

**Bioinformatics Core - Informatics and Analysis Core**  
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**A. Specific Aims**

The Bioinformatic Core (BINFOC) will have a number of very distinct functions, all of which will serve multiple INIA projects and help provide key integrative functions among the research projects. Additionally, the BINFOC will provide support for experimental design, advanced statistical analysis, data warehousing or database storage, and advanced bioinformatic analyses. The latter will include development or adaptation of novel algorithms for analysis of gene networks. Altogether the BINFOC will provide a forum for both data integration and advanced data analysis across all the primary projects of this proposal. In addition, the tools and resources provided by the BINFOC will provide service to the alcohol research community and other biomedical researchers.

The BINFOC will be divided up into subcores, to be based upon the different disciplines needed to accomplish the goals mentioned above. Each subcore will have a specific co-PI in charge of the aims and protocols inherent to that module. The subcores and related goals of the BINFOC are:

**Subcore 1: Communication and Collaboration. (M. Langston)**

This subcore will provide a web-based information system that will have both public and INIA-Stress restricted functions. Public resources will include information regarding INIA-Stress events, protocols, accomplishments and links to specific tools or databases developed/maintained by INIA-East. This Aim will provide evolution and improved implementation of the INIA-East web portal ([www.iniastress.org](http://www.iniastress.org))

**Subcore 2: Biostatistics Analysis and Design (E. Chesler)**

This subcore will provide advanced experimental design and statistical support for all INIA-Stress projects. An existing web-based data repository systems and analysis system will be expanded to provide rapid access to INIA-Stress behavioral and neurochemical data and produce a standardized set of statistical analyses.

**Subcore 3: Bioinformatic Support and Tool Development (J. Snoddy)**

This subcore will provide algorithms and assistance for gene-network annotation (INIAWebGestalt) analysis and gene network integration across INIA-Stress datasets. Advanced methods for integrating various bioinformatic gene-network resources will be expanded and developed to provide INIA-Stress investigators novel forums for in silico hypothesis generation and testing. This subcore will also provide for integration of other bioinformatics resources within individual projects such as the Ontological Discovery for Ethanol Research System (Chesler) or GeneNetwork (Williams).

**Subcore 4: Microarray Support and Analysis (M. Miles)**

This subcore will provide expertise and tools for experimental design, analysis and database management of microarray experiments for INIA-Stress. In addition, pilot microarray experiments will be performed in some instances, such as characterization of important mouse mutant lines. A GeneTraffic database will be set up for INIA-Stress microarray data and will be integrated with bioinformatics tools in subcore 3.