European Variation Archive at EMBL-EBI: webinar

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- DNA & RNA
- Beginner
- 0.5 hour

Variant submission and accessioning at the European Variation Archive

The European Variation Archive (EVA) is a primary open repository for archiving, accessioning, and distributing genome variation including single nucleotide variants, short insertions and deletions (indels), and larger structural variants (SVs) in any species. The EVA is in the process of releasing the first dbSNP data release which consists of RS ID-containing VCF files for each non-human species available in dbSNP. This webinar will provide an overview of the European Variation Archive including data ingestion, consumption, and how you can access and utilise dbSNP RS release batch files.

This webinar was recorded on 4 September 2019. It replaces previous webinars recorded in 2018 [2] and 2016 [3]. 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 [4].

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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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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