

Connecting diagnostic labs: Cafe Variome and DNA sequencing software

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There is a considerable need and desire for diagnostic labs to be able to check each other's databases for the presence of mutations they observe in their own patients. This is countered by the understandable reluctance and impracticability of sharing the content of each group's database with other labs, or indeed the world.

Cafe Variome core concept

Public API

Laboratory personnel can use "Cafe Variome-enabled" mutation interpretation software to push variant data to Cafe Variome

Other sources of variants are advertised and made discoverable via Cafe Variome

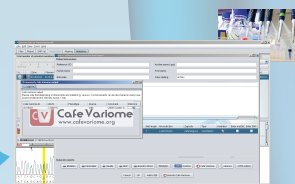


Open discovery of the existence of data through Cafe Variome Portal



End users can seek access to data under one of three models:

- openAccess**
Unrestricted access for anyone
- restrictedAccess**
Either pre-approved access for specific groups or access requested via automated email to the data owner
- linkedAccess**
Linking to source of variant to obtain full record

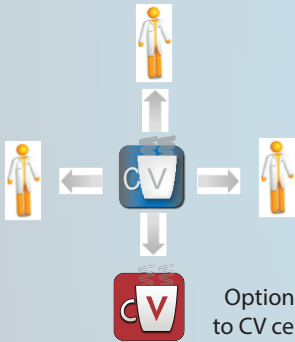


Lab personnel can use "Cafe Variome-enabled" software to query directly Cafe Variome for variants detected by the software

Cafe Variome for Rare Disease Networks

Use Cafe Variome to share variants between private networks of laboratories or groups.

Intuitive admin interface and sharing dashboard gives you fine grained access control over variants, sources, users and groups



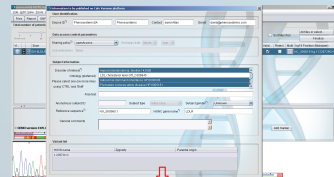
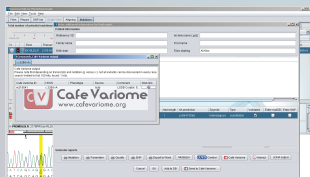
Installs can be hosted by the Cafe Variome team or on your own servers.

API use case examples

Capillary DNA sequencing

Checking a Cafe Variome instance for information on variants detected in a patient, using Genesearch.

Publish the variants on your local Cafe Variome instance or on the public instance. Annotate using HPO and OMIM terms



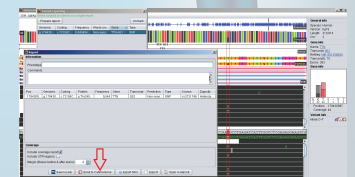
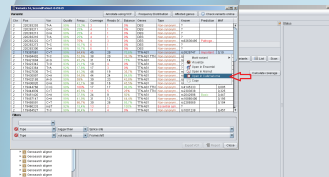
Query simultaneously all sources available in the public instance (dbSNP, HGMD, LSDBs,...) through federation, query own private data as well.

You control access rights as well as amount of details to be published. For fine grained access control use the CV control panels.

NGS sequencing

Looking up a Cafe Variome instance for information on variants detected in a patient, using GenesearchNGS.

Publish the variants on your local Cafe Variome instance or on the public instance.



Opens the Cafe Variome web page on the genomic position selected, presenting all available sources.

You control access rights as well as amount of details to be published. For fine grained access control use the CV control panels.



www.CafeVariome.org

