



VARIANT INTERPRETATION
FIND ANSWERS FASTER



VarSome

The Global Genomics Community

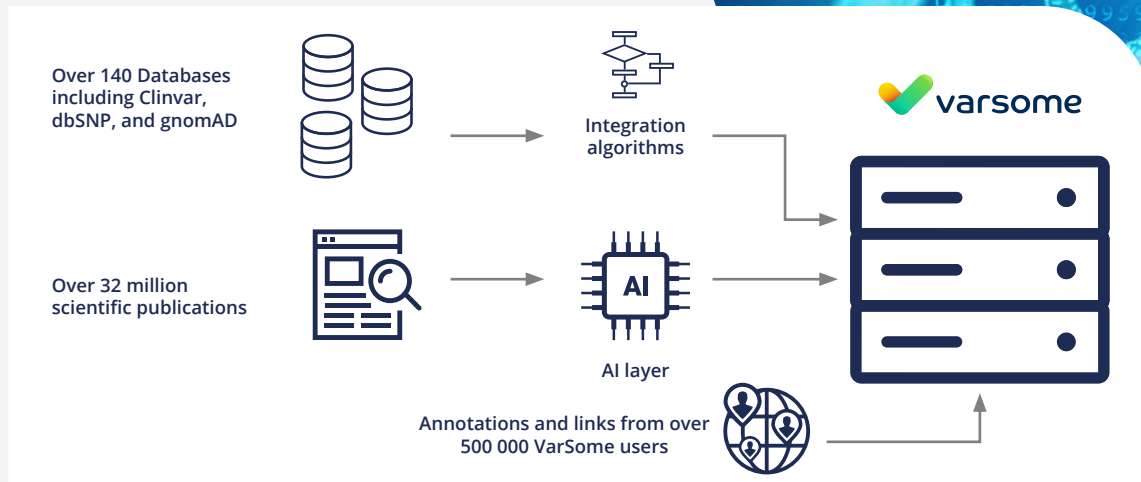


VarSome
used in
over
150
countries
across 6
continents

VarSome compliance and certifications

CE-IVD, HIPAA & GDPR Compliance, Hébergeur de Données de Santé Compliance, ISO 13485 (Quality Management Systems for Medical Devices), ISO 27001 (Information Security Management), IEC 62304 (Software Life Cycle Processes for Medical Devices), AgID Compliance.

What is VarSome



Your Variant Interpretation Engine

VarSome maintains, harmonizes, and integrates over 140 genomic databases and over 32 million publications to give you the most comprehensive variant interpretation engine there is. The complete list of data sources can be viewed at <https://varsome.com/datasources>.

VarSome's Network Effect

Over 500 000 users around the world add variant classifications, link publications, and provide additional annotation.

Industry-Leading Variant Classification

Cited in over 2 300 peer-reviewed publications, VarSome's proprietary ACMG*, AMP**, and CNV classifiers apply industry standard variant interpretation guidelines to help you understand your variants. Unlike other static platforms, our classifiers are dynamic and work in real-time making it possible to classify even novel variants. To ensure high levels of confidence, VarSome's classifiers provide transparency on evidence used and rules triggered as well as giving users the ability to adjust rule weighting.

Find Answers Faster with VarSome Professional

Search



Deep dive into genes and variants of interest using the VarSome search engine and classification tools.

Analyze



Upload your FASTQ and VCF files applying VarSome's best-in-class annotation to help you find variants of interest and solve your cases faster.

Code



Integrate the VarSome database and classifiers into existing in-house pipelines through cloud-based or on-premises installations.

*<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4544753/>

**<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5707196/>



A Complete Solution



VarSome Professional is our full suite of variant interpretation tools for labs analyzing NGS data in a research or clinical environment.



Your Variant Interpretation Engine

Whether you need to look up individual genes and variants, annotate your NGS files, or supplement in-house pipelines, VarSome Professional provides everything you need to Search, Analyze, and Code using our industry leading variant classification tools.

Customize and Control Your VarSome Experience

Every lab is different and has different requirements. VarSome Professional gives you the flexibility to work across the full suite of variant interpretation tools with a price plan you control based on your monthly usage.

Keeping Your Data Secure

We take data privacy and security very seriously, which is why we are HIPPA and GDPR compliant, as well as CE-IVD, ISO 27001 and ISO 13485 certified. However, we know that every organization is subject to different obligations when it comes to safeguarding data. This is why we offer on-premises installations upon request to ensure data protection compliance.

Looking After You Is Our Priority

We look after all of our VarSome users with a superbly responsive and helpful support team to ensure everything works perfectly for you.

As a VarSome Professional customer, you will also have your own personal Client Success Manager to make sure your experience is always first rate and to make sure we keep developing our tools around your needs.

Get Started Today

Contact us today at sales@varsome.com to arrange a free consultation.

Search



Who is it for: **Researchers in need of individual gene or variant lookups.**

VarSome Premium gives users powerful access to the VarSome search engine to query and work with the VarSome database at the variant and gene level. Users can search by HGVS nomenclature, rsID, gene name, transcript symbol or genome location. However, the VarSome database contains much more than just variant frequencies. Our complete search functionality supports word searches allowing you to find publications, diseases, phenotypes, genes, ClinVar & UniProt variants, and user comments.



Classifiers

The VarSome database powers the classification algorithms that apply ACMG* and AMP** interpretation guidelines to germline, somatic, and copy number variants. Every result provides clear natural language explanations as to why specific rules were triggered and the accompanying evidence. Similarly, a full explanation is provided when threshold criteria have not been met. As the rules were originally designed to be applied by clinicians with the benefit of case knowledge, VarSome allows users to adjust the weighting of rules to better fit their case.

VarSome and ClinVar

ClinVar links directly to VarSome result pages. Similarly, you can make ClinVar Submissions directly from VarSome.

Community

Over 500 000 users have visited VarSome.com, adding comments, linking publications, and providing advice. As many variants are rarely seen by any one individual, the VarSome Community ensures that knowledge and experience is shared. Users around the world have connected via VarSome to share expertise.



With access to over 140 data sources, and clear and transparent classification tools, VarSome is the most comprehensive and robust variant interpretation platform for human genome data.

*<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4544753/>

**<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5707196/>



Analyze



Who is it for: Labs generating NGS data.

VarSome Clinical is a CE IVD-certified and HIPAA-compliant platform that brings the power of VarSome to your Illumina and BGI FASTQs and any VCFs.

As genomic approaches have become more widespread in research and in the clinic, there are several reasons why VarSome Clinical is a crucial addition to your analysis pipeline.

Speed

VarSome Clinical employs dynamic and fully customizable algorithmic filters. This means that you can reduce your variant load dramatically to just your variants of interest – whether they be pathogenic variants, gene-list based, compound heterozygous, variants in imprinted genes or even *de novo* variants. VarSome Clinical's algorithmic filters put you and your workflow in control.

Interpret Novel Variants

VarSome applies ACMG* and AMP** interpretation guidelines to germline, somatic, and copy number variants. These are applied dynamically, rather than being looked up from a database as with other systems. This means that every variant will have the full weight of the VarSome database applied to it by the selected classifier algorithm to provide a suggested level of pathogenicity.

Family Analysis

VarSome Clinical's Trio analysis takes advantage of parental information to aid in diagnosing children with rare disease. Our Trio filters, combined with our variant classification filter, makes pediatric whole genomes and exomes much easier to interpret.

Illumina BaseSpace

You can integrate your Illumina BaseSpace account with VarSome Clinical for easy direct uploads of your FASTQs and VCFs.

Customizable Reports

VarSome Clinical recognizes that every lab has its own way of doing things. For that reason, reports are fully customizable to include only the information you need and your own branding.

Your Data; Your Rules

Although we are HIPAA and GDPR compliant, CE-IVD and ISO 27001 and ISO 13485 certified, we recognize that every organization has different obligations when it comes to safeguarding data. If your country does not allow data to leave its borders, we offer an on-premises installation of VarSome Clinical to ensure data protection compliance.



Code



Who is it for: Bioinformatics groups needing to integrate the VarSome database and classifiers into existing inhouse pipelines.

Free Your Team

VarSome was designed to support all types of users. As the field of genomics matures, we know that many groups have already built robust analysis pipelines. In these instances, maintaining databases can be a costly and time-consuming endeavor. VarSome API is the perfect solution for these groups. By connecting to our API, you can free your team to focus on analysis rather than database management.

Use The Best

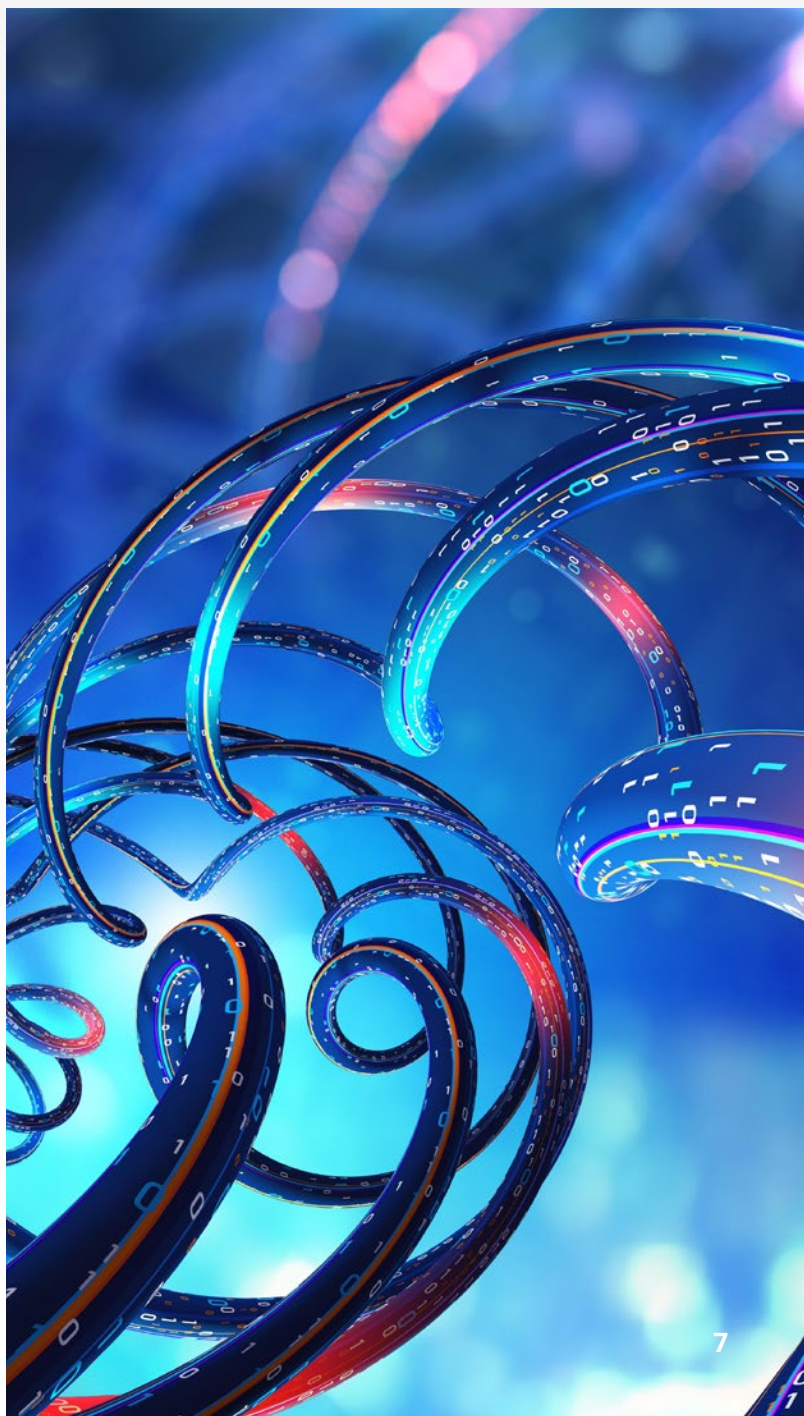
The way we apply ACMG* and AMP** guidelines to classify pathogenicity of germline, somatic, and copy number variants makes it ideally suited to exomes and whole genomes. As a result, clinical labs, academic and industry research labs, and even other analysis platforms have accessed the VarSome API to integrate our industry-leading variant classifiers.

Easy To Use

The API has been designed to be as simple as possible. A REST API is provided and data requests are returned as JSON. This makes it ideal to integrate into Python, R, Perl, Java, or any other programming language.

Secure and Private

Although we are HIPPA and GDPR compliant, CE-IVD and ISO 27001 and ISO 13485 certified, we recognize that every organization has different obligations when it comes to safeguarding data and metadata. For the highest levels of privacy, we offer the installation of the VarSome API on a dedicated server that we will update in line with our own API servers.



Getting Started with VarSome

Get in touch with our team at sales@varsome.com for a free consultation. Our team will work with you to define your variant interpretation needs and help you to test VarSome in your workflow.

Partnerships Opportunities

If you are a technology developer interested in partnering to further develop an opportunity with VarSome, or becoming a distribution partner, contact our Head of Strategic Alliances Tomáš Kučera at tomas.kucera@varsome.com



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