BBMRI-FUNCTIONALGENOMICS RP3 USER CODE OF CONDUCT (v08-04-2013)

The following is the Code of Conduct that the research investigators agrees to abide by as an Approved User of data part of the BBMRI Rainbow Project Functional Genomics RP3 ("RP3"). Failure to abide by any term within this Code of Conduct may result in revocation of approved access to any or all datasets obtained through RP3.

BBMRI-FunctionalGenomics comprises sensitive data that is provided by contributing biobanks. This data is property of the contributing biobanks, and shall not be used for any analyses unless explicit permission has been granted by BBMRI to perform predefined analyses. Specifically, researchers will work according to the following rules:

1. Investigator will use requested datasets solely in connection with the research project described in the approved Data Access Request for each dataset;
2. Investigator's permission to access RP3 data is strictly personal and cannot be transferred under any circumstance;
3. Investigator will perform all analyses solely on the LifeScience GRID and local GRID clusters ensuring data security;
4. When working on a local GRID-cluster, the Investigator will ensure that all downloaded data as well as intermediate/output data generated through analyses, are solely accessible by the Investigator him or herself, i.e. all original and subsequent data will not be readable, writable or executable by anyone other than the Investigator.
5. Investigator will refrain from downloading data to local non-GRID clusters or personal computers;
6. Investigator is aware that all activities with regards to viewing and downloading data will be monitored at the level of individual researcher;
7. Investigator will make no attempt to identify or contact individual participants from whom these data were collected;
8. Investigator will not distribute RP3 data to any entity or individual;
9. Investigator will adhere to computer security practices that ensure that only authorized individuals can gain access to data files;
10. Investigator will not submit for publication or any other form of public dissemination analyses or other reports on work using or referencing RP3 datasets prior to written permission by BBMRI;
11. Investigator acknowledges the BBMRI in any publication;
12. Investigator will report any inadvertent data release, breach of data security, or other data management incidents contrary to the terms of data access to m.h.moed@lumc.nl and b.t.heijmans@lumc.nl.

I read and understand the User Code of Conduct and its addendum. I declare that I will act accordingly. I understand that failure to adhere to the Code of Conduct will have repercussions for my role in RP3.

Name Signature Institute

Place Date

Please, scan the signed User Code of Conduct and return to b.t.heijmans@lumc.nl

ADDENDUM BBMRI-FUNCTIONAL GENOMICS RP3 USER CODE OF CONDUCT

For the BBMRI-Rainbow Project 3 Functional Genomics (RP3) substantial amounts of genotype and phenotype data will be generated and shared.

Within RP3 existing data contributed and owned by participating biobanks, including GWAS and phenotype data, will be brought together with newly generated transcriptome and methylome data.

The data is only to be used for pre-specified purposes to establish a comprehensive catalogue how genetic variation is impacting DNA methylation and gene expression levels, and how these effects eventually affect phenotypic variation. A description of a planned set of primary analyses according to the grant application is given below. Proposals for follow-up analyses using RP3 data are welcomed and will require approval.

To ensure this data is only accessible to bonafide researchers who obtained proper and explicit permission to conduct such analyses, the following data access and security measures will apply. RP3 data are stored on a centralized ABD secure BBMRI storage facility on the national LifeScience GRID as maintained by SARA. This facility includes tape back-up and fast lightpath connections to Dutch UMCs and GoNL data (RP1+2) are already stored here. To prevent inappropriate use and distribution to the genotype, phenotype, RNA-seq and DNA methylation data, researchers should request and obtain access to the data through the RP3 Data Access Procedure; accept and abide the rules of the Data Access Procedure with regards to security and conduct; request a personal GRID-certificate (enabling a strictly personal authentication procedure and logging of activities on the Grid).

All analyses will take place on the GRID. This implies that is not allowed for researchers to download data and analyze them on their own computing facilities not part of the GRID (e.g. non-GRID clusters and personal computers). When working on a local GRID-cluster, all downloaded data as well as intermediate/output data generated through analyses, must only be accessible by the researcher responsible (i.e. all original and subsequent data will not be readable, writable or executable by anyone other than the researcher). Activities with regards to viewing and downloading data will be monitored at the level of individual researcher to ensure data security.

Planned primary RP3 analyses

- RNA-seq based eQTL catalogue
- 450k-based meQTL catalogue
- DNA methylation vs. gene expression comparisons
- RNA-seq based discovery of exotic mechanisms of post-transcriptional modification (fusion, trans-splicing, editing, alternative poly-adenylation)
- Micro-array expression imputation using RNA-seq
- Next generation DNA methylation in GoNL subset: 'imputation' 450k, epigenetic landscape near insertions/deletions, alternative splicing effects, transmission, allele-specific methylation
- Proof of concept: Functional genomics of GWAS-identified SNPs sets associated with lipids and anthropometry (SNP > Methylation > RNA > Phenotype)