Want easy analysis of your own variant calls? The Ensembl Variant Effect Predictor (VEP) allows you to annotate variants with the genes and regulatory features they hit and what effect they have on them. It can also tell you if your variant is known or novel, and give you more information about known variants, such as population frequencies. You can use data from the VEP to prioritise variants from GWAS and whole variant calling studies, or from smaller scale single gene sequencing.

This webinar will guide you through using the easy web interface for the VEP - suitable for annotating small numbers of variants, and using the standalone script - suitable for fast analysis of genome-wide variant calls. Learning objectives:

- Discuss what the Ensembl VEP is and when you can use it
- Explore the Ensembl VEP interface

Your feedback

Please tell us what you thought about this webinar. Your feedback is invaluable and helps us to improve our courses and thus enhance your learning experience.

Contributors

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