User guide

Visualization concept

The DSNetwork approach was designed to assist researchers in the prioritization process of functional variants derived from GWAS association tests. Indeed, this type of analysis pinpoints genetic loci statistically associated to a particular phenotypic trait. These loci may contain several independent signals and these signals may themselves include hundreds of genetic variants associated with the trait. Those variants being sometimes statistically indistinguishable, it becomes essential to add exogenous knowledge to help identify potential functional causal variants among the background variants. Among the available methods, many are based on the evaluation or the prediction of functional impact of variants. However, the multiplication of approaches as well as their different implementations makes the interpretation of the predictions and the decision making very challenging.

In this context, we created a web application called DSNetwork for **D**ecision **S**upport **N**etwork. This tool aims to provide the users with deleteriousness predictions for human variants (hg19 build) recovered from several sources, and to present these scores in a user-friendly web interface.

The following paragraphs describe DSNetwork's approach through the hypothetical analysis of a loci containing 5 variants rs4233486, rs35054111, rs11808410, rs11804913 and rs7554973 using the deleteriousness scores of 5 distinct fictive predictors namely A, B, C, D and E. Table 1 summarizes the scores generated by these 5 predictors, reflecting their predictions regarding the functional impacts of the candidate variants.

DSNetwork integrates the characteristics of the different predictors and creates a reference frame containing the lower and upper boundaries as well as the direction (ascending [ASC], or descending [DESC]) of their prediction scores (Figure 1). The direction is used to rank variants from the most deleterious to the least deleterious on the basis of their respective scores. The boundaries are used to establish the absolute deleteriousness level of each variant.



Figure 1: Predictor reference frame

Once the different reference frames are integrated, they can be used to prioritize the variants according to 3 types of representations: the intra-predictor relative ranks, the intra-predictor absolute scores and the global ranks.

Here are the scores obtained for the 5 candidate variants for these 5 approaches:

	А	В	с	D	E
rs4233486	0.13	0.40	0.78	0.23	0.12
rs35054111	NA	0.70	0.21	NA	0.43
rs11808410	0.51	0.40	0.21	0.20	0.77
rs11804913	0.01	0.40	0.21	0.30	0.37
rs7554973	0.20	0.5	0.55	NA	0.01

Table 1: Annotations for the five candidate variants

Intra-predictor ranks

Intra-predictor ranks allow the prioritization of a list of variants relative to one another. According to the reference frames illustrated in Figure 1, the 5 predictors produce scores ranging from 0 to 1. We can classify the 5 variants of interest from the most deleterious (rank 1) to the least deleterious (rank 5) with each predictor (Table 2).

	А	В	с	D	E
rs4233486	2	4	1	2	2
rs35054111	NA	1	4	NA	4
rs11808410	4	4	4	3	5
rs11804913	1	4	4	1	3
rs7554973	3	2	2	NA	1

Table 2: Intra-predictor ranking

In order to summarize this information in an easy-to-interpret representation, each variant is depicted as a pie chart where each slice represents the rank of the variant for one of the predictors. Thus, in the current analysis, five pie charts are generated and each pie chart is divided into five slices of the same size. The slices are ordered by predictor by default.



Figure 2: Pie chart and slice distribution

We used a color gradient ranging from red to green, where red corresponds to the most deleterious variant (rank 1) among the candidates for a given predictor. The gray color represents missing data. Figure 3 depicts the pie charts generated for the five candidate variants. The slices can be ordered by color to allow easy identification of variants that appear the most deleterious across predictors.



Figure 3: Visualization of intra-predictor ranking

Intra-predictor absolute scores

Intra-predictor absolute scores allow prediction of variant deleteriousness in reference to the thresholds established for a particular predictor. Given these boundaries, we can determine where each variant is located on the deleteriousness spectrum for each predictor. We chose to divide the score range of each approach into 20 equal intervals. The first interval contains the most deleterious scores and the 20th, the least deleterious. Thus, the annotation scores obtained for each variant are translated into their corresponding intervals. This allows the user to know if a variant is predicted as deleterious by a particular approach without having to know the implementation details of this approach. For clarity purposes, in this example the range of scores has been divided into 4 intervals (instead of 20) (Table 3).

	А	В	с	D	E
rs4233486	1	3	1	4	1
rs35054111	NA	2	4	NA	2
rs11808410	3	3	4	4	4
rs11804913	1	3	4	3	2
rs7554973	1	3	2	NA	1

Table 3: Intra-predictor intervals

As for intra-predictor ranks, each variant is depicted as a pie chart where each slice represents the score interval of the variant for a particular predictor.

We used a color gradient ranging from red to blue. The red color represents the most deleterious interval for a given predictor. The gray color represents missing data. Figure 4 depicts the pie charts

generated for the five candidate variants. The slices can be ordered by color to easily identify variants with the most predictions of deleteriousness.



Figure 4: Visualization of intra-predictor scores intervals

Global ranking

In order to further facilitate the prioritization, we propose to summarize the information regarding the relative ranks in an overall rank for each variant.

To do so, we calculate the average rank of each variant based on its intra-predictor ranks. Then, we order the variants according to their average rank. Variants with the lowest average ranks are considered as the best candidates for being deleterious. Because in some cases there may be missing values for some of the predictors when analysing a specific set of variants, we propose three strategies for calculating a consistent average rank which will be comparable between variants and which will take into account these missing values: 1) replace missing values with the average value (default one, Table 4); or 2) replace missing values with the median value (Table 5). Once the necessary substitutions are made, the average ranks can be calculated and the global ranks generated.

	Score A	Rank with missing value exclusion	Score A with mean substitution	Rank with mean substitution
rs4233486	0.13	2	0.13	2
rs35054111	NA	NA	0.2125	4
rs11808410	0.51	4	0.51	5

rs11804913	0.01	1	0.01	1
rs7554973	0.20	3	0.20	3

Table 4: Mean-based substitution

	Score A	Rank with missing value exclusion	Score A with median substitution	Rank with median substitution
rs4233486	0.13	2	0.13	2
rs35054111	NA	NA	0.165	3
rs11808410	0.51	4	0.51	5
rs11804913	0.01	1	0.01	1
rs7554973	0.20	3	0.20	4

Table 5: Median-based substitution

Once the necessary substitutions have been made, the average ranks can be calculated and the global ranks generated (Table 6).

	А	В	с	D	E	Mean rank	rank
rs4233486	2	4	1	3	2	2.4	1.5
rs35054111	3	1	4	3	4	3.0	4
rs11808410	5	4	4	5	5	4.6	5
rs11804913	1	4	4	1	3	2.6	3
rs7554973	4	2	2	3	1	2.4	1.5

Table 6: Global ranking

As for the intra-predictor scores and ranks, the global ranks are made available for each variant under the form of a pie chart where the rank is represented by a color gradient ranging from red to green. The color red represents the most deleterious variant among the candidates for all approaches (Figure 5).



Figure 5: Global ranking representation according to the substitution method

Variants network

DSNetwork offers the possibility to simply visualize scores and linkage disequilibrium between variants in order to identify potential haplotypes. The scores are the nodes of the network and the LD between the different variants is represented by the links between the nodes. The level of LD is estimated via the r2 measure and represented in a color gradient ranging from yellow to red. The red representing a total imbalance is $r_2 = 1$. The gray color represents the missing information (Figure 6).



Figure 6: Linkage disequilibrium between variants

Conclusion

Considering the relative ranks, the two best candidate variants of our hypothetical analysis are rs4233486 and rs7554973. Indeed, depending on the substitution approach, these two variants are respectively first, first ex aequo or second among the 5 analysed variants. However, despite an apparent draw, rs4233486 could be the best candidate when taking into account the absolute score intervals. For three of the five approaches, rs4233486 is found in the most deleterious intervals. However, one cannot exclude the putative functional impact of rs7554973 with regard to its scores and the high LD with rs4233486.

Tool usage

The application is divided into 3 panels : 1) Input, 2) Selection, 3) Visualization.

Enter variant ids Please enter one variant id per line (rs123455 or 1:1324:A:C)	
Enter variant ids Please enter one variant id per line (rs123455 or 1:1324:A:C)	
Please enter one variant id per line (rs123455 or 1:1324:A:C)	
Load 1p36 data, load 1p34 data, load 7q22 data, load 11p15 data. or load text file (one variant id per line)	
Browse No file selected	
Fetch annotations from SNPnexus (significatively increases fetching duration) Q Fetch Annotations	
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Input

Users can analyse a specific set of variants either by pasting the SNP list in the text area provided for this purpose or by uploading a text file. This file should contain only the SNP list with one identifier per line.

Variants should be referenced through their dbSNP (Sherry et al. 2001) identifiers or their genomic positions and alleles (e.g 5:44527739:A:ATACT). The selected variants must be located on the same chromosome.

Once the variant list is uploaded, the "Fetch annotations" button will trigger the score retrieval process.

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Either paste your variants list in the text area ...

or upload a text file containing a variant id per line.

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Please enter one variant id per line (rs123455 or 1:1324:A:C)	
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Load 1p36 data, load 1p34 data, load 7q22 data, load 11p15 data.	
or load text file (one variant id per line)	
Browse locus_1p36.txt	
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Once your data has loaded, you may choose to trigger SNPNexus data retrieval. As the data needs to be retrieved from the server, a certain processing time should be expected. You can configure the waiting time (in minutes) through a slide bar.

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 Fetch annotations from SNPnexus (significatively inc fetching duration) 	reases
How long are you willing to wait ? (default: 5 min)	
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Press "Fetch annotations" to trigger annotation retrieval.

DSNetwork	=	
DSNetwork		+
Request panel		-
Selection panel		-
Network panel		-
		× Fetching annotations Extracting COTS data

An overview of the results is presented in a scatter plot representing the requested variants along the map of sequence constraint **C**ontext-**D**ependent **T**olerance **S**core (CDTS) - determined through alignment of genomes from thousands of individuals.

Request panel C Rest for new query Data retrieval No Annotations for the following variants: rs200439148.	COTS plot This plot represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U T Build represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U T Build represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U T Build represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U T Build represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U T Build represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U Build represents the requested variants along the map of sequence constant - Context-Dependent Tolerance Score (COTS) - determined throught alignment of thousands human genomes. U Build represent - Dependent - Depe
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Legend :

- Color code: selected variants, unselected variants
- Shape code enables to distinguish variants according to their regulatory consequences. 7 different shapes are available. If there is more than 7 different annotations, the rarer annotations will all have the same shape, the square.

By default, the best variants with regards to the overall global mean ranking are selected (up to 30).

You can download all the annotations by pressing "Download results (TSV)"

Selection

In the second panel, for consistency purposes, non-synonymous and regulatory variants are processed separately. Once the annotations are fetched, a summary table will appear in the selection panel. Without user specific selection, the first regulatory variants, up to a maximum of thirty, will be highlighted in the table and CDTS plot.

The summary table contains 6 columns: query, HGVS ids, CADD consequences and 3 columns containing overall global mean ranks (OGMR) according to the three substitution approaches.

Selection panel						-
Choose the network to build	Copy Print	Download CSV Download XLSX	Download PDF			Search:
synonymous and non-coding variants	query	hgvs ID	¢ consequences	OGMR (NA = median)	OGMR (NA = mean) 🔅	OGMR (NA = worst) 🕴
	rs2992735	chr1:g.18800387T>A	INTERGENIC	14	14	11
	rs3007733	chr1:g.18800911C>T	INTERGENIC	13	16	13
	rs3049905	chr1:g.18801607_1880	01609del	16	11	34
	rs1360916	chr1:g.18801697G>A	INTERGENIC	3	3	3
	rs1360915	chr1:g.18801804T>C	INTERGENIC	11	13	10
	rs34136920	chr1:g.18801848del		15	9	27
	rs1316327	chr1:g.18802387G>A	INTERGENIC	28	29	16
	rs2992732	chr1:g.18802825G>A	UPSTREAM	30	31	17
	rs3007734	chr1:g.18803022T>C	UPSTREAM	8	12	8
	rs2992764	chr1:g.18804144G>A	UPSTREAM	33	34	20
	rs2992763	chr1:g.18804386G>A	UPSTREAM	22	28	15
	Showing 1 to 12 o *OGMR = global m	f 36 entries nean rank computed by taking info acco	unt all with all the available annotations.			
						C Build Network

 \triangle Please notice that OGMR are computed by taking into account <u>all the variants</u> and <u>all the</u> <u>available annotations</u> and are <u>not updated</u> when some variants or annotations are excluded from the analysis in the following steps.

Users can change the type of variants to visualise through the dropdown list at the right of the selection panel.

Selection panel						-
Choose the network to build	Copy Print	Download CSV Download	I XLSX Download PDF		Search	:
non synonymous variants	query	hgvs ID	consequences	0 OGMR (NA = median)	OGMR (NA = mean) 0	OGMR (NA = worst) 🗄
synonymous and non-coding variants	rs2992755_C.A	chr1:g.18807897C>A	NON_SYNONYMOUS,REGULATORY	1	1	1
non synonymous variants	rs2992755_C.G	chr1:g.18807897C>G	NON_SYNONYMOUS,REGULATORY	4	4	4
	rs2992755_C.T	chr1:g.18807897C>T	NON_SYNONYMOUS,REGULATORY	2	2	2
	rs11261022	chr1:g.18807953C>A	NON_SYNONYMOUS,REGULATORY	6	6	6
	rs2992753	chr1:g.18808292C>A	NON_SYNONYMOUS	3	3	3
	rs2992752_A.C	chr1:g.18808526A>C	NON_SYNONYMOUS	8	8	8
	rs2992752_A.G	chr1:g.18808526A>G	NON_SYNONYMOUS	5	5	5
	rs2992752_A.T	chr1:g.18808526A>T	NON_SYNONYMOUS	7	7	7
	Showing 1 to 8 of 8 e	ntries				
	*OGMR = global mea	in rank computed with all the	available annotations.			

Which will automatically update the CDTS plot and highlight the preselected coding variants.



You can also change the selected variants through this table.

The number of selectable variants is restricted to 30 for ergonomic reasons.

Selection panel						-
Choose the network to build	Copy Print	Download CSV Download XLSX	Download PDF		Sear	ch:
synonymous and non-coding variants	query	hgvs ID	consequences	0 OGMR (NA = median) *	OGMR (NA = mean)	OGMR (NA = worst)
	rs1316327	chr1:g.18802387G>A	INTERGENIC	26	29	14 🔺
	rst				25	33
	rs:	(\mathbf{D})	м	28	28	15
	rs			29	27	35
	rs:		м	30	32	17
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	rs:			32	30	34
	rs:	ed selection limit (suppress at l	east 1 variant(s))	33	31	36
	rs:	ОК	м	34	34	19
	rs:		м	35	35	21
	rs2992762_A.G	chr1:g.18804609A>G	UPSTREAM	36	36	22
	- <u></u>					¥
	Showing 25 to 36 o	f 36 entries				
	UGMR = global me	an rank computed with all the availab	(e annotations.			
						Suild Network

You can use the reported global scores in the summary table to select a particular subset of variants. In the following picture, we selected regulatory variants which global rank is inferior to 5 with one of the substitution approaches.

Selection panel						-
Choose the network to build	Copy Print Download	I CSV Download XLSX Download PDF			Search:	
synonymous and non-coding variants	query	hgvs ID	consequences \$	OGMR (NA = median) 🗄	OGMR (NA = mean) *	OGMR (NA = worst) 🕴
	rs1360916	chr1:g.18801697G>A	INTERGENIC	1	1	1
	rs2992756	chr1:g.18807339T>C	REGULATORY, UPSTREAM	4	2	2
	rs3007718	chr1:g.18808465T>A	SYNONYMOUS	6	3	7
	rs12061708	chr1:g.18809916G>A	3PRIME_UTR	2	4	3
	rs2992761	chr1:g.18804674G>A	UPSTREAM	7	5	6
	rs2992740_G.T	chr1:g.18810344G>T	3PRIME_UTR	3	6	5
	rs2992757	chr1:g.18807137T>C	REGULATORY, UPSTREAM	5	7	4
	rs3049905_AAAAA.A	chr1:g.18801616_18801619del		11.5	9.5	22.5
	rs3049905_AAAA.A	chr1:g.18801617_18801619del		11.5	9.5	22.5
	rs3049905_AAA.A	chr1:g.18801618_18801619del		11.5	9.5	22.5
	rs3049905_AA.A	chr1:g.18801619del		11.5	9.5	22.5
	Showing 1 to 11 of 38 entries *OGMR = global mean rank con	nputed by taking into account all variants with all the availab	le annotations.			
	Build Network					

It will automatically load the CDTS plot.



 \triangle The automatic update of the CDTS plot can affect the responsiveness of the selection table. To avoid this behaviour, collapse the "Request panel" by clicking on the minus sign located at the top right.

Visualization

Once the variants are selected, press "Build Network" to build the decision support network. By default, the relative intra-predictor ranks - ordered by predictors - are displayed.

Network panel		-
Focus on		
None		1
This option enables to focus the network on a particular variants. Select 'None' to zoom out and visualize the whole network.	rs2992756 rs12061708	2.5
Choose the population to use		3
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Update		
This option enables to select the set of prediction and scoring algorithms used to compute the metascore (color of the database-shaped nodes)		

Once your mouse is the network area, you can use it to interact with the network in the following matter:

- Scroll in or out to zoom

Network panel	-
Choose the population to use	· · · · · · · · · · · · · · · · · · ·
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iwscoring_novel linsight remm	
Update	rs3007718
This option enables to select the set of prediction and scoring algorithms used to compute the metascore (color of the database-shaped nodes)	

- Drag and drop to move the network within the network area
- Grab the right bottom border and drag to the desired width or height to adjust the size of the network

- Double click on a variant pie	chart to get variant annotation	details
Network panel		
Choose the population to use		
African Caribbean in Barbados (ACB)	rs2992756	
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LD range	cadd.phred 2.192	
00	cadd.rawscore -0.043	
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	gwava_tss 0.57	
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	cadd.phast_cons.tranmalan 0.05	
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- Right click in the network area and select the "Save image as" option to save the network image in "png" format

to Update

Network panel		-
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None		13
This option enables to focus the network on a particular variants. Select 'None' to zoom out and visualize the whole network.	8	2
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African Caribbean in Barbados (ACB)		4
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cadd.phast_cons.primate		
cadd.phylop.mammalian cadd.phylop.primate	1	
cadd.phylop.vertebrate cadd.rawscore		

Visualization parameters are available at the left of the Network panel and will be described from the top to the bottom.

Focus

This first parameter enables to automatically focus the network on a particular variant. This is a useful option when dealing with big networks. The "none" option restores the initial visualization.



Linkage disequilibrium

By default, no linkage disequilibrium (LD) data are shown. To map LD on the network edges, choose a 1000 Genomes population and press "Add LD information" in the left panel.

This process can take a few seconds (up to 1 minute)



You can restrict the LD range you want to display after doing this, press "Update" to update the network.

Network panel			-
Focus on			
None			.*
This option enables to focus the network on a particular variants. Select 'None' to zoom out and visualize the whole network.	*		15
Choose the population to use			
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Add LD Information		1312001700	* -
			45
Data retrieval 🛛 👋			-
LD computation succeed for all variants	rs3007718		55
		rs2992757	4
D range			544
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- Opuace			
Those options enable to select the interval of LD values represented between all variants or for a single variant.			0.0
	rs2992740	rs1360916	0.8
Prediction visualization			0.6
Relative rank 👻			a 83
			0.3

You can use the "Between" option to restrict the LD information to a particular variant. Press "Update" to update the visualization.

Network panel				-
Focus on				
None				2
This option enables to focus the network on a particular variants. Select 'None' to zoom out and visualize the whole network.	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~			2
Choose the population to use				3
African Caribbean in Barbados (ACB) 👻	rs2992756	rs12061708		3.5
Add LD Information		1312001100		4
				13
Data retrieval ×				•
LD computation succeed for all variants	rs3007718			5.5
		rs2992757		
LD range				NA
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0 0.2 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 2				Rank
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Those options enable to select the interval of LD values represented				
between au variants or for a single variant.	rs2992740 rs126	30016		0.8
Prediction visualization	15130	0.910		9.7
Relative rank				0.5
			*	0.4
				0.2

These two parameters can be combined to display a specific range of LD for a particular variant. This is very useful when dealing with big networks.



Score visualization

You can change the visualization through the dropdown list "Prediction visualisation". For example, the intra-predictor ranks can be ordered by color to emphasize the rank distribution.

Network panel		-
F		
Focus on		
None		
This option enables to focus the network on a particular variants. Select 'None' to zoom out and visualize the whole network.	rs2992756 rs12061708	2
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	rs3007718	· · · ·
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	152552151	
Production of the Head on		15
Prediction visualization		
Relative rank (group by color)		
		NA
Predictors selection		
bayesdel cadd.consscore cadd.fitcons cadd.gerp.n		Rank
cadd.phast_cons.mammalian cadd.phast_cons.primate		
cadd.phast_cons.vertebrate_cadd.phred	rs2992740 rs1360916	
cadd.phylop.vertebrate cadd.rawscore deepseq_sig_log2	15150510	
eigen_nc eigen_pc_nc fathmm_nc fitcons_nc funseq		4
gwava_region gwava_tss gwava_unmatched		
iwscoring_known_iwscoring_novel_linsight_remm		
¢ Update		
This option enables to select the set of prediction and scoring		
algorithms used to compute the metascore (color of the database-		
snaped notes)		

You can choose to visualize the absolute scores ordered by predictors or by color gradient.



The dropdown list enables to select a global mean rank according to the substitution method of your choice among "mean", and "median".

Network panel	-
Focus on	
None	
This option enables to focus the network on a particular variants. Select 'None' to zoom out and visualize the whole network.	rs2992756 rs12061708
Choose the population to use	
African Caribbean in Barbados (ACB) 🗸	
	rs3007718
Add LD Information Remove LD Information	rs2992757
Prediction visualization	
Mean relative rank (NA = median)	
Predictors selection	
bayesdel cadd.consscore cadd.fitcons cadd.gerp.n	
cadd.phast_cons.mammalian_cadd.phast_cons.primate	
cadd.phylop.mammalian cadd.phylop.primate	rs2992740 rs1360916
cadd.phylop.vertebrate cadd.rawscore deepseq_sig_log2	
eigen_nc eigen_pc_nc fathmm_nc fitcons_nc funseq gwava region gwava tss gwava unmatched	
iwscoring_known iwscoring_novel linsight remm	
Update	
This option enables to select the set of prediction and scoring algorithms used to compute the metascore (color of the database- shaped nodes)	

Predictors selection

Predictors providing predictions for at least one variant in the selection are displayed in the "Prediction selection" area. You can easily select a subset of predictors you are interested in by adjusting the list of predictors.

Network panel				
P				
ocus on				
None	-			
his option enables to focus the elect 'None' to zoom out and v	e network on a particular variants. visualize the whole network.			
Choose the population to use				
Utah residents with Northern	and Western Europen ancestry	rs2992756	rs12061708	
()			.012001100	
Add LD Information	Remove LD Information			
			()	
Data retrieval	×	rs3007718		
	all variants		ro20027E7	
			152992757	
rediction visualization				
Relative rank	•			
edictors selection				
bayesdel cadd.consscore ca	add.fitcons cadd.gerp.n			
fitcons_nc funseq gwava_n	egion gwava_tss			
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msigne remm		rs2992740		
add.phast_cons.mammalia	n 🄺	132332140	IST300AT0	
add.phast_cons.primate				
.add.pnast_cons.vertebrate				
cadd.phileo.mammaliao				
cauo.phytop.mammalian				

After doing so press "Update" to update the network.

Network panel			-
Focus on			
None	•		,
This option enables to focus the Select 'None' to zoom out and v	network on a particular variants. isualize the whole network.		
Choose the population to use			
Utah residents with Northern (CEU)	and Western Europen ancestry 👻	rs2992756 rs12	061708
Add LD Information	Remove LD Information		
Data retrieval	×	rc2007718	
LD computation succeed for a	all variants	153007710	rs2992757
Prediction visualization			54
Relative rank			Park
Predictors selection			
bayesdel cadd.consscore ca	add.fitcons cadd.gerp.n		
fitcons_nc funseq gwava_re	egion gwava_tss		
linsight remm	E_klown_imsconing_liover		
Update		rs2992740 rs1360916	
This option enables to select the algorithms used to compute the shaped nodes)	e set of prediction and scoring e metascore (color of the database-		

Complementary information

The predictor descriptions are available in the sidebar application.

IELWOIK	Predictors				
scription	Print Download CS	V Download XI SX Download PDF		Search:	
	Score	≑ Id	Range	Ref	
	⊖ BayesDel	bayesdel	[-1.3_0.76]	Feng 2017	
	⊕ CADD	cadd.consscore; cadd.phred; cadd.rawscore	[0_7]; [1_99]; [-6_33]	Kircher et al. 2014;Rentzsch et al. 2018	
	te CADD	cadd.rawscore	[-6_33]	Kircher et al. 2014;Rentzsch et al. 2018	
	CDTS	cdts_percentile	[0_100]	di Iulio et al. 2018	
	0 0013		121112	Quang et al. 2015	
	⊕ DANN	dbnsfp.dann.rankscore	[0_1]		
	 ⊕ DANN ⊕ DeepSEA 	dbnsfp.dann.rankscore deepseq_sig_log2	[0_1] [1_100]	Zhou et al. 2015	
	 DANN DeepSEA Eigen 	dbnsfp.dann.rankscore deepseq_sig_log2 eigen_nc; dbnsfp.eigen.pc.raw_rankscore; eigen_pc_nc	[0_1] [1_100] [-2_5]; [0_1]; [0_1]; [-2_5]	Zhou et al. 2015 Ionita-Laza et al. 2016	