



BiQ Analyzer Software for DNA Methylation Analysis, Visualization and Quality Control

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Summary

BiQ Analyzer is a software tool for easy visualization and quality control of DNA methylation data. With more than a thousand users worldwide, BiQ Analyzer has become a standard tool for processing DNA methylation data from bisulfite sequencing. BiQ Analyzer has been selected by ABI to be part of the [Applied Biosystems Software Community Program](#).

Ansprechpartner

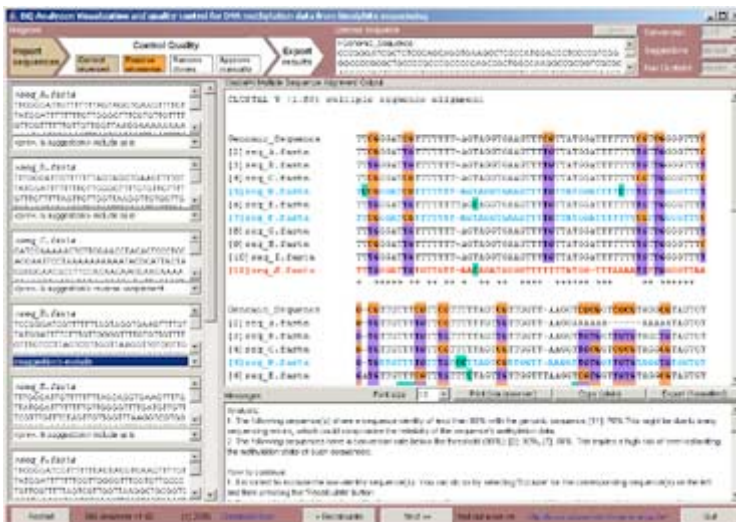
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Feature Highlights

- End-to-end support of the analysis process: from raw sequence files to comprehensive documentation and visualization
- Automatical generation of publication-quality 'lollipop diagrams'
- Integrated 1-click multiple alignment of clonal sequences
- Automated CpG highlighting
- Factor 5 speedup over manual analysis, plus systematic quality control

Targeted Users

Anyone who works with DNA methylation data from bisulfite sequencing; occasional users as well as experts (beginners will benefit from help with quality control whereas experts will save hours and days of tedious work by using BiQ Analyzer).



Detailed description (this section is based on the [Bioinformatics journal paper](#) in which BiQ Analyzer was first described):

Manual processing of DNA methylation data from bisulfite sequencing is a tedious and error-prone task. BiQ Analyzer significantly simplifies this task and provides start-to-end interactive software support. In an easy-to-use manner the tool helps the user to import the sequence files from the sequencer, to align them, to exclude or correct problematic sequences, to

document the experiment, to perform basic statistics and to produce publication-quality diagrams. Emphasis is put on quality control: The program automatically assesses data quality and provides warnings and suggestions for dealing with problematic sequences. The BiQ Analyzer program is implemented in the Java programming language and runs on any platform for which a recent Java virtual machine is available.

BiQ Analyzer is the first tool to provide comprehensive support for the analysis of DNA methylation data from bisulfite sequencing. It provides significant improvements over the only comparable software, namely a set of Perl scripts called **MethTools**: First, BiQ Analyzer imports sequence files directly from the sequencer without the need for any manual intervention and assists the user in all steps of alignment and quality control. Second, BiQ Analyzer does not only calculate summary statistics but can export the methylation data in full detail and in a format that makes it easy to import them into any statistics package or spreadsheet program. Third, BiQ Analyzer supports standardized experiment documentation. Finally, BiQ Analyzer provides an interactive graphical interface that guides the user through quality control and gives continuous feedback on problematic sequences.

BiQ Analyzer is designed to mimic the manual process of DNA methylation analysis. In several steps, the user is guided from the import of sequences, across several phases of quality control and multiple sequence alignment, to a questionnaire documenting the experiment. In each of the quality control steps, the program makes suggestions on how to handle critical sequences, but the ultimate decision for or against inclusion of a sequence always stays with the user. Based on the user decisions during that process, the program finally generates a one-file HTML documentation (including publication-quality methylation diagrams in the widely-used 'lollipop' style) and saves the derived methylation data to the system clipboard, ready for subsequent analysis in a spreadsheet or with a statistics software.

In summary, BiQ Analyzer provides start-to-end support for the visualization and quality control of DNA methylation data from bisulfite sequencing. For the frequent user of bisulfite sequencing it will lead to significant speed up of the data analysis process. The occasional user will benefit from the extensive hints that help to perform a rigorous quality control. Beyond that, BiQ Analyzer facilitates standardized quality control and documentation.

Selected publications in which the BiQ Analyzer software is described and / or applied:

- Bock, C. et al. BiQ Analyzer: visualization and quality control for DNA methylation data from bisulfite sequencing. *Bioinformatics* 21, 4067-8 (2005).
- Bock, C. et al. CpG island methylation in human lymphocytes is highly correlated with DNA sequence, repeats and predicted DNA structure. *PLoS Genetics* 2, e26 (2006).
- Williamson, C.M. et al. Identification of an imprinting control region affecting the expression of all transcripts in the *Gnas* cluster. *Nature Genetics* 38, 350-5 (2006).
- Shames, D.S. et al. A genome-wide screen for promoter methylation in lung cancer identifies novel methylation markers for multiple malignancies. *PLoS Medicine* 3, e486 (2006).
- Ho, S.M. et al. Developmental exposure to estradiol and bisphenol A increases susceptibility to prostate carcinogenesis and epigenetically regulates phosphodiesterase type 4 variant 4. *Cancer Research* 66, 5624-32 (2006).

Ordering and Pricing

Users from academia and from non-profit research institutes can obtain their BiQ Analyzer license directly from the Max Planck Institute for Informatics (see project website at <http://biq-analyzer.bioinf.mpi-inf.mpg.de/>).

Commercial users can choose between the following licensing schemes:

License Type	Annual Price in EUR (1)
Standard single-PC license	750,--
Site license (2)	3.000,--
Developer license with source code (3)	On request
Two-month evaluation license (4)	FREE

(1) Commercial licenses are valid for one year (365 days) from the day of ordering. All updates within this period are included. Payments in US-\$ are welcome and will be based on the actual exchange rate EUR / US \$.

(2) A site license permits use of BiQ Analyzer on all PCs at one company site (i.e. single postal address). Branches of the same company at different sites will have to acquire individual licenses.

(3) BiQ Analyzer is written entirely in Java. Parts of its source code (diagram generation and quality control) have already been used for the construction of a customized data analysis pipeline. It is possible to license the source code for custom adaption or integration into larger systems.

(4) The evaluation license is identical to the site license but valid only for two months after initial ordering.

To request a free test version or to order BiQ Analyzer, please contact Dr. Bernd Ctortecka.

Business Case: "Does it pay off to buy BiQ Analyzer for my company?"

Based on the experiences and usage data of hundreds of researchers that used BiQ Analyzer during 2006, it is possible to estimate the annual cost savings from a single BiQ Analyzer license:

- A typical user runs 20 to 50 bisulfite sequencing analyses per year
- Evaluating a single analysis takes approximately an hour using traditional tools (or significantly more if publication-quality diagrams are required)
- Using BiQ Analyzer, a significantly more accurate and reliable analysis can be performed in 5 to 10 minutes
- Assuming that an hour wasted on tedious data analyses has opportunity cost of 100 Euros, BiQ Analyzer helps saving several thousand Euros per user and year
- In addition, it provides many invaluable features, such as standardized documentation and quality control, the experience of bisulfite sequencing experts coded into a software and publication-quality diagrams that give DNA methylation results a professional look.

As a free bonus, all labs that order one or more licenses of BiQ Analyzer may freely use the web-based DNA methylation diagram generator at <http://biq-analyzer.bioinf.mpi-inf.mpg.de/>. This is a web service for users who analyze (part of) their DNA methylation data outside BiQ Analyzer and want to generate high-quality 'lollipop diagrams' directly.

Additional Information

For biological and technical questions,
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