Villez, K, Venkatasubramanian, V (2012). Fault diagnosis of a benchmark fermentation process based on probabilistic qualitative analysis of trends. Proceedings of the 2012 AIChE Annual meeting, Pittsburgh, PA, USA, October 28-November 2, 2012, 145

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282505 Fault Diagnosis of a Benchmark Fermentation Process Based On Probabilistic Qualitative Analysis of Trends

Monday, October 29, 2012: 10:30 AM
323 (Convention Center)

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Fault Diagnosis of a benchmark fermentation process based on Probabilistic Qualitative Analysis of Trends
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Qualitative analysis of trends consists of the task to segment a time series into contiguous time windows in which the first and/or second derivative of the trend underlying to the (noisy) data is considered to be unique. As such, one identifies so called episodes in which the trend is of a selected type: A – convex antitonic (monotone decrease); B – convex isotonic (monotone increase); C – concave isotonic; D – concave antitonic; etc. The resulting segmentation is referred to as a qualitative representation.

Such an analysis has been proposed frequently for the purpose of fault diagnosis of batch and continuous processes. Indeed, because process knowledge is often formulated or obtained easily in qualitative terms by communication with plant operators. However, recent research (Villez et al., 2011) points out that at least some of these existing methods are hardly robust to realistic noise levels. All existing methods are either based on recursive schemes or the application of heuristic rules which offer computational advantages at the loss of accuracy. For this reason, a spline based method has recently been proposed for improved accuracy (Villez et al., 2012a). In this line of research, focus is given to accuracy and statistical validity, while ignoring computational efforts as of yet. In essence, this spline method fits a spline subject to a supposed qualitative representation. This is a convex Second Order Cone Problem (SOCP) as long as the type and location of the episodes are known in advance and the spline function is of order four (cubic splines) or less (Nesterov, 2000; Papp, 2011). In Villez et al. (2012a) it is proved and demonstrated that the location of the episodes can be identified in a globally optimal fashion, given a qualitative sequence. Such qualitative sequence is the ordered series of episode types.

Given this method, the remaining problem is to identify the proper qualitative sequence. In Villez et al. (2012b), a probabilistic strategy is developed. To this end, each considered fault is associated with a unique qualitative sequence and a prior likelihood. Given a time series, the conditional likelihood (the likelihood of the data conditional to a qualitative sequence) is approximated with the maximum likelihood. This maximum likelihood follows from maximization of the spline function fit by searching the optimal locations of the episodes as given by the proposed qualitative sequences. By use of Bayes' rule, fault diagnosis boils down to the selection of the maximum a posteriori (MAP) likelihood qualitative sequence. This means that the qualitative sequence leading to the MAP likelihood, following global optimizition of the episode locations, is selected.

The provided method is applied to the simulated benchmark simulation model of [Birol]. This model was set up for benchmarking of fault diagnosis methods, amongst others. In Villez et al. (2011), noisy Penicillin concentration profiles were analyzed with an existing, wavelet-based method. Profiles of three conditions were selected, each of which have distinct qualitative representations based on visual inspection. In Figure 1, one can see that Normal Operational Conditions (NOC) correspond to a BC sequence. Fault 2 correspond to BCBC sequence. Fault 3 correspond to BCDA a sequence. The results in Villez et al. (2011) indicated extreme sensitivity to noise. The shown results are the initial results obtained with the newly proposed spline-based method and are obtained in the contex of larger, comparitive study of techniques for qualitative analysis.

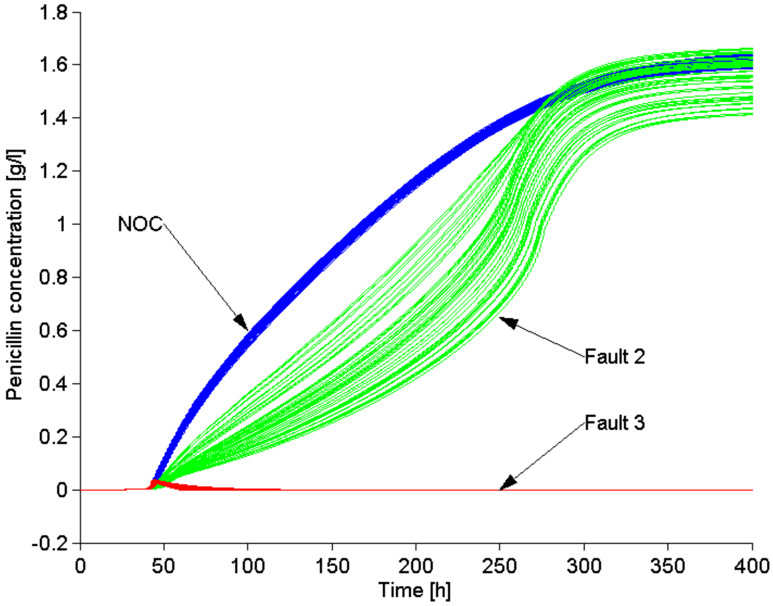

Figure 1: Simulated contration profiles for different conditions in the benchmark fermentation model.

Figure 2 shows the maximum likelihood fits for one batch with Fault 2 and for each of the proposed qualitative sequences. One can see that the spline fits for each shape constraints can hardly be distinguished.

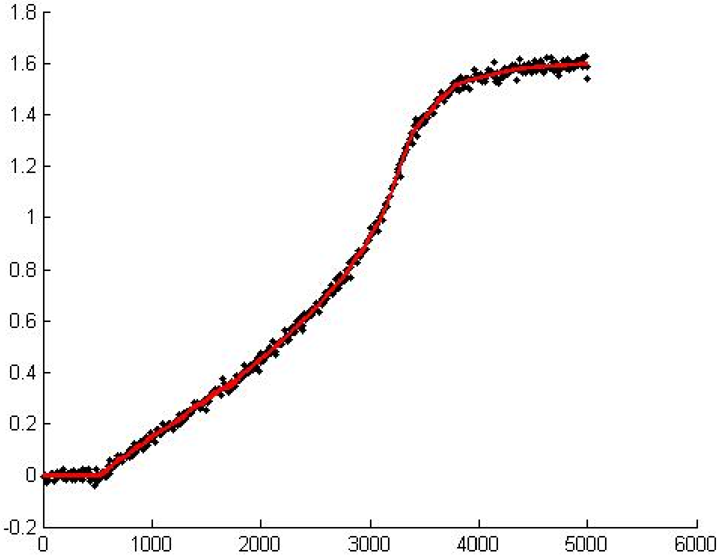

Figure 2: Maximum likelihood fits for a batch with Fault 2. The fits of different sequences are hard to distinguish.

Figure 3 shows the a posteriori likelihoods (normalized) which are obtained for a batch with Fault 2 and for three qualitative sequences (BC/BCBC /BCDA). Prior likelihoods for each of the qualitative sequences were set equal, implying complete ignorance. One can see that the maximum a posteriori (MAP) selection of a qualitative sequence is correct. Indeed, the BCBC sequence is selected. Note that the difference in likelihood is rather subtle as would be expected from the almost equal fits.

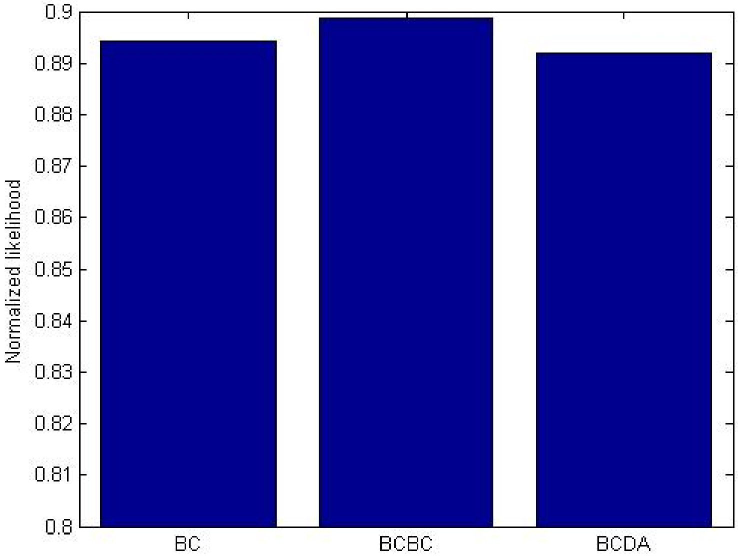

Figure 3: A posteriori likelihoods for three batches and three qualitative sequences. The maximum a posteriori (MAP) likelihoods lead to a correct matching.

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