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***Human Genome Variation* database launches**

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Today marks the launch of a fully searchable open access database of human genome variants. The data accompanies Data Reports (a new article type) published in the open access [Human Genome Variation](#) journal, providing a valuable resource for clinicians and researchers.

The database allows users to search and filter genomic data by different variables, including specific disease, gene, population or region. Collating data from anonymised patients across the globe will have positive implications for clinicians and researchers trying to learn more about disease and human health. All data is licensed under a CCo waiver.

The database will be managed by *Human Genome Variation* and is powered by [Figshare](#), a technology company who work with publishers and institutions to help manage and enhance their research data. *Human Genome Variation*, a new open access journal from Nature Publishing Group, publishes its first Data Reports this month. Data Reports are standardized reports about genomic variation and variability, especially in relation to disease.

The fact that both the data and the journal articles are open access will facilitate data and text mining and large-scale systematic analysis, which is particularly important in this field, as most clinicians may only see one or two examples of any particular genome variant in their lifetime.

Professor Katsushi Tokunaga, Editor-In-Chief of *Human Genome Variation* said: "It is early days for the HGV database, but our hope that our partnership between *Human Genome Variation* and Figshare will mature and grow into an important resource for the genomics community, enabling researchers, clinicians, genetic counsellors and all those interested in genomics, access to genetic data and the resulting findings."

Nature Publishing Group partnered with Figshare on this project to utilise their experience of creating innovative digital academic publishing solutions. Mark Hahnel the founder of Figshare said "We're proud to be partnering with Nature Publishing Group on this project. We are always looking for new ways to open up and improve the dissemination of scientific content and we're really excited about the impact the HGV database will have on the genomic community."

Human Genome Variation is an online-only, open access journal launched in partnership with Japan Society of Human Genetics that contains articles and reports about variation and variability in human genomes and the consequences, implications and future impacts for the study of human genomics. An important and innovative feature of the journal is the Data Report article; these are short reports about human genome variation and variability which describe disease-causing variation and/or their frequencies. In addition, Data Reports can describe and analyse human multifactorial disease associated variations and/or their frequencies. Authors publishing in HGV are offered a choice of Creative Commons licenses.

The APC for publishing a Data Report in *Human Genome Variation* is 1000GBP (with waivers available in 2014). Authors are invited to deposit their dataset in the database at no extra cost, although they are welcome to deposit their dataset in other repositories too.

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About Figshare

Figshare was the brainchild of Mark Hahnel who, whilst studying for his PhD in stem cell biology at Imperial College, London became frustrated at not being able to publish ALL his scientific research. Figshare is the research data management tool for researchers, academic institutions and publishers. The platform allows any file format to be made visualisable in the browser so that figures, datasets, media, papers, posters, presentations and filesets can be disseminated in a way that the traditional scholarly publishing model does not allow. Figshare is a portfolio company of Digital Science. For more information, visit figshare.com and www.digital-science.com

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