R. P., Snoswell, M., Bioprocess simulation: an integrated approach to process development. *Computers Chem. Eng.* 1989, 13, 553–561.
- [19] Dassau, E., Zadok, I., Lewin, D. R., Combining six-sigma with integrated design and control for yield enhancement in bioprocessing. *Ind. Eng. Chem. Res.* 2006, 45, 8299–8309.
- [20] Sin, G., Ödman, P., Petersen, N., Eliasson Lantz, A., Gernaey K. V., Matrix notation for efficient development of first-principles models within PAT applications: Integrated modeling of antibiotic production with *Streptomyces coelicolor*. *Biotechnol. Bioeng.* 2008, 101, 153–171.
- [21] Degerman, M., Westerberg, K., Nilsson, B., Determining critical process parameters and process robustness in preparative chromatography A model-based approach. *Chem. Eng. Technol.* 2009, 32, 903–911.

- [22] Singh R., Gernaey K. V. Gani R., Model-based computer aided framework for design of process monitoring and analysis systems. *Computers Chem. Eng.* 2009, 33, 22–42.
- [23] Sin, G., Woodley, J. M., Gernaey K. V., Application of modeling and simulation tools for the evaluation of biocatalytic processes: A future perspective. *Biotechnol. Prog.* 2009, 25, 1529–1538.
- [24] Gernaey, K. V., Eliasson Lantz, A., Tufvesson, P., Woodley J. M. Sin, G., Application of mechanistic models to fermentation and biocatalysis for next generation processes. *Trends Biotechnol.* 2010, 28, 346–354.
- [25] Roels, J. A., Application of macroscopic principles to microbial metabolism. *Biotechnol. Bioeng.* 1980, 22, 2457–2514.
- [26] Gernaey, K. V., Gani, R., A model-based systems approach to pharmaceutical product-process design and analysis. *Chem. Eng. Sci.* 2010, 65, 5757–5769.
- [27] Noorman, H. J., Heijnen, J. J., Luyben, C. K. A. M., Linear relations in microbial reaction systems: A general overview of their origin, form and use. *Biotechnol. Bioeng.* 1991, 38, 603– 618
- [28] Sin, G., Gernaey, K. V., Eliasson Lantz, A., Good modelling practice (GMoP) for PAT applications: Propagation of input uncertainty and sensitivity analysis. *Biotechnol. Prog.* 2009, 25, 1043–1053.
- [29] Kiparissides, A., Kucherenko, S. S., Mantalaris, A., Pistikopoulos, E. N., Global sensitivity analysis challenges in biological systems modeling. *Ind. Eng. Chem. Res.* 2009, 48, 7168–7180.
- [30] Sayar, N. A., Chen, B.H., Lye, G.J., Woodley, J. M., Modelling and simulation of a transketolase mediated reaction: Sensitivity analysis of kinetic parameters. *Biochem. Eng. J.* 2009, 47, 1–9.
- [31] Striedner, G., Cserjan-Puschmann, M., Pötschacher, F., Bayer, K., Tuning the transcription rate of recombinant protein in strong *Escherichia coli* expression systems through repressor titration. *Biotechnol. Prog.* 2003, 19, 1427–1432.
- [32] Clementschitsch, F., Bayer, K., Improvement of bioprocess monitoring: development of novel concepts. *Microb. Cell Fact.* 2006, 5, 19.

- [33] Clementschitsch, F., Jürgen, K., Florentina, P., Bayer, K., Sensor combination and chemometric modelling for improved process monitoring in recombinant *E. coli* fed-batch cultivations. *J. Biotechnol.* 2005, 120, 183–196.
- [34] Striedner, G., Pfaffenzeller, I., Markus, L., Nemecek, S et al., Plasmid-free T7-based *Escherichia coli* expression systems. *Biotechnol. Bioeng.* 2010, 105, 786–794.
- [35] Wurm, F., Production of recombinant protein therapeutics in cultivated mammalian cells. *Nat. Biotechnol.* 2004, 22, 1393–1398.
- [36] Farid, S. S., Process economics of industrial monoclonal antibody manufacture. J. Chromatogr. B 2007, 848, 8–18.
- [37] Morrow, K. J., Advances in antibody manufacturing using mammalian cells. *Biotechnol. Annu. Rev.* 2007, 13, 95–113.
- [38] Werner, R. G., Economic aspects of commercial manufacture of biopharmaceuticals. J. Biotechnol. 2004, 113, 171–182.
- [39] Wong, D. C. F., Wong, K. T. K, Goh, L. T., Heng, C. K., Yap, M. G. S., Impact of dynamic online fed-batch strategies on metabolism, productivity and N-glycosylation quality in CHO cell cultures. *Biotechnol. Bioeng.* 2005, 89, 164–177.
- [40] Gawlitzek, M., Estacio, M., Fürch, T., Kiss, R., Identification of cell culture conditions to control N-glycosylation site-occupancy of recombinant glycoproteins expressed in CHO cells. Biotechnol. Bioeng. 2009, 103, 1164–1175.
- [41] Kell, D. B., Brown, M., Davey, H. M., Dunn, W. B. et al., Metabolic footprinting and systems biology: The medium is the message. *Nat. Rev. Microbiol.* 2005, 3, 557–565.
- [42] Lenz, E. V., Wilson, I. D., Analytical strategies in metabonomics. J. Proteome Res. 2007, 6, 443–458.
- [43] Bruggeman, F. J. Westerhoff, H. V., The nature of systems biology. *Trends Microbiol.* 2007, 15, 45–50.
- [44] Teixeira, A. P., Alves, C., Alves, P. M., Carrondo, M. J. T., Oliveira, R. Hybrid elementary flux analysis/nonparametric modeling: application for bioprocess control, *BMC Bioinfor*matics 2007, 8, 30.
- [45] Teixeira, A. P., Carinhas, N., Dias, J. M. L., Cruz, P. et al., Hybrid semi-parametric mathematical systems: Bridging the gap between systems biology and process engineering. J. Biotechnol. 2007, 132, 418–425.