



MEMORANDUM OF UNDERSTANDING

Working with the HSPH Bioinformatics Core

The HSPH Bioinformatics Core (HBC) supports researchers with 1) the management, integration and contextual analysis of biological high-throughput data, 2) integration of phenotypes and environment data, and 3) deployment and maintenance of databases and tools to support ongoing projects.

Procedure

Groups and individuals interested in working with the HBC should make initial contact with Dr. Oliver Hofmann, Associate Core Director (ohofmann@hsph.harvard.edu) to discuss the nature of work and how the HBC could assist. *The initial consultation is free of charge.* Dr. Hofmann will work with the requestor to determine the specifications of the project work, and will then create a time estimate with deliverables. HBC will charge an hourly rate (currently set at \$125) which covers all involved personnel, computing time, basic data storage cost, and all other technical expenses.

The requesting researcher will notify HBC staff in advance of fixed deadlines (e.g., paper or grant submission dates) so that the project can be scheduled accordingly. Prior to the start of the project, the requesting researcher will inform HBC staff of any security requirements or confidentiality agreements associated with shared data. In particular, any data requiring IRB approval needs to be declared before the start of the project to ensure that the necessary applications can be made in time.

Please initial here to acknowledge this requirement: _____

Once the project costs and deliverables have been proposed, the requestor will sign off on the project. Project completion will be defined in the scope of the project and deliverables.

Reporting

Progress reports and billing information will be provided together with detailed timesheets on a monthly basis. Project progress will be documented on a secure project management website available to clients; all data sets, results and documentation will be shared at regular intervals. *The requesting researcher will receive monthly invoices even for projects which are covered from external sources and for which no transfer of funds is required.*

The client will provide associated grant information to HBC. The HBC requires basic information on any grant application that is developed as a result of core consultation as part of our reporting process.

Acknowledgments and authorship

The requesting researcher and Oliver Hofmann will discuss authorship. The HBC does not require or request co-authorship on studies using data generated solely by using off-the-shelf software on a fee-for-service basis by our facilities. However, in cases where significant intellectual contributions are made by HBC members, co-authorship follows commonly-accepted scientific practice (also see the Acknowledgment section below).

In order to monitor our support service and satisfy institutional reporting requirements, we require clients acknowledge work performed by HBC in peer-reviewed publications in either one of the following two ways:

- in the acknowledgement section by stating that “The authors would like to thank [Name of Consultant] of the HSPH Bioinformatics Core, Harvard School of Public Health, Boston, MA for assistance with [services performed],” or
- in the appropriate body text section for which HBC provided a service by stating that “[Service] was provided by the HSPH Bioinformatics Core, Harvard School of Public Health, Boston, MA.”

Projects that made significant use of computational resources are kindly asked to acknowledge the FAS Research Computing environment as follows:

“The computations in this paper were run on the Odyssey cluster supported by the Harvard University FAS Research Computing Group.”

ABOUT THE HSPH BIOINFORMATICS CORE

Resources and people

The HBC is comprised of a team of research analysts, software engineers, database developers and support staff at the master's and doctoral level working under the direction of the HBC Core Scientific Director, Winston Hide, and Associate Director, Oliver Hofmann. It is also associated with the School's Program for Quantitative Genomics (PQG) and serves as the consulting group for the HSCI Center for Stem Cell Bioinformatics. HBC's staff handle biomedical data analysis, scientific systems administration, software and algorithm development, and high-throughput data analysis as well as data curation. Core staff are allocated as needed to best meet project requirements.

Services

The HBC offers a broad range of support and consultations. Requests range from basic questions in research computing, bioinformatics and computational biology during initial stages of study design and grant proposals to supporting ongoing studies requiring external expertise.

The HBC has experience in secure large-scale data management, database design, and software development. Staff members can provide assistance in quality assurance and analysis of gene expression arrays, genome-wide SNP arrays, and different aspects of second-generation sequencing technologies such as ChIP-seq, RNA-Seq or re-sequencing efforts of mammalian and pathogen genomes.

Services also include provision of external information generated from public databases, data curation, and assistance in choosing the right data format and annotation standard to ensure that best practices in data management and submission are being maintained.

Facilities & equipment

The HBC has access to the Faculty of Arts and Sciences computing resources, including a state-of-the-art Linux computing cluster that provides high performance, parallel processing computing and is designed for future growth. Support is provided by the FAS Research Computing group who offer considerable user support to researchers with accounts on the cluster. The cluster currently uses a variety of statistical software programs, including R, SAS, STATA, Matlab, and Mathematica, as well as modern bioinformatics tools and packages such as Bioconductor (Array and short-seq data), PLINK (GWAS), Birdsuite (CNV) and common next-generation sequencing tools (GATK, Picard, etc.).

Additionally, HBC operates a number of dedicated servers to process larger data sets, provide interactive access, and disseminate data to collaborators as necessary. The cluster and SANs are behind a Cisco internal firewall.

Contact information

Scientific Director Winston Hide (whide@hsph.harvard.edu)
Associate Director Oliver Hofmann (ohofmann@hsph.harvard.edu)
Program Coordinator Carolyn Ingalls (cingalls@hsph.harvard.edu)

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I acknowledge receipt of this memorandum:

Project name

Name

Oliver Hofmann, Associate Core Director

dated

dated