Opening up the BBMRI genomics infrastructure in The Netherlands

Venue: The Atrium, VU Medical Faculty, Van der Boechorststraat 7, Amsterdam. Directions: From the main entrance of the VU Medical Faculty, go straight until you can not continue. Here you can take the elevator or stairs to the first floor. On the first floor walk into the hall and you will find the Atrium.

09.45 – 10.00	**Coffee & registration**

Session 1: 10:00-12:00 **Practical guide into using the BIOS genomics infrastructure** **Moderator: Rick Jansen, VUMC**		
10.00 – 10.15	Rick Jansen (VUMC)	Introduction: The BIOS data infrastructure
10.15 – 10.30	Joost Verlouw (EMC)	BIOS data: What, Where and How
10.30 – 11:00	Annique Claringbould (UMCG)	RNA-seq QC and important parameters for analyses
11.00 – 11.30	Maarten van Iterson (LUMC)	BIOSRutils: R-package for loading and processing BIOS data
11.30 - 12.00	Jan-Bert van Klinken (LUMC)	Online BIOS QTL atlases

12.00 - 13:00	**Lunch**

Session 2: 13:00-14:30 **Showcasing the utility of the infrastructure in daily science** **Moderator: Joyce van Meurs, Erasmus MC**		
13.00 – 13.15	Bas Heijmans (LUMC)	Overview of past and present use of BIOS data
13.15 – 13.30	Annique Claringbould (UMCG)	Trans eQTL analysis
13.30 – 13.45	Jenny van Dongen (VUMC)	Epigenome-wide association study of educational attainment
13.45 – 14.00	Koen Dekker (LUMC)	Identifying methylome-metabolome interactions
14.00 - 14.15	Michiel Adriaens (MU)	Epigenetic and transcriptional markers of cardiometabolic disease
14.15 – 14.30	Martijn Dekker	Fetal differentially DNA-methylated regions, childhood lung function, and the risks of asthma and COPD across the life course

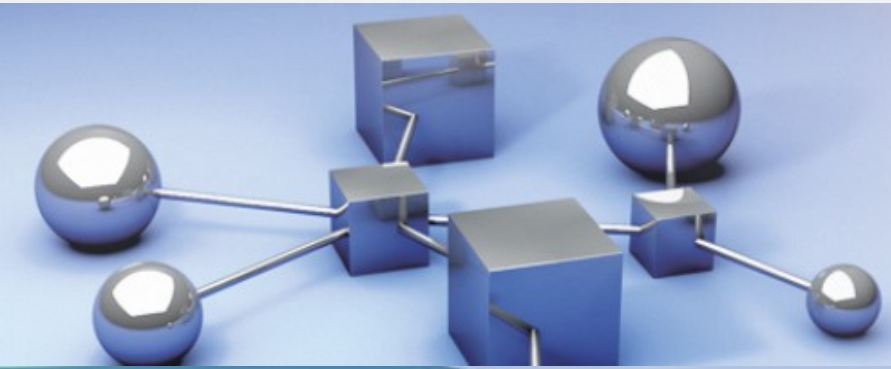
14:30 - 15:00	**Coffee Break**

Session 3: 15:00- 16:00 **Key note lecture on personalized medicine** **Moderator: Lude Franke, UMCG**		
15.00 – 16.00	Alain van Gool (RadboudMC)	Biomarkers in Personalized Health(care): time for quality not quantity

16:00 - 17.30	**Drinks**

- BIOS is a BBMRI Rainbow project starting in 2011

-The Goal: enabling mechanistic insights into how SNPs (identified with GWAS) influence complex disease phenotypes



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-The Goal: enabling mechanistic insights into how SNPs (identified with GWAS) influence complex disease phenotypes

-The Means: Enrich existing samples (genotyped) with Transcriptomic and Methylomic data: map relations between 3 levels of data.

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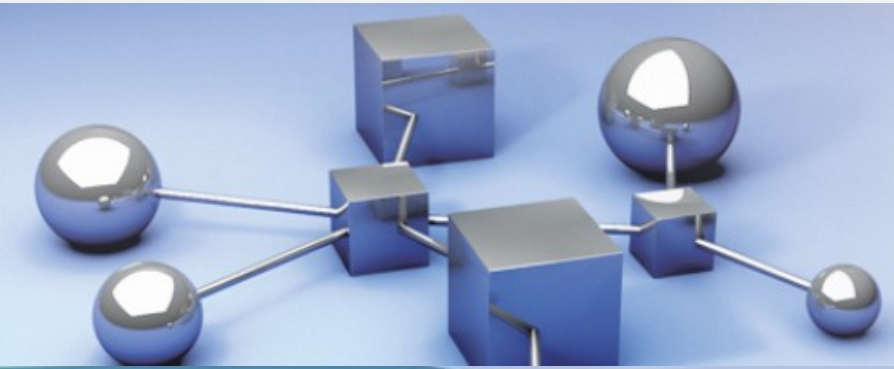
-The Team: bringing together Dutch (international) omics-experts and the biobanks they represent



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The BIOS Team

Management team
Bastiaan T. Heijmans (chair)1, Peter A.C. ’t Hoen2, Joyce van Meurs3, Rick Jansen5, Lude Franke6.

Cohort collection
Dorret I. Boomsma7, René Pool7, Jenny van Dongen7, Jouke J. Hottenga7 (Netherlands Twin Register); Marleen MJ van Greevenbroek8, Coen D.A. Stehouwer8, Carla J.H. van der Kallen8, Casper G. Schalkwijk8 (Cohort study on Diabetes and Atherosclerosis Maastricht); Cisca Wijmenga6, Lude Franke6, Sasha Zhernakova6, Ettje F. Tigchelaar6 (LifeLines Deep); P. Eline Slagboom1, Marian Beekman1, Joris Deelen1, Diana van Heemst9 (Leiden Longevity Study); Jan H. Veldink10, Leonard H. van den Berg10(Prospective ALS Study Netherlands); Cornelia M. van Duijn4, Bert A. Hofman11, Aaron Isaacs4, André G. Uitterlinden3 (Rotterdam Study).

Data Generation
Joyce van Meurs (Chair)3, P. Mila Jhamai3, Michael Verbiest3, H. Eka D. Suchiman1, Marijn Verkerk3, Ruud van der Breggen1, Jeroen van Rooij3, Nico Lakenberg1.

Data management and computational infrastructure
Hailiang Mei (Chair)12, Maarten van Iterson1, Michiel van Galen2, Jan Bot13, Dasha V. Zhernakova6, Rick Jansen5, Peter van ’t Hof12, Patrick Deelen6, Irene Nooren13, Peter A.C. ’t Hoen2, Bastiaan T. Heijmans1, Matthijs Moed1.

Data Analysis Group
Lude Franke (Co-Chair)6, Martijn Vermaat2, Dasha V. Zhernakova6, René Luijk1, Marc Jan Bonder6, Maarten van Iterson1, Patrick Deelen6, Freerk van Dijk14, Michiel van Galen2, Wibowo Arindrarto12, Szymon M. Kielbasa15, Morris A. Swertz14, Erik. W van Zwet15, Rick Jansen5, Peter-Bram ’t Hoen (Co-Chair)2, Bastiaan T. Heijmans (Co-Chair)1.

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Department of Gerontology and Geriatrics, Leiden University Medical Center, Leiden, The Netherlands
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BIOS Data generation: 2 omics levels:

Epigenome: Illumina 450k methylation arrays:
N = 4805 (510 GONL and 43 complete genomics samples)
N = 1538 non BIOS samples

Transcriptome: RNA-seq, >15M x 50bp Paired End:
N = 3824 (510 GONL and 43 complete genomics samples)
N = 2030 non BIOS samples

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Already present for these samples:
- genotype data
- a large amount of phenotypes

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Additional elements of The BIOS data infrastructure

-Storing & processing BIOS data: SARA computation facilities

- the BIOS wiki: http://www.bbmriwiki.nl/wiki/BIOS_start-

-Data request procedure (see BIOS wiki):
  1) Use SARA VM to process BIOS data
  2) Download BIOS data from EGA (https://www.ebi.ac.uk/ega/studies/EGAS00001001077)

-R package to access and process BIOS data

-Online BIOS eQTL and mQTL browser (http://genenetwork.nl/biosqtlbrowser/)

-Scientific output: >40 data requests, BIOS is co-author on >10 papers & counting!

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The Future of BIOS:

Many low hanging fruits are still there to be harvested in BIOS data (infrastructure) and expert support!!!! We welcome YOU!!

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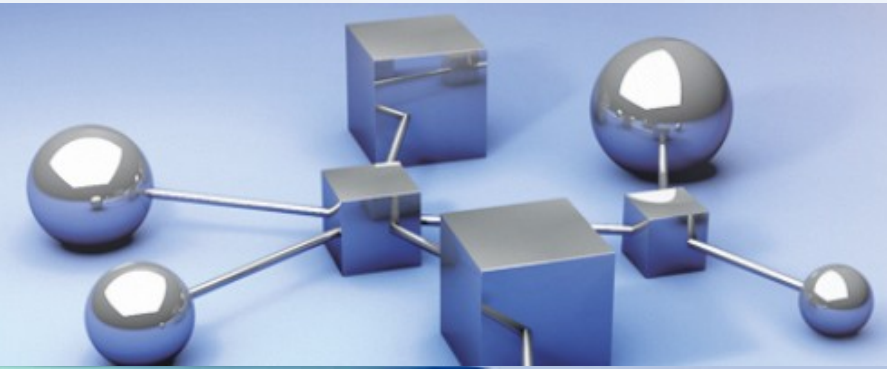

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