Scripps Clinic Bio-Repository & Bio-Informatics Core (SCBBC)

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The SCBBC consists of the
Scripps Clinic Bio-Repository,
which offers collected,
categorized and clinically
documented biological samples,
and the Scripps Clinic BioInformatics Core, which provides
numerous analytic tools and
services for individualized
research studies.

Staff are available for study specific consultations.

Study Protocol IRB-14-6499

SCBBC

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processing and storage resource for the centralized banking of blood, bio-fluids and tissue specimens procured from patients with malignancies and diseases or normal controls. All malignant samples will be accompanied by clinical and pathological data. All samples are stored in accord with the International Society of Biologic and Environmental Repositories (ISBER) Best Practices and specific protocol defined sample parameters.

· Bio-Repository: Serves as a procurement

Beyond simply serving as a repository of blood, tissue and bio-fluids, the Bio-Repository is be a shared resource of samples that will be made available to researchers and other collaborators approved by the SCBBC Oversight Committee.

 Bio-Informatics: Provides data management and analysis services for SCMG and SH investigators, as well as for external researchers/collaborators. We offer scientific support to assist in the planning, collection, analysis, integration and dissemination of biomedical data and knowledge. Projects will often vary in time and cost depending on the scientific goals of the work, and the desired level of detail.

Our goal is to use existing software & tools developed by the group, along with open source software, to support science in a cost-effective manner. We have expertise in analyzing data and building tools across many different scientific areas.

The main focus area centers on Next-Generation Sequencing (NGS) and RNA Microarrays. Additionally, statistical data analysis on primary data and downstream functional analyses are available.





Services Available

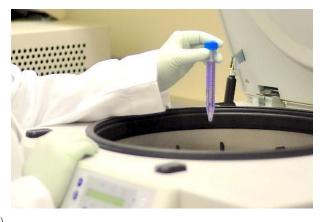
- Bio-Repository
 - I. Sample Collection:
 - Blood
 - Tissue
 - Urine
 - Stool
 - Saliva
 - II. Sample Processing:
 - Whole Blood
 - Plasma
 - Serum
 - MNCs
 - Urine (Pellet & Supernatant)
 - Stool

III. Sample Storage & Tracking:

- -80°C Thermo Scientific Freezers (x3)
- LN₂ Thermo Scientific CryoPlus Tank (Vapor Phase)
- Freezerworks Sample Management Software (Biobanking information management system)

IV. DNA/RNA Isolation:

- QIAcube (Fully automated nucleic acid extraction with QIAGEN spin-column kits.)
 - Allows automated DNA, RNA and protein sample processing
 - o Eliminates manual processing steps
- V. Individualized/Study Specific Data Collection & Entry
- VI. Equipment & Laboratory Space:
 - Thermo Scientific 1300 Series A2 Class II Biological Safety Cabinet (with SmartFlow, Digital Airflow Verification and Night Set-Back mode)
 - Thermo Scientific Heraeus Megafuge (centrifuge)
 - Thermo Scientific Pico Microfuge
 - Thermo Scientific Lab-Line Waterbath
 - Thermo Scientific S1 Pipet Filler
 - Thermo Scientific F1-ClipTip Pipette's
 - CO₂ Incubator
 - 400 Sq Feet Communal Laboratory Space







Services Available

Bio-Informatics

I. Experimental Planning & Optimization:

- Framing the clinical question/s for conducting the experiment.
- Sample size planning, optimization and power calculations.
- Designing the ideal experimental setup to investigational methods.
- Design control and validation.

II. NGS and Microarray Data Analysis Services Include:

- RNA-Seq and microRNA-Seq data analysis.
- ChIP-Seq data analysis.
- Custom Bio-informatics workflows for NGS applications (RNA-Seq, ChIP-Seq, microRNA-Seq).
- Gene expression analysis of in house and published microarray datasets (Affymetrix, Illumina, ...).
- Quality control, alignment/mapping.
- de novo genome/transcriptome assembly (in the absence of a reference genome).
- Integration and application of published and popular algorithms and tools.
- Multiple genome browser support for visualization of NGS results.
- Develop and integrate data analysis and visualization tools, including leveraging of R and other programming languages.
- Establishing and maintaining customized genomic databases.
- Statistical support and consultation including providing advice on various aspects of statistical design and analysis.
- Support grant applications with experimental design recommendations and power/sample analysis.

III. Downstream Analysis Services Include:

- Pathway and gene ontology analysis using publicly available tools (NIH DAVID, Panther, KEGG) as well as commercial software such as Partek Pathways and Ingenuity Pathway Analysis.
- Classification/Clustering analysis using R based pipelines for building prognostic and diagnostic classifiers.
- Preparation of research section and planning an analysis of research grants.
- Help with writing high quality manuscripts for peer reviewed journals.



