

Contract Concept Review for Bioinformatics Support Services

B. Alex Merrick, Ph.D.

National Institute of Environmental Health Sciences

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Bioinformatics Support Contract

- What is the purpose of the contract? The contract provides bioinformatics support for projects within the NIEHS research portfolio.
- What needs does a bioinformatics contract fill? Bioinformatics analysis
 provides biocomputational capabilities for NIEHS needs in diverse fields of
 study including:
 - Toxicology
 - Genomics
 - Structural chemistry
 - High throughput screening

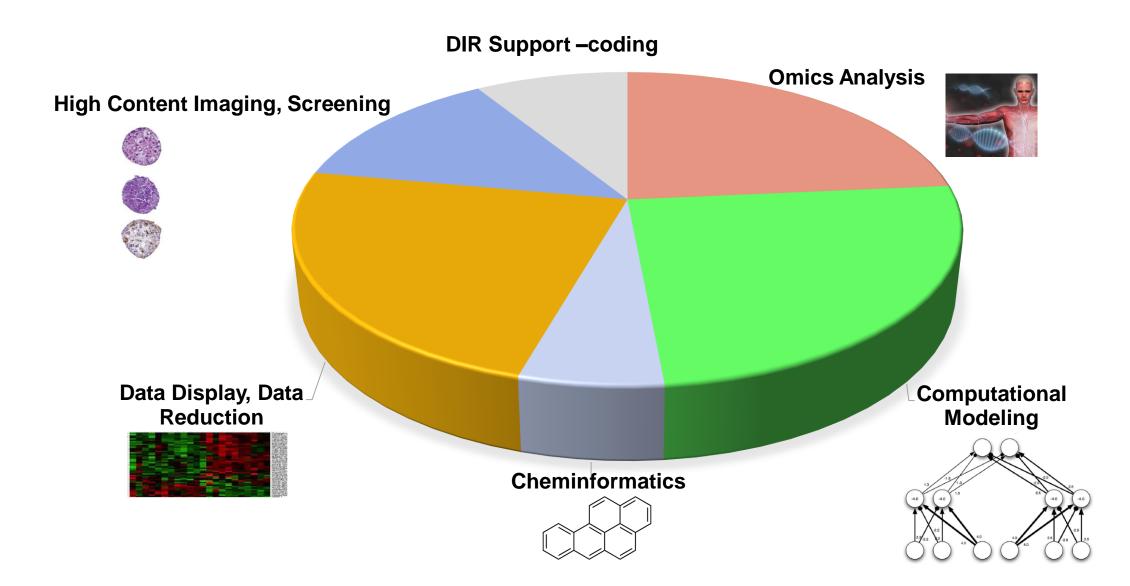


Bioinformatics Support Contract

- Who can use the contract? Primarily support (90%) for Division of the NTP (DNTP) but can also provide some support (10%) for Division of Intramural Research (DIR). Currently, all branches and programs in DNTP are using the contract.
- New contract length: 7 years (current contract is 5 years)
- **History**: Outgrowth of biostatistics contract
- Statement of Work: Similar capabilities to previous Statement of Work. It requires contractor to have flexibility to analyze numerous types of research data that may involve multi-scale modeling and provide tools and unique methods for data visualization. Receipt of source code for program needs.



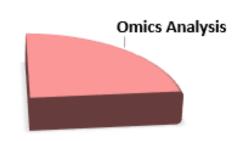
Percentage Technical/Programmatic Effort

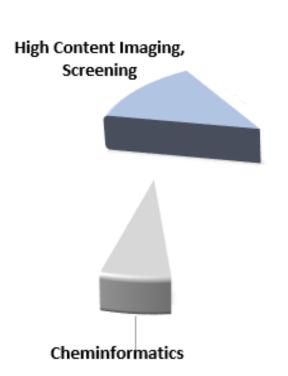




Technical Capabilities

- Data analysis for genomic and epigenomic sequencing data
- Transcriptomics and toxicogenomics support. Data reference, extraction, deposits in GEO*, SRA*
- High throughput transcriptomics support; e.g., S1500+ platform
- In vitro image analysis and pattern recognition related to in vitro models; e.g., cellular and subcellular morphology in toxicity
- QSAR and read-across support for HTS* screening assays to support Tox21 program; e.g., cheminformatics



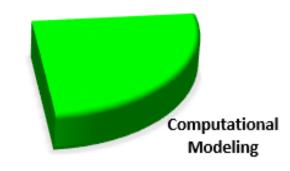


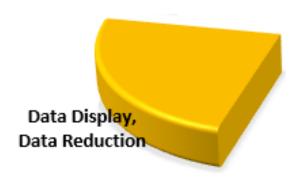
^{*} GEO: Gene Expression Omnibus; SRA: Short Read Archive; HTS: High Throughput Screening



Technical Capabilities

- Computational, biostatistical, and informatic methods. e.g., machine learning, data extraction, multi-scale and mathematical modeling, provide coding support.
- Informatics methods and data mining for systematic scientific literature reviews. Use of machine learning, text mining, natural language processing from government or public resources.
- Computational support. Biostatistical, software engineering, computational programs may involve Java, C++ and R for text mining, natural language processing, machine learning methods.
- Study designs and analysis. Data reduction methods, KEGG*, IPA*, GSEA*, SVM* analysis.
- Publication and meeting support. Organize data for publication, technical reports, presentations, e.g., graphs, tables and figures.





^{*} KEGG: Kyoto Encyclopedia of Genes & Genomes; IPA: Ingenuity pathway analysis; GSEA: Gene Set Enrichment Analysis; SVM: Support Vector Machines



Representative Bioinformatics Projects and Capabilities

- BMDExpress* development/support; DrugMarix, Tox21, TG-GATES*
- Cardiomyocytes Ca⁺⁺ flux data, electrophysiology
- Exome-seq analysis, RNA-seq, DNA-seq ccfDNA*
- HepaRG, hepatocytes, renal spheroid cultures, embryoid bodies
- High throughput transcriptomics TempO-seq (BioSpyder)
- Mouse aging study whole genomic analysis
- Orbitox
- S1500 platform developments: human, mouse, rat, zebrafish
- Tagging protocols, data mining, machine learning, AI*

^{*} AI: Artificial Intelligence; TG-GATES: Japanese ToxicoGenomics Database; BMDExpress: BenchMarkDoseExpress; ccfDNA: circulating cell free DNA



The BSC members are asked to review the concept for overall value and scientific relevance, as well as for fulling NIEHS' goal of protecting public health. Consideration should be given to:

- The significance of the goals of the proposed research activity.
- The availability of technology and other resources necessary to achieve those goals.
- The extent to which there are practical scientific or clinical uses for the expected results.
- The adequacy of the proposed methodology.

The DNTP seeks approval from the BSC to continue this type of activity using a contract mechanism.



Questions?

