BBMRI-Omics hands on course

10:00-10:15 Introduction to available omics data within BBMRI-omics.nl. (Rick Jansen)

10.15-10.45: Introduction to the BBMRIomics R package for integrated analysis of BBMRI-omics data using R (Maarten van Iterson)

10:45-11.45: Practicum (Maarten van Iterson)

11.45-12:30: Lunch (demo: using BBMRI-Omics.nl online atlases (Jan-Bert van Klinken))

12.30-13.00: Joost Verlouw: QTL lookup of GWAS hits. Take the SNP hits from a recent GWAS, extract corresponding BIOS genotype data, run association with full Methylation, Expression and Metabolomics data sets.

13.00-14.00: Practicum (Joost Verlouw)

14.00-14.15- Tea break

14:15-14:: Introduction to the Brainshake 1H-NMR metabolomics platform (Marian Beekman)

14:45-15.30: Practicum. Analyzing Metabolomics data (Koen Dekker)

15:30-16:00: Allele specific expression (Niek de Klein & Freerk van Dijk)

16:00-17:00: Practicum (Niek de Klein & Freerk van Dijk))

17:00 Drinks

Wifi: eduroam or ask frontdesk. Course material:
http://wiki.bbmri.nl/wiki/BIOS_BBMRI-omics_course

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BBMRI-omics = GONL + BIOS + BBMRI Metabolomics

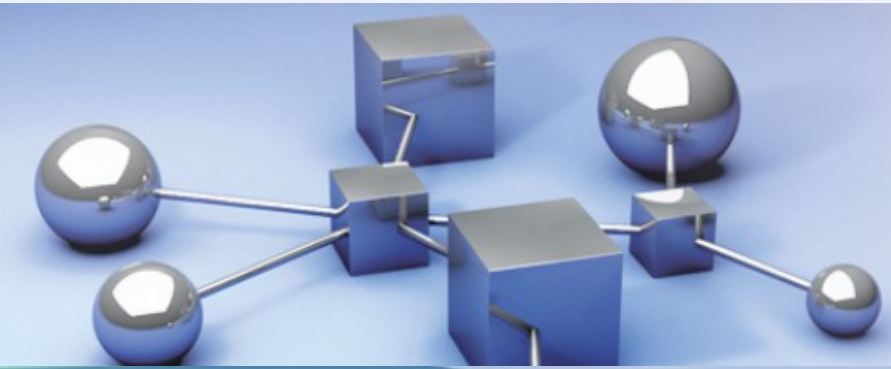
GONL = Genotype sequencing (*N*=769)
BIOS = RNA-seq + Methylation + already measured genotypes and phenotypes
BBMRI Metabolomics = Brainshake 1H-NMR

BIOS RNA-seq: Illumina HiSeq 2000, >15M x 50bp Paired End, whole blood
N = 3824 BIOS samples, including 510 GONL, *N* = 2030 non BIOS samples)

BIOS Methylation: Illumina 450k methylation, whole blood
N = 4805 BIOS samples, including 510 GONL, *N* = 1538 non BIOS samples

BBMRI Metabolomics: Brainshake 1H-NMR (247 markers), whole blood
(N = 23,729, overlap with BIOS: *N* = 3880 methylation, *N*= 2728 RNA-seq, *N*=2716 both)

Samples from 6 biobanks: Twin Register (Amsterdam), Rotterdam Study, Leiden Longevity Study, LifeLines (Groningen), PAN (Utrecht), CODAM (Maastricht)



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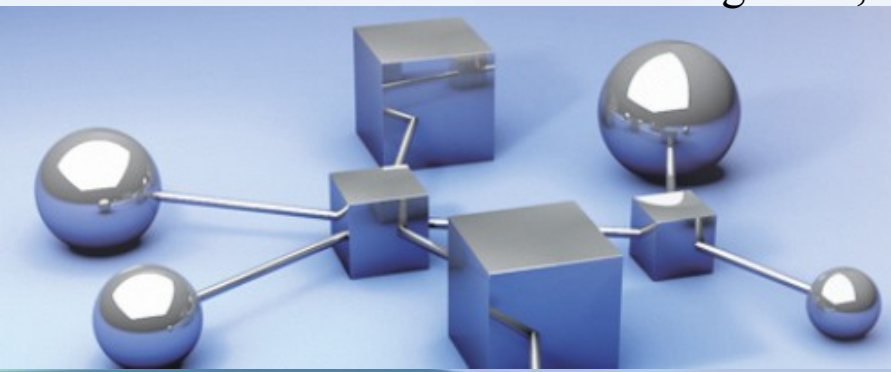
Management teams:
GONL = Cisca Wijmenga (PI), Morris Swertz, P. Eline Slagboom, Gertjan B. van Ommen, Cornelia M. van Duijn, Jasper A. Bovenberg (ELSI), Dorret I. Boomsma, Paul I.W. de Bakker
BIOS = Bastiaan T. Heijmans (chair), Peter A.C. 't Hoen, Joyce van Meurs, Rick Jansen, Lude Franke.
BBMRI Metabolomics = Eline Slagboom, Dorret Boomsma, Cornelia van Duin



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BBMRI-omics: access to data

Work in progress: one central data sharing interface (http://www.bbmri.nl/omics/)

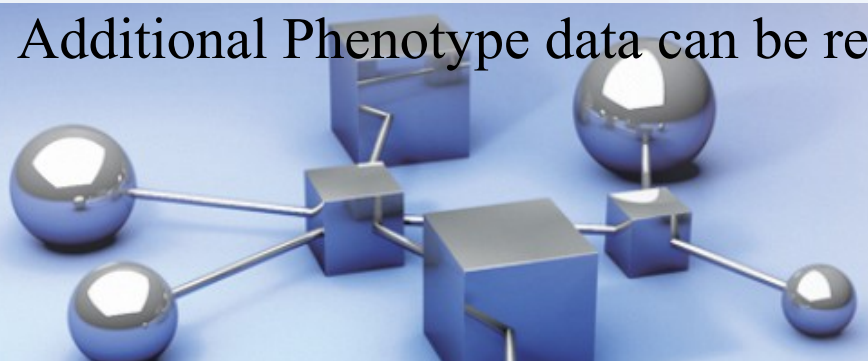
Currently:

GONL: request via http://www.nlgenome.nl/

BIOS: request via http://wiki.bbmri.nl/wiki/BIOS_start-
-BIOS data is available at a Sara Virtual Machines: 16 cores, 128 GB ram, 5TB storage
-BIOS data analysis has to be done at this VM (like today)
OR download freeze 1 at EGA (https://www.ebi.ac.uk/ega/studies/EGAS00001001077)

Metabolomics: Overlap with BIOS is accessible at the BIOS VM, data access procedure and website are being made.

Additional Phenotype data can be requested at the Biobanks!!



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Using the BIOS Virtual Machine (VM)

Three ways to access the VM: 1) ssh, 2) GUI, 3) R studio server

File locations: /virdir/Backup/RP3_data/, see http://wiki.bbmri.nl/wiki/BIOS_PreparedData

Genotype data is imputed vs GONL and HRC, present in vcf files.

When you work in R: use the packake BBMRIomics by Maarten van Iterson.
All data is available via this package and easy to link (we do this today)

Questions: we suggest our forum https://www.biostars.org/t/bbmri-nl-bios/ (or email)

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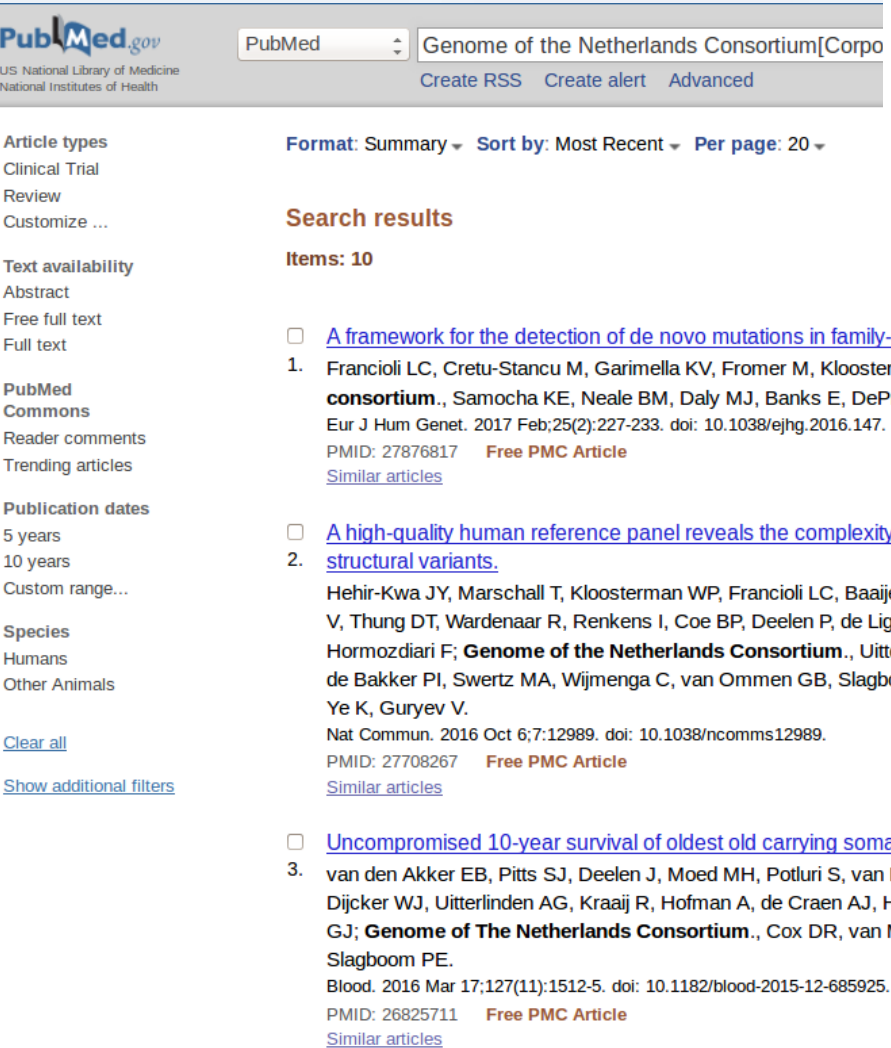
Current research in BBMRI omics

GONL



Current research in BBMRI omics

Metabolomics

Several projects ongoing for the relation with:

Dementia (submitted)
Osteoarthritis
Ageing and mortality
Depression
Recurrent CVD risk
Complications in Type 2 diabetes
Migraine

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Current research in BBMRI omics

BIOS (> 70 data requests)

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1. Epigenome-wide association study (EWAS) on lipids: the Rotterdam Study.
Braun KV, Dhana K, de Vries PS, Voortman T, van Meurs JB, Uitterlinden AG; **BIOS consortium.**, Hofman A, Hu FB, Franco OH, Dehghan A.
Clin Epigenetics. 2017 Feb 7;9:15. doi: 10.1186/s13148-016-0304-4. eCollection 2017 Feb 7.
PMID: 28194238 **Free PMC Article**
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2. Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk.
Warren HR, Evangelou E, Cabrera CP, Gao H, Ren M, Mifsud B, Ntalla I, Surendran P, Liu C, Cook JP, Kraja AT, Drenos F, Loh M, Verweij N, Marten J, Karaman I, Lepe MP, O'Reilly PF, Knight J, Snieder H, Kato N, He J, Tai ES, Said MA, Porteous D, Alver M, Poulter N, Farrall M, Gansevoort RT, Padmanabhan S, Mägi R, Stanton A, Connell J, Bakker SJ, Metspalu A, Shields DC, Thom S, Brown M, Sever P, Esko T, Hayward C, van der Harst P, Saleheen D, Chowdhury R, Chambers JC, Chasman DI, Chakravarti A, Newton-Cheh C, Lindgren CM, Levy D, Kooner JS, Keavney B, Tomaszewski M, Samani NJ, Howson JM, Tobin MD, Munroe PB, Ehret GB, Wain LV; International **Consortium** of Blood Pressure (ICBP) 1000G Analyses.; **BIOS Consortium.**; Lifelines Cohort Study.; Understanding Society Scientific group.; CHD Exome+ **Consortium.**; ExomeBP **Consortium.**; T2D-GENES **Consortium.**; GoT2DGenes **Consortium.**; Cohorts for Heart and Ageing Research in Genome Epidemiology (CHARGE) BP Exome **Consortium.**; International Genomics of Blood Pressure (iGEN-BP) **Consortium.**; UK Biobank CardioMetabolic **Consortium** BP working group..
Nat Genet. 2017 Mar;49(3):403-415. doi: 10.1038/ng.3768. Epub 2017 Jan 30.
PMID: 28135244
Similar articles

3. Controlling bias and inflation in epigenome- and transcriptome-wide association studies using the empirical null distribution.
van Iterson M, van Zwet EW; **BIOS Consortium.**, Heijmans BT.
Genome Biol. 2017 Jan 27;18(1):19. doi: 10.1186/s13059-016-1131-9.
PMID: 28129774 **Free PMC Article**
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Disease variants alter transcription factor levels and methylation of their binding sites

Marc Jan Bonder, René Luijk, Daria V Zhernakova, Matthijs Moed, Patrick Deelen, Martijn Vermaat, Maarten van Iterson, Freerk van Dijk, Michiel van Galen, Jan Bot, Roderick C Slieker, P Mila Jhamai, Michael Verbiest, H Eka D Suchiman, Marijn Verkerk, Ruud van der Breggen, Jeroen van Rooij, Nico Lakenberg, Wibowo Arindrarto, Szymon M Kielbasa, Iris Jonkers, Peter van 't Hof, Irene Nooren, Marian Beekman, Joris Deelen + *et al.*

Affiliations | Contributions | Corresponding authors

Nature Genetics **49**, 131–138 (2017) | doi:10.1038/ng.3721
Received 02 December 2015 | Accepted 18 October 2016 | Published online 05 December 2016

NATURE GENETICS | LETTER

日本語要約

Identification of context-dependent expression quantitative trait loci in whole blood

Daria V Zhernakova, Patrick Deelen, Martijn Vermaat, Maarten van Iterson, Michiel van Galen, Wibowo Arindrarto, Peter van 't Hof, Hailiang Mei, Freerk van Dijk, Harm-Jan Westra, Marc Jan Bonder, Jeroen van Rooij, Marijn Verkerk, P Mila Jhamai, Matthijs Moed, Szymon M Kielbasa, Jan Bot, Irene Nooren, René Pool, Jenny van Dongen, Jouke J Hottenga, Coen D A Stehouwer, Carla J H van der Kallen, Casper G Schalkwijk, Alexandra Zhernakova + *et al.*

Affiliations | Contributions | Corresponding authors

Nature Genetics **49**, 139–145 (2017) | doi:10.1038/ng.3737
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genenetwork.nl/biosqtlbrowser/

GONL data

BLAS R | eQTL database | BIOS WIki | Journals | BIOS wiki | personal | software | gene

BIOS QTL browser

This web page accompanies the manuscripts titled '**Disease variants alter transcription factor levels and methylation of their binding sites**', by *Bonder et al* and '**Identification of context-dependent expression quantitative trait loci in whole blood**', by *Zhernakova et al*, both have been published to Nature Genetics.
For further questions, contact the corresponding author: lude@ludesign.nl

Download meQTL results

You can download the independant top *cis*- and *trans*-meQTL and eQTMs, detected at a false-discovery rate of 0.05:
Cis-meQTLs independent top effects
Cis-eQTMs independent top effects
Trans-meQTLs top effects

Download eQTL results

You can download the *cis*-eQTLs detected at a false-discovery rate of 0.05:
Cis-eQTLs Gene-level independent top effects with context specific effects
Cis-eQTLs Gene-level all primary effects
Cis-eQTLs Exon-level independent top effects
Cis-eQTLs Exon-ratio independent top effects
Cis-eQTLs PolyA-ratio independent top effects

Query results

Or, you can query our independent eQTL, meQTL and eQTMs below (examples: rs3774937, cg10154826, ENSG00000226979 or *LTA*):

Gene or SNP name: Search