European Variation Archive at EMBL-EBI: webinar

Hannah McLaren [1], Gary Saunders [2]

- DNA & RNA
- Beginner
- 0.5 hour

EVA: A database of all types of genetic variation data from all species

The European Variation Archive (EVA) is a primary open repository for archiving, accessioning, and distributing genomic variation in any species. Since launching in 2014, the EVA and sister project DGVa have archived approximately 700 million unique variants across 351 studies and 46 species including cow, chicken, goat, pig and sheep.

A key function of the EVA is to provide long term, stable identifiers so that studies and variants can be referenced in publications, cross-linked between databases and integrated with successive reference genome builds. This webinar will include the latest information on the EVA’s responsibility for issuing and maintaining variant identifiers (rs#) for non-human species and the progress of importing data from dbSNP.

For those new to the resource we will demonstrate what data is available and how to access it via the website and REST API. We will also clarify the data requirements for submission.

This webinar is an update to a webinar recorded by Gary Saunders in 2016.

This webinar was recorded on 5 September 2018. It is best viewed in full screen mode using Google Chrome. The slides from the webinar can be downloaded below.

See the EMBL-EBI training pages for a list of upcoming webinars [3].

Learning objectives:

- List the key functions of the EVA resource
- Discover how to access variation data at EVA through the website and REST API
- Outline the submission process and data requirements
- Provide latest updates on the dbSNP import and generation of rs IDs.

Your feedback

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Contributors
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Genetic Variation Scientific Curator - Paschall team: Variation

Gary Saunders is an EBI curator of the European Variation Archive and related resources: the Database of Genomics Variants archive and the European Genome-phenome Archive. It is Gary's responsibility to manage the data within these resource(s) to ensure accuracy, clarity and discoverability. Previous to this position, Gary was a curator of the GENCODE project, which provides the gene set for the Ensembl genome browser.

Gary moved into curation following the completion of his PhD at the University of Glasgow, where he employed a variety of phylogenomic and bioinformatic methods to investigate drug resistance in nematode parasites of human and livestock importance. ORCID iD: 0000-0002-7468-0008

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[1] https://www.ebi.ac.uk/training/online/trainers/hannahm_18904
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