Received: 17 June 2019 | Accepted: 27 June 2019

DOI: 10.1002/humu.23858

SPECIAL ARTICLE

Human Mutation HGVS HUMAN GENOME VARIATION SOCIETY WILEY

VIPdb, a genetic Variant Impact Predictor Database

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Funding information
NIH, Grant/Award Numbers: U41 HG007346, R13 HG006650; TATA Consultancy Services Ltd.

Abstract

Genome sequencing identifies vast number of genetic variants. Predicting these variants' molecular and clinical effects is one of the preeminent challenges in human genetics. Accurate prediction of the impact of genetic variants improves our understanding of how genetic information is conveyed to molecular and cellular functions, and is an essential step towards precision medicine. Over one hundred tools/resources have been developed specifically for this purpose. We summarize these tools as well as their characteristics, in the genetic Variant Impact Predictor Database (VIPdb). This database will help researchers and clinicians explore appropriate tools, and inform the development of improved methods. VIPdb can be browsed and downloaded at https://genomeinterpretation.org/vipdb.

KEYWORDS

genotype-phenotype relationship, SNV phenotype, SV impact, variant impact, variant impact prediction, VIPdb

Genomic data hold the promise of revolutionizing our understanding and treatment of human disease. There is a growing gap between the rapid increase of data generation and the functional interpretation of these data (Lappalainen, Scott, Brandt, & Hall, 2019; Muir et al., 2016). Understanding the effects of genetic variants on phenotype is crucial for several fields, including annotation of large-impact variants in resequencing projects (e.g., Pabinger et al., 2014), interpretation of genome-wide association results (e.g.,Visscher et al., 2017), and detection of disease-related variants in a clinical context (e.g., Richards et al., 2015). However, it is presently impractical to experimentally and clinically study effects of all possible genetic variants. Therefore, it is crucially important to develop computational tools for variant impact prediction. To date, over a hundred of tools and databases have been developed for specific contexts. Tools can be developed for specific types of variants. For example, most tools are developed for predicting impact of single nucleotide variations (SNVs), while a smaller number can address small insertions and deletions (indels), and only a handful of tools are able to predict impact of large structural variations (SVs). Moreover, the impact of a variant can be evaluated at different levels, such as molecular damage (e.g., gene expression (Zhou et al., 2018), protein functionality (Vaser, Adusumalli, Leng, Sikic, & Ng, 2016), RNA splicing [Park, Pan, Zhang, Lin, & Xing, 2018]) and pathogenicity (e.g., visible phenotypes [Landrum et al., 2016]). As these tools' purpose differ, the information or training data they draw upon is also diverse, including but not limited to, pathogenicity and clinical phenotypes, cross-species and within-species sequence conservation, protein sequence and protein structure, RNA splicing, RNA binding protein recognition, miRNA binding activity, transcriptional gene regulation, epigenetic signals and translation efficiency. In addition, some tools are optimized for a specific species, and some are developed for a specific disease or gene. The main

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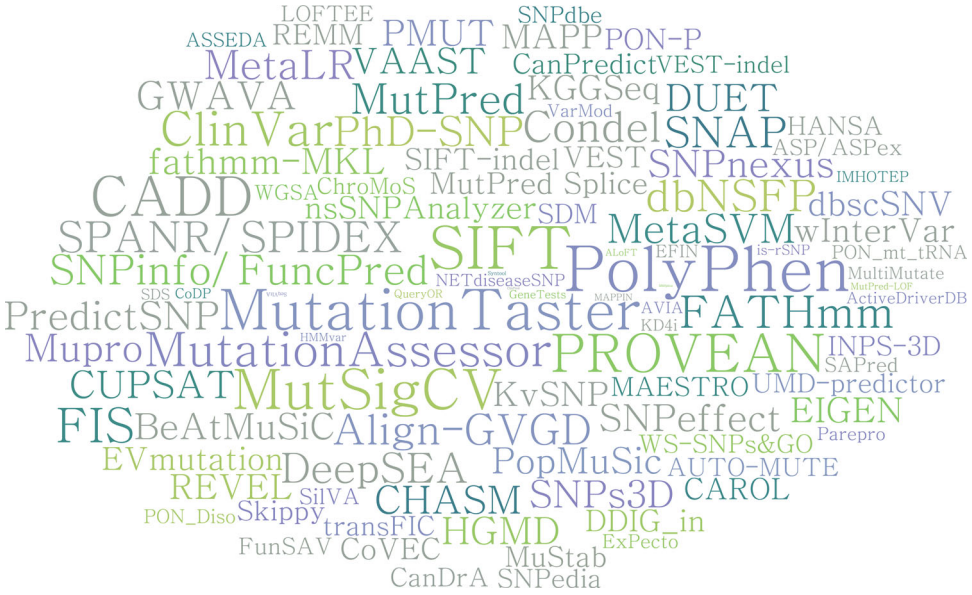

FIGURE 1 Wordle of variant impact predictors. Only tools primarily designed for variant impact prediction were plotted. Character sizes represent the logarithm of recent citations (from Jan 1, 2017 to Jun 1, 2019). For tools with multiple publications, we plotted the sum of all citations. Colors were randomly selected. The Wordle tool (http://www.wordle.net) was used to generate the plot

TABLE 1 Tools and databases used for genomic variant impact predictions

Tool	Primarily for variant impact prediction	Reference
ActiveDriverDB	● DB	Krassowski et al. (2017)
AGGRESCAN		Conchillo-Solé et al. (2007)
AGGRESCAN3D		Zambrano et al. (2015)
Align-GVGD	●	Tavtigian et al. (2006)
ALoFT	●	Balasubramanian et al. (2017)
ANNOVAR		Yang and Wang (2015)
ASP/ASPex	●	Marini, Thomas, and Rine (2010)
ASSEDA	●	Nalla and Rogan (2005)
AUTO-MUTE	●	Masso and Vaisman (2010)
AVIA	●	Vuong et al. (2015)
BeAtMuSiC	●	Dehouck, Kwasigroch, Rooman, and Gilis (2013)
CADD	●	Kircher et al. (2014)
CanDrA	●	Mao et al. (2013)
CanPredict	●	Kaminker, Zhang, Watanabe, and Zhang (2007)
CAROL	●	Lopes et al. (2012)
CHASM	●	Wong et al. (2011)
ChroMoS	●	Barenboim and Manke (2013)
ClinPred	●	Alirezaie, Kernohan, Hartley, Majewski, and Hocking (2018)
ClinVar	● DB	Landrum et al. (2016)
CoDP	●	Terui, Akagi, Kawame, and Yura (2013)
CoMEt		Leiserson, Wu, Vandin, and Raphael (2015)
Condel	●	González-Pérez and López-Bigas (2011)
COSMIC	DB	Tate et al. (2019)
CoVEC	●	Frousios, Iliopoulos, Schlitt, and Simpson (2013)

(Continues)

TABLE 1 (Continued)

Tool	Primarily for variant impact prediction	Reference
CUPSAT	●	Parthiban, Gromiha, Abhinandan, and Schomburg (2007)
DANN		Quang, Chen, and Xie (2015)
DBD-Hunter		Gao and Skolnick (2008)
dbNSFP	● DB	X. Liu et al. (2016)
dbscSNV	●	Jian, Boerwinkle, and Liu (2014)
dbSNP	DB	Sherry et al. (2001)
dbVar	DB	Lappalainen et al. (2013)
DDIG_in	●	Livingstone et al. (2017)
DeepSEA	●	Zhou and Troyanskaya (2015)
DFIRE/DDNA2		B. Xu, Yang, Liang, and Zhou (2009)
DUET	●	Pires, Ascher, and Blundell (2014)
Dmutant		Zhou and Zhou (2002)
EFIN	●	Zeng, Yang, Chung, Lau, and Yang (2014)
EGAD		Pokala and Handel (2005)
EIGEN	●	Ionita-Laza, McCallum, Xu, and Buxbaum (2016)
Eris		Yin, Ding, and Dokholyan (2007)
EVmutation	●	Hopf et al. (2017)
Exome Variant Server (EVS)	DB	Altshuler et al. (2010)
Exomiser		Smedley et al. (2015)
FATHmm	●	Shihab et al. (2014)
fathmm-MKL	●	Shihab et al. (2015)
FIS	●	Reva, Antipin, and Sander (2011)
fitCons		Gulko, Hubisz, Gronau, and Siepel (2015)
FOLD-RATE		Gromiha, Thangakani, and Selvaraj (2006)
FoldAmyloid		Garbuzynskiy, Lobanov, and Galzitskaya (2009)
FOLDEF(core of FOLDX)		Schymkowitz et al. (2005)
FunSAV	●	M. Wang et al. (2012)
GeneTests	DB	Pagon et al. (2002)
GenoCanyon		Lu et al. (2015)
GERP + +		Davydov et al. (2010)
GWAVA	●	Ritchie, Dunham, Zeggini, and Flicek (2014)
HANSA	●	Acharya and Nagarajaram (2012)
HGMD	● DB	Stenson et al. (2017)
HMMvar	●	M. Liu, Watson, and Zhang (2015)
HOPE		Dunlavy, O'Leary, Klimov, and Thirumalai (2005)
Human Splicing Finder		Desmet et al. (2009)
IMHOTEP	●	Knecht et al. (2016)
INPS-3D	●	Savojardo, Fariselli, Martelli, and Casadio (2016)
INSIGHT		Thompson et al. (2014)
is-rSNP	●	Macintyre, Bailey, Haviv, and Kowalczyk (2010)
K-FOLD		Capriotti and Casadio (2007)
KD4i	●	Bermejo-Das-Neves, Nguyen, Poch, and Thompson (2014)
KGGSeq	●	M. J. Li et al. (2017)
KvSNP	●	Stone and Sidow (2005)

(Continues)

TABLE 1 (Continued)

Tool	Primarily for variant impact prediction	Reference
LocTree		Goldberg et al. (2014)
LOFTEE	●	Karczewski et al. (2019)
LUMC LSDB	DB	Fokkema et al. (2011)
LS-SNP/PDB		Ryan, Diekhans, Lien, Liu, and Karchin (2009)
MAESTRO	●	Laimer, Hofer, Fritz, Wegenkittl, and Lackner (2015)
MAPP	●	Stone and Sidow (2005)
MAPPIN	●	Gosalia, Economides, Dewey, and Balasubramanian (2017)
MaxEnt		Yeo and Burge (2004)
MetaLR	●	Dong et al. (2015)
MetaSVM	●	Dong et al. (2015)
MMSplice	●	Jun Cheng et al. (2019)
MultiMutate	●	Deutsch and Krishnamoorthy (2007)
Mupro	●	Cheng, Randall, and Baldi (2006)
MuSiC		Dees et al. (2012)
MuStab	●	Teng, Srivastava, and Wang (2010)
MutationAssessor	●	Reva et al. (2011)
MutationTaster	●	Schwarz, Cooper, Schuelke, and Seelow (2014)
MutPred Splice	●	Mort et al. (2014)
MutPred	●	B. Li et al. (2009)
MutPred-LOF	●	Pagel et al. (2017)
MutSigCV	●	Lawrence et al. (2013)
MuX-48		Kang, Chen, and Xiao (2009)
MuX-S		Kang et al. (2009)
NeEMO		Giollo, Martin, Walsh, Ferrari, and Tosatto (2014)
NETdiseaseSNP	●	Johansen, Izarzugaza, Brunak, Petersen, and Gupta (2013)
nsSNPAnalyzer	●	Bao, Zhou, and Cui (2005)
OMIM	● DB	Amberger and Hamosh (2017)
OncodriveCLUST		Tamborero, Gonzalez-Perez, and Lopez-Bigas (2013)
PAGE		Tartaglia, Cavalli, Pellarin, and Caflisch (2005)
Panther		Mi et al. (2017)
PantherPSEP		Tang and Thomas (2016)
Parepro	●	Tian et al. (2007)
PASTA		Walsh, Seno, Tosatto, and Trovato (2014)
Personal Genome Project	DB	Shringarpure and Bustamante (2015)
PharmGKB	● DB	Thorn, Klein, and Altman (2013)
phastCons		Siepel et al. (2005)
PhD-SNP	●	Capriotti, Calabrese, and Casadio (2006)
Phen-Gen		Javed, Agrawal, and Ng (2014)
phyloP		Pollard, Hubisz, Rosenbloom, and Siepel (2010)
PMUT	●	López-Ferrando, Gazzo, De La Cruz, Orozco, and Gelpí (2017)
PolyPhen	●	Adzhubei et al. (2010)
PON_Diso	●	Ali, Urolagin, Gurarslan, and Vihinen (2014)
PON_mt_tRNA	●	Niroula and Vihinen (2016)
PON-P	●	Niroula, Urolagin, and Vihinen (2015)

(Continues)

TABLE 1 (Continued)

Tool	Primarily for variant impact prediction	Reference
PopMuSic	●	Dehouck, Kwasigroch, Gilis, and Rooman (2011)
PPT-DB		Wishart et al. (2008)
PredictSNP	●	Bendl et al. (2016)
ProA		Fang, Gao, Tai, Middaugh, and Fang (2013)
PROFcon		Punta and Rost (2005)
PROVEAN	●	Choi and Chan (2015)
QueryOR	●	Bertoldi et al. (2017)
REMM	●	Smedley et al. (2016)
REVEL	●	Ioannidis et al. (2016)
SAAPdap/ SAAPred		Hurst et al. (2009)
SAPred	●	Ye et al. (2007)
Scide		Dosztányi, Magyar, Tusnády, and Simon (2003)
Scpred		Kurgan, Cios, and Chen (2008)
SDM	●	Pandurangan, Ochoa-Montaño, Ascher, and Blundell (2017)
SDS	●	Preeprem and Gibson (2014)
SeqVItA	●	Dharanipragada, Seelam, and Parekh (2018)
SIFT	●	Sim et al. (2012)
SIFT-indel	●	Hu and Ng (2013)
SignalP		Petersen, Brunak, Von Heijne, and Nielsen (2011)
SilVA	●	Buske, Manickaraj, Mital, Ray, and Brudno (2013)
SInBaD		Lehmann and Chen (2013)
SiPhy		Garber et al. (2009)
Skippy	●	Woolfe, Mullikin, and Elnitski (2010)
SNAP	●	Hecht, Bromberg, and Rost (2015)
SNPdbe	●	Schaefer, Meier, Rost, and Bromberg (2012)
SNPedia	● DB	Cariaso and Lennon (2012)
SnpEff		Cingolani, Platts et al. (2012)
SNPeffect	●	De Baets et al. (2012)
SNPinfo/FuncPred	●	Z. Xu and Taylor (2009)
SNPnexus	●	Dayem Ullah et al. (2018)
SNPs3D	●	Tian et al. (2007)
SPANR/SPIDEX	●	Xiong et al. (2015)
SPF_Cancer		Capriotti and Altman (2011)
SuRFR		Ryan, Morris, Porteous, Taylor, and Evans (2014)
Syntool	●	Zhang et al. (2017)
TANGO		Rousseau, Schymkowitz, and Serrano (2006)
TransComp		Qin, Pang, and Zhou (2011)
transFIC	●	Gonzalez-Perez, Deu-Pons, and Lopez-Bigas (2012)
UMD-predictor	●	Frédéric et al. (2009)
VAAST	●	Hu et al. (2013)
Variant Tools		Peng (2015)
VariBench		Sasidharan Nair and Vihinen (2013)
VariSNP		Schaafsma and Vihinen (2015)
VarMod	●	Pappalardo and Wass (2014)

(Continues)

TABLE 1 (Continued)

Tool	Primarily for variant impact prediction	Reference
VarWalker		Jia and Zhao (2014)
VEP		McLaren et al. (2016)
VEST	●	Carter, Douville, Stenson, Cooper, and Karchin (2013)
VEST-indel	●	Douville et al. (2016)
Waltz		Maurer-Stroh et al. (2010)
WGSA	●	X. Liu et al. (2016)
wInterVar	●	Q. Li and Wang (2017)
WoLF-PSORT		Horton et al. (2007)
WS-SNPs&GO	●	Capriotti et al. (2013)
Zyggregator		Tartaglia and Vendruscolo (2008)

Note: Tools that are primarily for predicting variant impact are indicated. All items shown are tools, except databases are also flagged with "DB".

challenges in using these tools include their large number and high diversity, lack of consistent output formats, unclear performance characteristics and limited use guidelines. The critical Assessment of Genome Interpretation (CAGI) conducts community experiments for a particular purpose to provide objective assessment of variant impact predictions of phenotype (Hoskins et al., 2017, Andreoletti et al. (this issue)).

Here, we describe the Variant Impact Predictor Database (VIPdb). In this database, we have attempted to collect a comprehensive list of genetic variant impact prediction tools, as well as tools that while not primarily designed for this goal, nonetheless contribute to this purpose, such as tools estimating conservation scores and databases holding population allele frequencies (Figure 1 and Table 1). We also include some particularly relevant databases. This database will help researchers choose appropriate tools, and inform the development of improved methods.

VIPdb is a publication-based database. It originated as a table of resources (Brenner, 2007) and a pilot impact tool list, which was first generated in 2010, manually updated in an ad hoc fashion and available via CAGI (https://genomeinterpretation.org/impact) since

TABLE 2 Description of fields in VIPdb (Table S1), that we collected for each tool or reference

Fields		Description
Ref ID		VIPdb literature reference ID
Tool ID		VIPdb tool or database ID
Name		Tool or database name
Database?		A binary value indicating if it is a database
Primarily for variant impact prediction		A binary value indicating if the tool is primarily designed for predicting variant impact information, or the database provides such information
Variant type	SNVs	A binary value indicating if the tool or database addresses single nucleotide variations
	Indel	A binary value indicating if the tool or database addresses small insertions and deletions
	SVs	A binary value indicating if the tool or database addresses large structural variations
	Nonsynonymous/nonsense	A binary value indicating if the tool addresses nonsynonymous and/or nonsense variants
	Synonymous	A binary value indicating if the tool addresses synonymous variants
	Splicing	A binary value indicating if the tool addresses splicing variants
	Regulatory regions	A binary value indicating if the tool addresses other regulatory variants, e.g., variants in enhancer region
Gene-specific		List of gene(s), if the tool is designed for specific gene(s).

(Continues)

TABLE 2 (Continued)

Fields			Description
In dbNSFP Academic			A binary value indicating if the tool is within dbNSFP academic database
In dbNSFP Commercial			A binary value indicating if the tool is within dbNSFP commercial database
License (Note: Users must evaluate the suitability of each tool and its licensing for their application. The license characterizations are for convenience, and we make no claims regarding their accuracy)		Free for academic use?	A binary value indicating if the tool or database is free for academic use
		Free for commercial use?	A binary value indicating if the tool or database is free for commercial use
		Description	Extracted description of the license
Downloadable precalculated annotation?			A binary value indicating if precalculated annotations/scores are available
Standalone?			A binary value indicating if a stand-alone version is available
Web server?			A binary value indicating if a web server is available
Website accessible as of Jun 1, 2019			A binary value indicating the homepage accessibility
Homepage			Homepage of the tool or database
Source code accessible			Source code link, if available
Reference and Citations	Per paper info	Latest publication?	A binary value indicating if this paper is the latest publication of the tool or database
		Title	Title of the publication
		Doi	DOI of the publication
		PubMed ID	PubMed ID of the publication
		Year	Published year of the publication
		Y<2014	Number of citations before 2014
		Y2014	Number of citations during 2014
		Y2015	Number of citations during 2015
		Y2016	Number of citations during 2016
		Y2017	Number of citations during 2017
		Y2018	Number of citations during 2018
		2019–2019.6	Number of citations between Jan 1, 2019 and Jun 1, 2019
		Y>2015	Number of citations after Jan 1, 2015
		Y>2017	Number of citations after Jan 1, 2017
		Total	Total citation number of the publication
	All tool citation		Total citation number of the tool (citations of multiple reference summed together)
Update date			Last update date for this reference

then. To collect a near-comprehensive list of recent tools, we manually reviewed all publications that cited at least one of the pioneering variant impact prediction tools, including SIFT (Kumar, Henikoff, & Ng, 2009; Sim et al., 2012; Vaser et al., 2016), or PolyPhen (Adzhubei et al., 2010; Adzhubei, Jordan, & Sunyaev, 2013; Ramensky, Bork, & Sunyaev, 2002); as well as annotation tools, such as ANNOVAR (K. Wang, Li, & Hakonarson, 2010; Yang & Wang, 2015) and SnpEff (Cingolani, Patel et al., 2012; Cingolani, Platts et al., 2012). Tools in dbNSFP (X. Liu, Wu, Li, & Boerwinkle, 2016) were also included. In addition, a small number of tools and databases were further collected by direct searches via PubMed database with a various key words list. We excluded LSDBs (Cotton et al., 2008), many of which can be found via LUMC LSDB (https://grenada.lumc.nl/LSDB_list/lsdbs). Next, we collected information about these included tools (Table 2), including their primary purposes (nonsynonymous/nonsense, splicing or other regulatory variants), accepted variant types (SNPs, indels, or SVs), platforms (standalone or online tool), use license (free for academic or for commercial use), whether in dbNSFP database (X. Liu et al., 2016), current website/source code accessibility and citations for publications (from Scopus database).

VIPdb is browsable at the CAGI website (https://genomeinterpretation.org/vipdb) and can be fully downloaded

as a spreadsheet (Table S1; latest version available at above website). We accept submissions of new resources.

ACKNOWLEDGMENT

The CAGI experiment coordination is supported by NIH U41 HG007346 and the CAGI conference by NIH R13 HG006650. This work was supported by TATA Consultancy Services Ltd.

DATA ACCESSIBILITY

VIPdb is browsable at https://genomeinterpretation.org/vipdb; and the full database can be also downloaded.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

How to cite this article: Hu Z, Yu C, Furutsuki M, et al. VIPdb, a genetic Variant Impact Predictor Database. *Human Mutation*. 2019;40:1202–1214. https://doi.org/10.1002/humu.23858