

ISMB 2005 Software Demo: Advanced micro-array probe design using OligoWiz 2.0

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Abstract

Tools for advanced microarray probe selection are becoming increasingly important as technologies for building inexpensive custom designed microarrays are becoming available. As an example, NimbleExpress from Affymetrix (California, U.S.) offers custom designed microarrays containing 280.000 24-30bp probes for app. 3000€ for the setup and app. 700€ per array manufactured. Hence, special purpose microarrays have become feasible. Examples of special purpose arrays includes arrays for detecting alternative splicing, determining transcription start and for ChIp-chip analysis. In addition, traditional expression microarrays can benefit both from the ability to place probes within exon regions, but also from the ability to place multiple probes per transcript.

OligoWiz 2.0 facilitates probe selection according to a series of probe quality scores: cross-hybridization, ΔT_m , position in transcript, probe folding and low-complexity. The program has a graphical user interface which assist the probe designer in getting an overview over these scores by presenting them as graphs along the input sequences. In addition, OligoWiz 2.0 allows for integration of sequence annotation such as exon/intron structure, UTR regions, intergenic regions, transcription start site etc. These are also presented in the graphical interface.

Microarray probes can be selected manually in the graphical interface by the user, but may also be placed automatically according to both quality scores and sequence annotation. The program supports rule-based automatic placement of multiple probes per transcript. Automatic probe selection is performed relative to a weighted total score, which combined the different quality scores. In addition probe placement can be restricted to certain sequence regions of interest for example exons or introns. This is done by specifying the desired sequence segments using regular expression search in a corresponding sequence annotation string. Together these functionalities make advanced probe design feasible for scientists inexperienced in computerized information management.

Input enriched with sequence feature annotation can automatically be generated from GenBank files by use of the FeatureExtract web server (see below).

The software demo will cover a thorough introduction to the probe quality scores, a walkthrough of the graphical interface, automatic placement of probes and extraction of sequence feature annotation using the FeatureExtract server. The software demo will use real-life examples as case-stories: Selecting multiple exon-probes per transcript, creating splicing specific arrays targeting exon, introns, exon/intron boundaries etc.

Availability

OligoWiz 2.0 is built as a client-server suite. The graphical user interface delegates the computational intensive calculations to a multi CPU supercomputer hosted at the Center for Biological Sequence Analysis at the Technical University of Denmark. The graphical user interface is written in Java 1.4 and can be run on virtually all platforms. All work on the OligoWiz data files created by the OligoWiz server is conducted using the GUI in a completely offline manner.

Both use of the server and the graphical client is free for both academic and commercial use. Since running the OligoWiz 2.0 server is computationally intensive, there is a limit of 50 submissions per day to the OligoWiz server. Each submission can contain thousands of sequences.

OligoWiz 2.0 is hosted at:

<http://www.cbs.dtu.dk/services/OligoWiz2/>

The FeatureExtract server used for creating sequence annotation containing datasets is hosted at:

<http://www.cbs.dtu.dk/services/FeatureExtract/>

References

OligoWiz 2.0 - integrating sequence feature annotation into design of microarray probes

Rasmus Wernersson and Henrik Bjørn Nielsen.

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Design of oligonucleotides for microarrays and perspectives for design of multi-transcriptome arrays.

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Sample screenshot of the graphical user interface of OligoWiz 2.0