

CLINVITAE: an open database of clinically observed variants, and other open source tools from Invitae

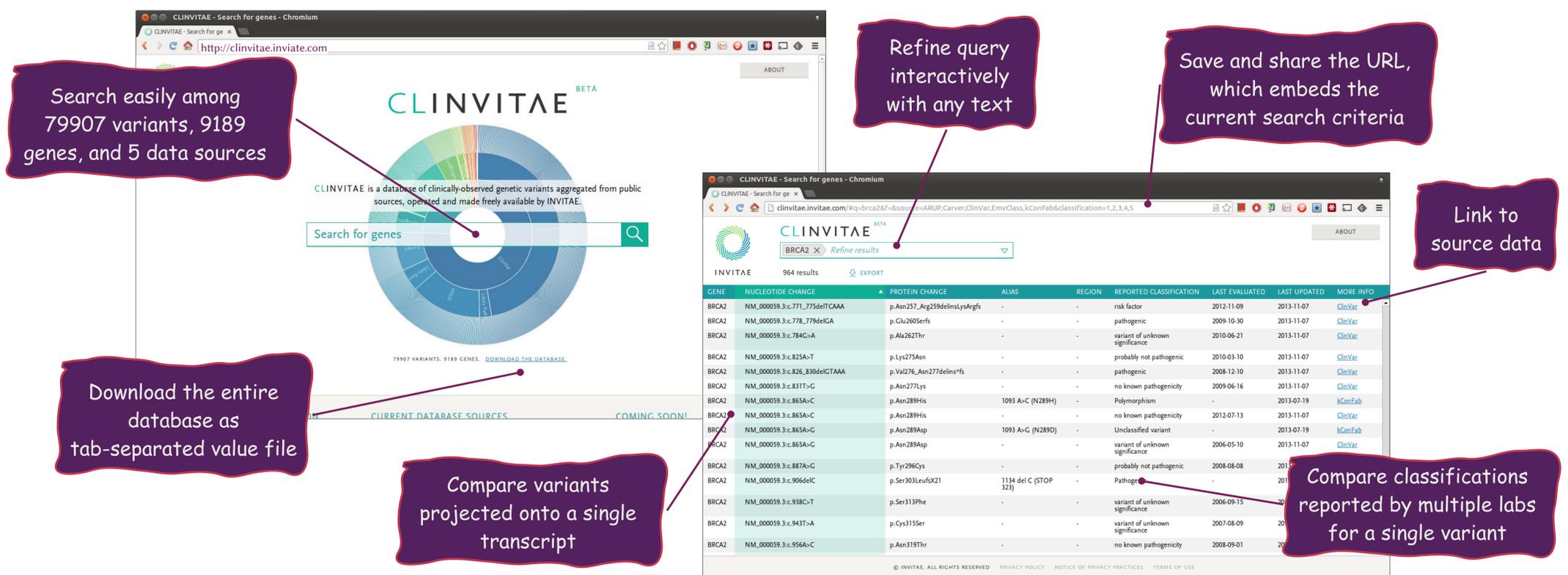
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Variants of uncertain significance (VUS) are routinely identified in clinical and research sequencing projects. Assessing these variants for clinical relevance presents a significant analysis burden for clinical geneticists and genetic counselors.

CLINVITAE is a free, comprehensive, and easy-to-use resource that aggregates variants and reported pathogenicity. It is especially focused on variants not currently in ClinVar.

The current beta release contains 79,907 variants in 9,189 genes from 5 sources. A new version of CLINVITAE with new sources, refreshed data, and additional features is underway.

CLINVITAE was built using our HGVS and UTA variant mapping tools, which are described at the bottom of this poster.



Search easily among 79907 variants, 9189 genes, and 5 data sources

Refine query interactively with any text

Save and share the URL, which embeds the current search criteria

Link to source data

Download the entire database as tab-separated value file

Compare variants projected onto a single transcript

Compare classifications reported by multiple labs for a single variant

GENE	NUCLEOTIDE CHANGE	PROTEIN CHANGE	ALIAS	REGION	REPORTED CLASSIFICATION	LAST EVALUATED	LAST UPDATED	MORE INFO
BRCA2	NM_000059.3:c.771_775delTCAAA	p.Asn257_Arg259delinsLysArgfs	-	-	risk factor	2012-11-09	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.778_779delTGA	p.Glu260Serfs	-	-	pathogenic	2009-10-30	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.784G>A	p.Ala262Thr	-	-	variant of unknown significance	2010-06-21	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.825A>T	p.Lys275Asn	-	-	probably not pathogenic	2010-03-10	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.826_830delGTAAA	p.Val276_Asn277delins*fs	-	-	pathogenic	2008-12-10	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.831T>G	p.Asn277Lys	-	-	no known pathogenicity	2009-06-16	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.865A>C	p.Asn289His	1093 A>C (N289H)	-	Polymorphism	-	2013-07-19	iConFab
BRCA2	NM_000059.3:c.865A>C	p.Asn289His	-	-	no known pathogenicity	2012-07-13	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.865A>G	p.Asn289Asp	1093 A>G (N289D)	-	Unclassified variant	-	2013-07-19	iConFab
BRCA2	NM_000059.3:c.865A>G	p.Asn289Asp	-	-	variant of unknown significance	2006-05-10	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.887A>G	p.Tyr296Cys	-	-	probably not pathogenic	2008-08-08	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.906delC	p.Ser303LeufsX21	1134 del C (STOP 323)	-	Pathogene	-	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.938C>T	p.Ser313Phe	-	-	variant of unknown significance	2006-09-15	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.943T>A	p.Cys315Ser	-	-	variant of unknown significance	2007-08-09	2013-11-07	ClinVar
BRCA2	NM_000059.3:c.956A>C	p.Asn319Thr	-	-	no known pathogenicity	2008-09-01	2013-11-07	ClinVar

Other open source tools from Invitae

HGVS Parsing, Formatting, and Mapping in Python

<http://bitbucket.org/invitae/hgvs>

Genome, transcript, and protein sequence variants are typically reported using recommendations provided by the Human Genome Variation Society (HGVS) [1]. The complexity of this standard makes it difficult to use in software.

We have developed a easy-to-use and freely-available Python library for parsing, representing, formatting, and mapping variants between genome, transcript, and protein sequences. The current implementation handles most of the standard for precisely defined sequence variants.

[1] <http://www.hgvs.org/mutnomen/>

```

In [1]: import bdi.sources.uta0_pg
import hgvs.hgvsmapper
import hgvs.parser

In [2]: bdi = bdi.sources.uta0_pg.UTA0()
hgvsmapper = hgvs.hgvsmapper.HGVSMapper(bdi)
hgvsparser = hgvs.parser.Parser()

In [3]: var_c1 = hgvsparser.parse_hgvs_variant('NM_001261456.1:c.1762A>G')
var_p1 = hgvsmapper.hgvs_c_to_hgvs_p(var_c1, None)
var_c1, var_p1

Out[3]: (Variant(ac=NM_001261456.1, type=c, posedit=1762A>G),
Variant(ac=NP_001248385.1, type=p, posedit=Met588Val))

In [4]: var_g = hgvsmapper.hgvs_c_to_hgvs_g(var_c1, 'GRCh37.p10')
var_g

Out[4]: Variant(ac=NC_008001.10, type=g, posedit=166793560A>G)

In [5]: txs = bdi.get_tx_for_gene('LY9')
len(txs)
[ tx['ac'] for tx in txs ]

Out[5]: ['NM_002348.3', 'NM_001261456.1', 'NM_001261457.1', 'NM_001033667.2']

In [6]: var_c2 = hgvsmapper.hgvs_g_to_hgvs_c(var_g, 'NM_001261457.1')
var_p2 = hgvsmapper.hgvs_c_to_hgvs_p(var_c2, None)
var_c2, var_p2

Out[6]: (Variant(ac=NM_001261457.1, type=c, posedit=1534A>G),
Variant(ac=NP_001248386.1, type=p, posedit=Met512Val))

```

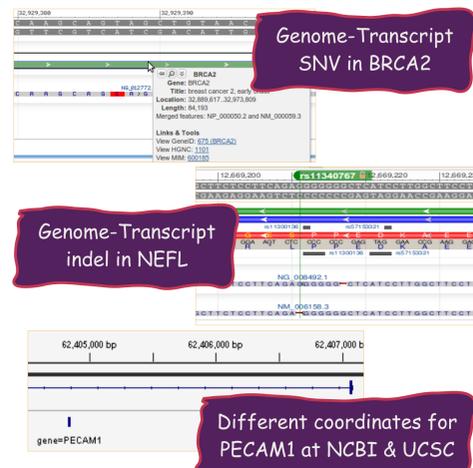
UTA: The Universal Transcript Archive

<http://bitbucket.org/invitae/uta>

PostgreSQL: uta.invitae.com:5432, [uta_public/uta_public](http://uta_public.invitae.com:5432)

Transcripts are the lens through which variants are reported and interpreted. Having a consistent, shared view of transcripts is essential to accurately inferring the clinical significance of sequence variants.

UTA provides the data necessary to map variants between genome assemblies and transcripts, and enables "liftover" between pairs of transcripts via a common reference assembly. The upcoming UTA release will identify alignment discrepancies across sources in order to identify regions where interpretation may be ambiguous.



Illuminate: shedding light on Illumina sequencing metrics

<http://bitbucket.org/invitae/illuminate>

Illuminate is a Python library that provides programmatic access to metadata and metrics from Illumina sequencers.

Illuminate provides access to every raw data point the Illumina sequencers collect during their runs, while streamlining delivery of the most commonly desired attributes like mean cluster density, q-score distribution, and indexing characteristics.

Illuminate enables monitoring of in-progress sequencing runs, aggregation of metrics for quality control, and interactive analysis via the Python pandas package.

```

In [1]: from illuminate import InteropDataset

In [2]: ID = InteropDataset('/Users/nthmost/projects/bitbuo

In [3]: QM = ID.QualityMetrics()

In [4]: print "Q Score HeatMap Across All Reads"
QM.idf.sum().plot()

Out[4]: <matplotlib.axes.AxesSubplot at 0x108c49e10>

In [8]: print "% >= Q30 Per Read"
print QM

% >= Q30 Per Read
Read 1: 92.598490
Read 2: 92.008049 (Index)
Read 3: 86.113045

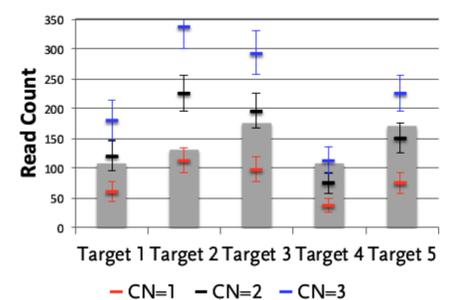
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CNVitae: Accurate detection of small and large copy number events from targeted next-generation sequence data

Coming Soon!

CNVitae is designed to detect single-exon CNVs as well as larger regions from next-generation sequence data. Its algorithm is based on a statistical model for read counts and employs model-based segmentation algorithms optimized for use with sparsely distributed and highly variable targets across the genome.

This framework estimates the most likely copy number for all segments, and, critically for clinical use, each called segment is assigned a robust quality score indicating confidence in the copy number determination.



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ASHG 2013 CNVite Poster
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