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MiDaR: Microarray Database Resource for Customized Chip Design

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Short Abstract: Often it is desirable to design a customized microarray chip for a subset of genes or a particular organism of interest. We have created a solution, MiDaR (Microarray Database Resource), to aid in the process of creating and storing custom microarrays based on gene information and GO annotations.

Long Abstract:
The invention of microarray technology allows biologists to study differential expression of genes under a variety conditions. While there are a number of commercially available solutions for commonly used organisms on a genome-wide basis, there are a large number of cases where it is desirable to design a customized microarray chip for a subset of genes or a particular organism of interest. Until now, there have not been any publicly available methods for aiding in the design of customized chips. We have created a solution, MiDaR (Microarray Database Resource) to aid in this process.

MiDaR provides a user-friendly graphical user interface (GUI) in order to facilitate custom chip design. It has been created to allow for the customized design for regions of interest. Genes can be selected for inclusion based on their Gene Ontology (GO) [1] annotations (biological process, molecular function, or cellular component), or by custom-defined groupings (such as different isoforms of a single gene). Positive and negative control groups can also be selected. Once the user has selected their genes of interest, MiDaR will allow the user to enter in either individual primer pairs for cDNA construction, or oligonucleotide probes. If the user wishes to automate this process, MiDaR will allow for on-the-fly probe design by using MPrime, a large-scale multiple primer/oligo design program [2]. The calls to MPrime will result in probes with uniform constraints. In order to deal with potential microarray position dependent biases, the user is given the option to randomly assign the positions for each probe.

After the microarray has been defined, it can be viewed graphically. The researcher then has the option of highlighting individual genes by their names, or based on their groups. This can be particularly useful in tracking both positive and negative controls. By clicking on an individual location, the user can retrieve information concerning any individual probe on the constructed array. We will demonstrate how MiDaR can be used to create a customized oligonucleotide microarray for studying neurodegenerative diseases in order to illustrate the capabilities of MiDaR.

MiDaR was developed using MicrosoftTM VisualStudio and MySQL. More information on acquiring MiDaR free of charge can be found at the MiDaR website: http:// bioinformatics.louisville.edu/MiDaR/.

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[1] Harris, M.A. et al. (2004) The Gene Ontology (GO) database and informatics resource. Nucleic Acids Res., 32, D258-D261.
[2] Rouchka, E.C., Khalyfa, A., and Cooper, N.G.F. (2005) MPrime: efficient large scale multiple primer and oligonucleotide design for customized gene microarrays. BMC Bioinformatics, 6, 175.