

PROGRAMME

Monday 19th May

Satellite Meetings

8.30	Registration UNESCO, 7 Place de Fontenoy			
9.30 – 11.00	LSDB Curation Course Salle III		Breast Cancer Interest Group Salle IV (by invitation only)	Oesophageal Cancer Meeting Salle V (by invitation only)
11.00 – 11.30	Coffee Break			
11.30 – 13.00	LSDB Curation Course Salle III	HVP Country Node Establishment Workshop: new directions Salle VI	Breast Cancer Interest Group Salle IV (by invitation only)	Oesophageal Cancer Meeting Salle V (by invitation only)
13.00 – 14.30	Lunch break at leisure			
14.30 – 16.00	LSDB Curation Course Salle III	HVP Country Node Establishment Workshop: new directions Salle VI	Breast Cancer Interest Group Salle IV (by invitation only)	
16.00 – 16.30	Coffee Break			
16.15 – 18.00	Joint meeting of Gene and Disease Specific Database Advisory Council with International Confederation of Countries Advisory Council Salle IV			



Tuesday 20th May

8.30 – 9.30 Registration
UNESCO, 7 Place de Fontenoy

9.00 **HVP Breast Cancer interest Group**
Salle III (by invitation only)

Human Variome Project – 5th biennial meeting Salle IV

SESSION I WELCOME & INFORMATION CHAIR: JOHN BURN

WELCOME ADDRESS

David Abraham

Chair, Human Variome Project International Board

Richard Cotton

Scientific Director, Human Variome Project International

9.35 – 9.45

WELCOME ADDRESS

Wendy Watson-Wright

Assistant Director-General for Natural Sciences *ad interim*, UNESCO

9.45 – 10.00

Report from the International Scientific Advisory Council

Garry Cutting, Chair

10.00 – 10.15

Report from Gene/Disease Specific Database Advisory Council

Raymond Dagleish, Chair

10.15 – 10.30

Report from International Confederation of Countries Advisory Council

Martina Wisch-Baumgartner, Chair

10.30 – 11.15

Global Alliance

Peter Goodhand

11.15 – 11.25

Assemble for group photograph

Foyer outside Salle IV

11.15 – 11.45

Coffee Break

SESSION II COLLABORATION BETWEEN DEVELOPED AND DEVELOPING COUNTRIES CHAIR: MARTINA WISCH-BAUMGARTNER

11.45 – 12.05

Datasharing in the Belgium/Congo

Thomy de Ravel

12.05 – 12.25

The Human Variome Project Australian Node in 2014

Graham Taylor

12.25 – 12.45

A Human Variome Project Country Node: Taking the HVPA-BioGrid Experience as a Data Sharing Model

Nik Nor Liza Nik Hassan

12.45 – 13.00 **Report from Minimum Content of a Country Specific Variant Database**
Martina Wisch-Baumgartner

13.00 – 14.20 Lunch break at leisure

SESSION III

CURRENT DEVELOPMENTS IN AFRICA

CHAIR: RAJ RAMESAR

- 14.20 – 14.30 **Introduction speech**
Lalla Aïcha Ben Barka
Assistant Director-General for Africa, UNESCO
- 14.30 – 14.35 **Introduction to H3Africa**
Raj Ramesar
- 14.35 – 14.50 **H3Africa Kidney Disease Research Network**
(GHANA)
Dwomoa Adu
- 14.50 – 15.05 **Clinical and Genetic Studies of Hereditary Neurological Disorders in Mali**
(MALI)
Guida Landoure
- 15.05 – 15.20 **Host and Microbial Genetic Determinants of febrile illness in West Africa**
(CAMEROON, NIGERIA)
Christian Happi
- 15.20 – 15.35 **Collaborative African Genomics Network (CAfGEN)**
(BOTSWANA, UGANDA)
Gabriel Anabwani
- 15.35 – 15.50 **TrypanoGEN: An integrated approach to the identification of genetic determinants of susceptibility to trypanosomiasis**
(UGANDA)
Enock Matovu
- 15.50 – 16.05 **Development of H3 Africa Biorepositories to facilitate studies on Biodiversity, Disease & Pharmacogenomics of African Populations**
(SOUTHERN AFRICA)
Akin Abayomi
- 16.05 – 16.20 **Visual Analytical Screening System for Disease Linked Gene Variants**
(NIGERIA)
Oyekanmi Nash

16.20 – 17.00 Poster Session I – Odd numbers (1, 3, 5 ...)
o Poster presenters for ODD NUMBERS to stand by their poster

SESSION IV

INTEGRATION OF NGS DATA

CHAIR: HEIDI REHM

- 17.00 – 17.20 **Informatics infrastructure for secure access, visualization and analysis of NGS data**
Ted Kalbfleisch
- 17.20 – 17.40 **Next-generation variant sharing between Dutch genome diagnostic laboratories**
Moris Swertz
- 17.40 – 18.00 **Dealing with Next Generation sequencing data not generated in the TSC context**
Rosemary Ekong



18.00 – 19.30

Welcome Reception

7th Floor Bar

Wednesday 21st May

Salle IV

SESSION V

DATABASES AND DATA CURATION 1

CHAIR: JOHAN T. DEN DUNNEN

9.30 – 9.45

Cracking rare disease: sharing exome/genome variant and phenotype data in LOVD3

Peter Taschner

9.45 – 10.00

Lightweight integration tool for data collection

Andrei Loukianov

10.00 – 10.15

Microattributions – increasing incentives for data submissions to Locus-Specific Databases

John-Paul Plazzer

10.15 – 10.30

Whole Exome and Genome Sequencing Analysis (PhenoDB) and Gene Matching Tool for Identification of Individuals with Mutations in the Same Gene (GeneMatcher)

Ada Hamosh

10.30 – 10.45

Cafe Variome: connecting diagnostic networks, disease consortia and diverse third parties

Raymond Dalgleish

10.45 – 11.00

MUTALYZER 2: Improved Sequence Variant Descriptions from next generation sequencing data and gene variant databases

Peter Taschner

11.00 – 11.10

Report from WG03: Minimal content for gene variant databases (LSDBs)

Peter Taschner

11.10 – 11.30

Coffee Break

SESSION VI

CONCURRENT WORKSHOPS

Workshop A
11.30 – 13.00
Salle IV

InSiGHT Interpretation Committee

Chair: Finlay Macrae
Observers welcome

Workshop B
11.30 – 13.00
Salle III

Institutional Support for Data Sharing

Chair: Richard Cotton

11.30 – 11.45

Report of World Health Organisation Project

Helen Robinson

11.45 – 12.00

Ethical issues

Dafna Fienholz, UNESCO



12.00 – 12.30	Attracting EC Funding Diana Salmen, European Commission
12.30 – 13.00	OPEN DISCUSSION

13.00 – 14.30 Lunch break at leisure

13.00 – 14.30	WG04: Sequence variant description committee meeting Salle III (by Invitation only)
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SESSION VII **DATABASES AND DATA CURATION 2**
CHAIR: MAUNO VIHINEN

14.30 – 14.45	ClinGen: The Clinical Genome Resource Heidi Rehm
14.45 – 15.00	ClinVar: A Central Repository for Clinically Relevant Variants Melissa Landrum
15.00 – 15.15	MseqDR consortium: a grass-roots effort to establish a global resource aimed to empower genomic studies of mitochondrion diseases Marcella Attimonelli
15.15 – 15.30	MSV3d 2014: Database of human MisSense Variants mapped to 3D protein structure Hoan Nguyen
15.30 – 15.40	Report from WG05: Variant Database Quality Assessment Mauno Vihinen
15.40 – 15.50	Report from WG01: Disclaimer Statements on G/DSDBs Websites John Paul Plazzer
15.50 – 16.00	Report from WG04: Sequence variant description committee Johan T. den Dunnen

16.00 – 16.30 Coffee Break

SESSION VIII **HUGO SESSION**
CHAIR: STYLIANOS ANTONARAKIS

16.30 – 17.00	The Renaissance of Personalized Medicine Stylianos Antonarakis
17.00 – 17.30	Functional annotation of personal genomes: transcriptome analysis in the GTEx project Tuuli Lappalainen
17.30 – 18.00	Clinical bioinformatics; a paradigm change in medicine Jacques Beckmann



Thursday 22nd May

Salle IV

SESSION IX

ASSESSMENT OF PATHOGENICITY OF VARIANTS 1
CHAIR: MARC GREENBLATT

- 9.30 – 9.50 **Development of rules for the interpretation of mismatch repair gene variants based on the 5-tiered IARC classification system**
Maurizio Genuardi
- 9.50 - 10.10 **Using The InSiGHT Consensus Criteria for Classification of Mismatch Repair Gene Variants to Validate New Lines of Evidence for Use in the Classification Process**
Marc Greenblatt
- 10.10 – 10.30 **Progress of the InSiGHT Mismatch Repair Gene Database and Variant Interpretation Committee - Application of Classification Rules and Dissemination of Results**
Finlay Macrae
- 10.30 – 10.50 **Exonic splicing mutations in Mendelian disorders: more prevalent than currently estimated**
Alexandra Martins
- 10.50 – 11.00 **Report from WG02: Assigning Pathogenicity to a Genetic Variant**
Marc Greenblatt

11.00 – 11.40

Poster Session 2 – Even numbers (2, 4, 6 ...)

- Poster presenters for EVEN NUMBERS to stand by their poster

SESSION X

ASSESSMENT OF PATHOGENICITY OF VARIANTS 2
CHAIR: MIKE WATSON

- 11.40 – 12.00 **Variant Server in a box**
Joeri van der Velde
- 12.00 – 12.20 **A powerful literature review: impact index, a gene-based bibliomic pathogenicity score**
Christopher Cassa
- 12.20 – 12.40 **A collaborative database for prospective studies in Lynch syndrome: First results and invitation to join**
Pal Moller
- 12.40 – 13.00 **Is the assessment of pathogenicity of a variant in isolation appropriate for clinical application in the context of multigenic analyses of complex genetic pathology?**
Desiree du Sart

13.00 – 14.30

Lunch break at leisure

SESSION XI

PHENOTYPE AND TRANSLATION TO THE CLINIC CHAIR: ADA HAMOSH

- 14.30 – 14.50 **Clinical Significance of Transcript Alignment Discrepancies**
Reece Hart
- 14.50 – 15.10 **The Curation of Molecular Pathology Cancer Samples**
Kenneth Doig
- 15.10 – 15.30 **VarElect: phenotype-based variation prioritizer in GeneCards**
Gil Stelzer
- 15.30 – 15.50 **Linking Genomic and Clinical Data: The HVPA-BioGrid Experience**
Maureen Turner
- 15.50 – 16.10 **Phenotype terminologies in use for genotype-phenotype databases: need for a standardization**
Ana Rath
- 16.10 – 16.20 **Report from WG06: Disease & Phenotype Descriptions in Gene/Disease Specific Databases**
Peter Robinson
- 16.20 – 16.40 Coffee Break
- 16.40 – 17.30 **Meeting Summary and thoughts**
Garry Cutting
- END HVP 5th biennial meeting**



Friday 23rd May

Advisory Council and International Scientific Advisory Committee Meetings

9.30 – 11.00

Combined HVP Council Meetings

- **Gene/Disease Specific Database Advisory Council Meeting**
- **International Confederation of Countries Advisory Council Meeting**
- **International Scientific Advisory Council**

Salle IV
(all welcome)

11.00 – 11.15

Coffee Break

11.15 – 13.00

Gene/Disease Specific Database Advisory Council Meeting

Salle IV (all welcome)

International Confederation of Countries Advisory Council Meeting

Salle III (all welcome)

MEETING END

