



THE HUMAN VARIOME PROJECT

# Bulletin

## From the Editor

We have been busy preparing for our third Human Variome Project meeting focusing on “Implementation and Integration” issues which will be held at the UNESCO Headquarters in Paris May 10-14, 2010. We already have a number of delegates registered for this meeting so please remember that there are

only 200 places available. If you are planning to attend, please register now to be assured of a place, the earlybird registration ends March 31. We particularly would like proposed or ongoing relevant work to be presented. Please contact the meeting secretariat if you haven't already sent in an abstract

even if you are not able to attend. We will be hosting four satellite meetings on May 10th and we hope you will also be able to attend one of these listed below:

- EMBL-EBI Workshop
- InSiGHT
- NUGO Micronutrient Genomics Project
- HVP Neurogenetics Consortium.

More information on the workshops are on pages 4-5.

We look forward to seeing you in Paris!

Lauren Martin,  
Editor.

### UNESCO Headquarters, Paris



## STOP PRESS—UNESCO PATRONAGE GRANTED OF 3RD HUMAN VARIOME PROJECT MEETING

We are pleased to announce that we have been honored by the granting of UNESCO patronage for our third Human Variome Project meeting. The meeting is co-organised with the Division of Basic and Engineering Sciences, Natural Sciences Sector, UNESCO.

## Human Variome Project

### Special points of interest:

- > HVP Satellite meetings on May 10th.
- > Australian Node of the HVP.
- > HVP Coordinating Office/European Research Exchange
- > UK's DMuDB extending access worldwide

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## Biocurator

The BioPortal team is pleased to announce the release of BioPortal 2.2 (<http://bioportal.bioontology.org/>). Release notes and known issues are listed below.

### New Features

- *Ontology Views*
  - Views in BioPortal are subsets or other derivatives of ontologies in the repository that you can share with the community. You can upload views for any ontology, and review them, add notes, create mappings, and use REST Web services to access them programmatically.
  - A view can also serve as a mechanism to define value sets, which are quite useful in combination with the BioPortal ontology-term selection widget.
  - View generation and storage in BioPortal is the result of collaboration with Dr. Jim Brinkley's group at the University of Washington.
- *NCBO Resource Index*
  - We have initiated automated indexing of the contents of public databases using ontology terms. The indexing is done using the same workflow that drives the previously released Annotator web service. Currently we index the following public databases: Array Express, Biositemaps, caNanoLab, Conserved Domain Database, ClinicalTrials.gov, DrugBank, Gene Expression Omnibus, Online Mendelian Inheritance in Man, PharmGKB, Reactome, ResearchCrossroads (Grant funding database), Stanford Microarray Database, UniProt KB, and WikiPathways. The resulting annotations are accessible for browsing via the Resources tab corresponding to any ontology concept. The annotations can also be accessed programmatically: [http://www.bioontology.org/wiki/index.php/Resource\\_Index](http://www.bioontology.org/wiki/index.php/Resource_Index).
  - If you have recommendations on additional publicly accessible resources to index, let us know at [support@bioontology.org](mailto:support@bioontology.org).
- *Search filter for Ontology Groups and Categories*
  - You can now limit your search to ontologies from a certain group (e.g., OBO Foundry, caBIG) or ontologies in a certain category (e.g., anatomy).

### New REST Web Services

- Services to access ontologies and ontology versions
  - List all Categories
  - List all Groups
  - Download by virtual ontology identifier
- Services to access ontology views and ontology view versions
  - List all Views of all Ontologies (lists the latest version)
  - List all versions for a given View
- Concept services
  - Get all concepts
- Search service – parameter added to enable search within an ontology branch
- Service to access the NCBO Resource Index

See [http://www.bioontology.org/wiki/index.php/BioPortal\\_REST\\_services](http://www.bioontology.org/wiki/index.php/BioPortal_REST_services) for the full list of BioPortal REST Web services.

### New Data

- Mapping data generated by the LOOM algorithm are now in BioPortal (close to 1 million new lexical-based mappings). See <http://www.bioontology.org/wiki/index.php/LOOM> for more details about this tool.
- Selected UMLS ontologies are now available in BioPortal. Email [support@bioontology.org](mailto:support@bioontology.org) to request loading of additional UMLS ontologies.

### Known Issues

- The tree navigation shows 'Too many children' in cases where the number of siblings is greater than 500.

Trish Whetzel, PhD  
Outreach Coordinator, The National Center for Biomedical Ontology  
<http://www.bioontology.org>

## Australian Node of the HVP

The aim of the Australian node of the Human Variome Project is to establish a system to collect and make available information on inherited genetic variations associated with human disease and to put this system into operation.

This project will review existing/available technology and IT system resources and then design and create a data repository called the Australian Human Variome Database (AHVD). The AHVD will provide a single interface to access information on genetic variants characterised by Australian

laboratories and clinics. A service to integrate submission of laboratory and clinical data to the AHVD into the existing workflows of these laboratories and clinics will also be provided.

These two services will mark the commencement of the Australian Node of the Human Variome Project. The ultimate goal of this Project is to create linkages between similar nodes in all countries. The Australian Node can act as a pilot system/model for the establishment of other country nodes.

During the past months an extensive

review of the existing software and systems has been undertaken and we are currently finalizing the IT architecture and specifications template.

The building of the system has now commenced and will be ready for laboratory testing in June 2010.

We have started on both the governance structure and ethical statement for the Australian Node which will assist in the ongoing sustainability and oversight of the project.

The necessary ethics applications have been researched and are underway.

## Publicity of the Human Variome Project

In this reporting period, the Human Variome Project has been publicised at the following meetings:

“Identifying Opportunities to Maximize the Utility of Genomics Research Data through Electronic Health Information Exchange” meeting in Washington, USA, 15 October 2009 (60 at-

tendees). See page 4 for more information.

The Technology in Healthcare Summit 2009, Melbourne, Australia 16-17 November 2009.

International Symposium on Applied Genomics 2009 (ISAG 2009) held in Tokyo, Japan 3-4 December 2009.

Richard Cotton, convenor of the Human Variome Project has been invited to speak at Rede Latino Americana de Genética Humana – Latin American Human Genetics Network (RELAGH) Meeting 2011, Costa Rica, May 11-13, 2011.

**The Australian Human Variome Database (AHVD) “will provide a single interface to access information on genetic variants characterised by Australian laboratories and clinics”**

## Clinical Genomics and Health Information Technology

Richard Cotton participated in a Clinical Genomics Workshop in Washington on 15 October 2009 entitled "Identifying Opportunities To Maximize the Utility of Genomics Research Data Through Electronic Health Information Exchange". The overall goal of this meeting was to enable information exchange

relevant to clinical research and health care applications to support broad needs. Standards and data architectures that support these cross-applications of information were the focus of the work in this workshop. The meeting summary can be found on the HHS Assistant Secretary for Planning and

Evaluation website (<http://aspe.hhs.gov/sp/reports/2009/clingenworkshop/index.shtml>).

The background information and presentation for the workshop have been migrated to a site on the BIG Health Consortium <http://bighealthconsortium.org/initiatives/clinicalgenomics/>.



**HVP Neurogenetics Consortium meeting Honolulu October 19th**

**The HVP Neurogenetics steering committee has now been formed and we already have 115 people from 25 countries interested in this initiative**

## HVP Neurogenetics Consortium

The HVP office assisted Dr. Maria-Jesus Sobrido in obtaining funds (€100,000) from the Universidade de Santiago do Compostela and Xunta de Galicia in Spain for funding Neurogenetic databasing.

This led to the HVP initiating a Neurogenetics Consortium which has been led by Dr. Sobrido who reserved some funding to start this initiative as a satellite meeting at ASHG in Honolulu on October 19th. The meeting proved to be very successful with international speakers

and 80 registrants, the full program can be seen on our website ([www.humanvariomeproject.org/fora/hawaii/Hvp\\_neuro\\_program.pdf](http://www.humanvariomeproject.org/fora/hawaii/Hvp_neuro_program.pdf)). Dick Cotton introduced the HVP to the attendees and Mike Woods from InSiGHT outlined their experience with inherited colon cancer in the HVP/InSiGHT pilot project.

A steering committee has now been formed and we already have 115 people from 25 countries interested in this initiative. A summary of the meeting can be found

online [http://www.humanvariomeproject.org/images/stories/summary\\_neurogenetics\\_honolulu.pdf](http://www.humanvariomeproject.org/images/stories/summary_neurogenetics_honolulu.pdf).

The start of the HVP Neurogenetics Consortium and its progress and projects will be documented at a satellite meeting at our third HVP meeting in Paris as a satellite meeting on May 10th (see <http://www.humanvariomeproject.org/meetings/paris/neuro.html>).

If you are interested in finding out more about this consortium please [email us](#).

## The European Bioinformatics Institute Training Workshop

The European Bioinformatics Institute encompasses genome databases such as Ensembl, the European Genotype Archive (EGA) a repository of genotype experiments including case control, population and family studies (which will be extended to include SNPs and CNV genotypes from array based methods), and the HUGO Gene Nomenclature Committee amongst other large databanks. We

are part of the 1000 Genomes project which aims to create the most detailed and medically useful picture of human genetic variation and Gen2Phen an EU funded project which aims to unify human and model organism genetic variation databases, linking resources into other biomedical knowledge sources amongst other relevant efforts to encapsulate human variation.

Most modules of this workshop consist of a presentation, followed by the opportunity to do exercises. Participants are encouraged to bring problems/questions about their research to try to tackle these during the workshop using Ensembl.

For more information about this Workshop including the programme, please see <http://www.humanvariomeproject.org/meetings/paris/ebi.html>.

## International Society for Gastrointestinal Hereditary Tumours

The International Society for Gastrointestinal Hereditary Tumours (InSiGHT) is the peak organization representing health professionals committed to the care of individuals and their families with inheritable gastrointestinal cancers.

In 2010, InSiGHT will have a special meeting with the Human Variome Planning Committee in the UNESCO Building in Paris on May 10th. The meeting will build on the initiatives founded at the 2009 meeting in Dusseldorf between InSiGHT,

the HVP and the National Institutes of Health Colon Family Register.

Please see <http://www.humanvariomeproject.org/meetings/paris/insight.html> for more information on this satellite meeting.



**HVP Satellite meetings to be held at UNESCO Headquarters, Paris**

## The Micronutrient Genomics Project (MGP) Workshop

The Micronutrient Genomics Project (MGP) is a community driven project facilitating the development of systematic capture, storage, management, analyses, and dissemination of data and knowledge generated by biological studies focused on micronutrient – genome interactions. MGP's workshop is the third in a series which aims to demonstrate the potential, elucidate the strategy, establish the necessary multidisciplinary links, build the organizational structures and develop the knowledge base. This MGP workshop is being held at UNESCO to foster collaborations with the Human Variome Project (HVP). The HVP and MGP share a common interest in analyzing, characterizing, and databasing genetic variation in the world's populations. The MGP is focusing on micronutrients since they influence multiple metabolic pathways and optimum micronutrient supply is important for maintenance of homeostasis in metabolism and maintaining health throughout the lifecycle.

This MGP Workshop is sponsored by NuGO and the Division of Personalized Nutrition and Medicine of the US FDA/National Center for Toxicological Research. More information can be seen at <http://www.humanvariomeproject.org/meetings/paris/nugo.html>.

## Papers of interest

Pruitt KD, Harrow J, Harte RA, Wallin C, Diekhans M, Maglott DR, Searle S, Farrell CM, Loveland JE, Ruef BJ and others. 2009. The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. *Genome Res* 19 (7):1316-23.

Gao S, Zhang N, Duan GY, Yang Z, Ruan JS, Zhang T. Prediction of function changes associated with single-point protein mutations using support vector machines (SVMs). *Hum Mutat.* Aug 2009;30(8):1161-1166.

Philp AR, Jin M, Li S, et al. Predicting the pathogenicity of RPE65 mutations. *Hum Mutat.* Aug 2009;30(8):1183-1188.

Calabrese R, Capriotti E, Fariselli P, Martelli PL, Casadio R. Functional annotations improve the predictive score of human disease-related mutations in proteins. *Hum Mutat.* Aug 2009;30(8):1237-1244.

Tiffin N, Andrade-Navarro MA, Perez-Iratxeta C. Linking genes to diseases: it's all in the data. *Genome Med.* Aug 7 2009;1 (8):77.

Paterson T, Law A. An XML transfer schema for exchange of ge-

nomomic and genetic mapping data: implementation as a web service in a Taverna workflow. *BMC Bioinformatics.* Aug 14 2009;10(1):252.

Biesecker LG. A silent majority? *Am J Med Genet A.* Aug 2009;149A(8):1623.

Birney E, Hudson TJ, Green ED, Gunter C, Eddy S, Rogers J, Harris JR, Ehrlich SD, Apweiler R, Austin CP and others. 2009. Prepublication data sharing. *Nature* 461(7261):168-70.

Kohler S, Schulz MH, Krawitz P, Bauer S, Dolken S, Ott CE, Mundlos C, Horn D, Mundlos S, Robinson PN. 2009. Clinical diagnostics in human genetics with semantic similarity searches in ontologies. *Am J Hum Genet* 85(4):457-64.

Check Hayden E. 2009. Genomics shifts focus to rare diseases. *Nature* 461(7263):458.

Cotton RG. 2009. Collection of variation causing disease--the Human Variome Project. *Hum Genomics* 3(4):301-3.

Thorisson GA. 2009. Accreditation and attribution in data sharing. *Nat Biotechnol* 27 (11):984-5.

Practice guidelines for the Interpretation and Reporting of Unclassified Variants (UVs) in

Clinical Molecular Genetics (<http://cmgs.org/BPGs/pdfs%20current%20bpgs/UV%20GUIDELINES%20ratified.pdf>).

Yu, W., et al., Phenopedia and Genopedia: disease-centered and gene-centered views of the evolving knowledge of human genetic associations. *Bioinformatics*, 2010. **26**(1): p. 145-6.

Credit where credit is due. *Nature*, 2009. **462** (7275): p. 825.

Cotton, R.G., Al Aqeel, A. I., Al-Mulla, F., Carrera, P., Claustres, M., Ekong, R., Hyland, V. J., Macrae, F. A., Marafie, M. J., Paalman, M. H., Patrinos, G. P., Qi, M., Ramesar, R. S., Scott, R. J., Sijmons, R. H., Sobrido, M. J., Vihinen, M. Capturing all disease-causing mutations for clinical and research use: toward an effortless system for the Human Variome Project. *Genet Med*, 2009. **11**(12): p. 843-9.

Abdulla, M.A., et al., *Mapping human genetic diversity in Asia*. *Science*, 2009. **326**(5959): p. 1541-5.

An article on the HVP appeared in the September 2009 Issue of *Muy Interesante*, a Spanish language magazine. Please [contact us](#) if you would like a copy.

A way  
"Capturing  
all disease-  
causing  
mutations  
for clinical  
and  
research  
use" can be  
seen in  
*Genet Med*,  
2009. **11**(12):  
p. 843-9

## Marie Curie International Research Staff Exchange Scheme (IRSES)

If anyone is interested in working in the HVP's Coordinating Office, please read this Exchange Scheme.

The European Commission has published a new call for the Marie Curie International Research Staff Exchange Scheme (IRSES) targeting projects starting at the end of 2010. The International Research Staff Exchange Scheme aims at strengthening research partner-

ships through short staff exchanges between 2 or more European research organisations and organisations from countries like Australia, Canada, NZ, USA, etc and for a period of 24-48 months. Individual staff exchanges will not exceed 12 months.

These actions have a bottom-up approach, and research fields are chosen freely by the applicants. Since the start of the pro-

gram in 2008, 29 selected projects involved Australian teams.

Due: Thursday 25<sup>th</sup> March 2010

Funding Organisation: [European Commission](#)

Url: [cordis.europa.eu/fp7/dc/?fuseaction=UserSite.PeopleDetailsCallPage&call\\_id=245](http://cordis.europa.eu/fp7/dc/?fuseaction=UserSite.PeopleDetailsCallPage&call_id=245).

**The lead participant or coordinator must be from Europe.**



HVP Coordinating office  
Melbourne, Australia

## UK's Diagnostic Mutation Database extends access to geneticists worldwide

The United Kingdom's Diagnostic Mutation Database (DMuDB), a central repository for sharing gene variant data between UK diagnostic genetics laboratories, was established by the National Genetics Reference Laboratory (NGRL) Manchester in 2002.

DMuDB allows UK scientists working within the National Health Service to determine the significance of variants not previously identified by their own laboratory. Now, the DMuDB is launching a new enquiry service

that extends the knowledge of DMuDB to geneticists throughout the world. The DMuDB has established a secure web page through which international geneticists with "a legitimate interest" are able to request information on a particular variant. Should the requested variant be present in DMuDB, inquirers will receive contact details for the relevant National Health Service laboratory so that they can establish contact. Nearly 6,000 records for 83 genes are currently

recorded in DMuDB, containing over 12,000 individual variants. Well represented genes include *MLH1*, *MSH2*, *MSH6*, *APC*, *CFTR*, *MEN1*, *NF1*, *NF2*, *RPGR* and *TSC2*. For further information see [http://www.ngrl.org.uk/Manchester/dmudb\\_query\\_launch.html](http://www.ngrl.org.uk/Manchester/dmudb_query_launch.html)

Extracted from OrphaNews Europe 28 October 2009  
<http://www.orpha.net/actor/Euro-paNews/2009/091028.html>.

**"DMuDB allows UK scientists working within the National Health Service to determine the significance of variants not previously identified by their own laboratory"**



## THE HUMAN VARIOME PROJECT

### Vision

The Human Variome Project will establish systems to collect and make available information on all genetic variations associated with human disease.

### Mission

The Human Variome Project is dedicated to improving health outcomes by facilitating the unification of data on human genetic variation and its impact on human health. It supports the use of human variation information in clinical & research environments across the world.

### Values

- Free public access to information
- Inclusive of all countries, peoples and disciplines
- Provision of appropriate credit and acknowledgement
- Respect ethical, legal and social issues

## Human Variome Project

Contact: [Prof. Richard G.H. Cotton](#)

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See our website <http://www.humanvariomeproject.org>

## Databases currently collecting worldwide

Please contact the curators if you have data to contribute

*Cystic Fibrosis (CFTR)*—[G. Cutting](#)

*Fanconi Anaemia*—[A. Auerbach](#)

*HNPCC genes*—[Finlay Macrae](#)

## Meetings of interest

The Human Variome Project - Implementation and Integration Meeting, 10-14 May 2010, UNESCO Headquarters, Paris, France. <http://www.humanvariomeproject.org/meetings/paris>. Satellite meetings on May 10th can be seen at <http://www.humanvariomeproject.org/meetings/paris/satellites.html>

Human Genome Variation Society "Informatics for Next Generation Sequencing" 18 May 2010  
Le Corum, Montpellier, France (satellite to HUGO) <http://www.hgvs.org/mont/>

8th Australasian Mutation Detection Meeting  
3rd- 6th August 2010  
Cradle Mountain Chateau, Cradle Mountain, Tasmania <http://www.mutationdetection.org/>

Workshop: The Human Variome Project, to be held during the International Conference on Nutrigenomics (INCON), <http://www.nutrigenomicabrasil.org/congresso/ingles/index.html>, in Guarujá, SP, Brazil, September 26-29, 2010.