

vtpNet: variant-transcription factor-phenotype networks

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1 Introduction

In a wide-ranging paper (PMID 22955828 Maurano et al. (2012)), Maurano and colleagues illustrate the concept of “common networks for common diseases” with a bipartite graph. One class of nodes is a set of autoimmune disorders, the other class is a set of transcription factors (TFs). In this graph, an edge exists between a disorder node and a TF node if a SNP that is significantly associated with the risk of the disorder lies in a genomic region possessing a strong match to the binding motif of the TF. This package defines tools to investigate the construction and statistical interpretation of such bipartite graphs, which we will denote VTP (variant-transcription factor-phenotype) networks.

2 Illustrative example of an unpruned VTP

The following code uses the `graphNEL` class to construct an approximation to the complete bipartite graph underlying Figure 4A of the Maurano paper; Figure 1 illustrates an arbitrary complete subgraph. The elements of `diseaseTags` are formatted to allow multiline rendering of the strings in node displays. It will be useful to distinguish a display token type and an analysis token type to simplify programming.

```
> #  
> # tags formatted for display  
> #  
> diseaseTags = c("Ankylosing\\nspondylitis", "Asthma",  
+ "Celiac\\ndisease", "Crohn's\\ndisease",  
+ "Multiple\\nsclerosis", "Primary\\nbiliary\\ncirrhosis",  
+ "Psoriasis", "Rheumatoid\\narthrititis",  
+ "Systemic\\nlupus\\nerythematosus",  
+ "Systemic\\nsclerosis", "Type 1\\ndiabetes",
```

```

+       "Ulcerative\\nocolitis"
+ )
> TFtags = c("ELF3", "MEF2A", "TCF3", "PAX4", "STAT3",
+ "ESR1", "POU2F1", "STAT1", "YY1", "SP1", "CDC5L",
+ "NR3C1", "EGR1", "PPARG", "HNF4A", "REST", "PPARA",
+ "AR", "NFKB1", "HNF1A", "TFAP2A")
> # define adjacency matrix
> adjm = matrix(1, nr=length(diseaseTags), nc=length(TFtags))
> dimnames(adjm) = list(diseaseTags, TFtags)
> library(graph)
> cvtp = ugraph(aM2bpG(adjm)) # complete (V)TP network; variants not involved yet

```

3 Data on GWAS variants: their associated phenotype, locations, and other characteristics

We will use the GWAS data provided at <https://www.sciencemag.org/content/suppl/2012/09/04/science.1222794.DC1/1222794-Maurano-tableS2.txt>, which was manually imported to a GRanges instance in hg19 origin-1 coordinates.

```

> library(vtpnet)
> data(maurGWAS)
> length(maurGWAS)

[1] 5654

> names(values(maurGWAS))

[1] "name" "disease_trait"
[3] "disease_class" "internally_replicated"
[5] "independently_replicated" "In_DHS"
[7] "fetal_origin" "X.LOG.P."
[9] "sample_size"

```

4 Data on transcription factor binding sites

We have included the result of using FIMO Grant et al. (2011) to scan for motif matches for TF PAX4 as modeled in the Bioconductor *MotifDb* collection. The `-max-stored-scores` parameter was set to 10000000 so that p of up to 10^{-4} are retained.

```

> data(pax4)
> length(pax4)

```

```

> library(Rgraphviz)
> #flat = function(x, g) c(x, edges(g)[[x]])
> #sub = subGraph(unique(c(flat("Crohn's\\ndisease", cvtp),
> #   flat("Ulcerative\\ncolitis", cvtp))), cvtp)
> sub = subGraph(unique(c(diseaseTags[1:4], TFtags[1:6])), cvtp)
> plot(sub, attrs=list(node=list(shape="box", fixedsize=FALSE)))
> #plot(cvtp, attrs=list(graph=list(margin=c(.5,.5), size=c(4.1,4.1)),
> #   node=list(shape="box", fixedsize=FALSE, height=1)))

```

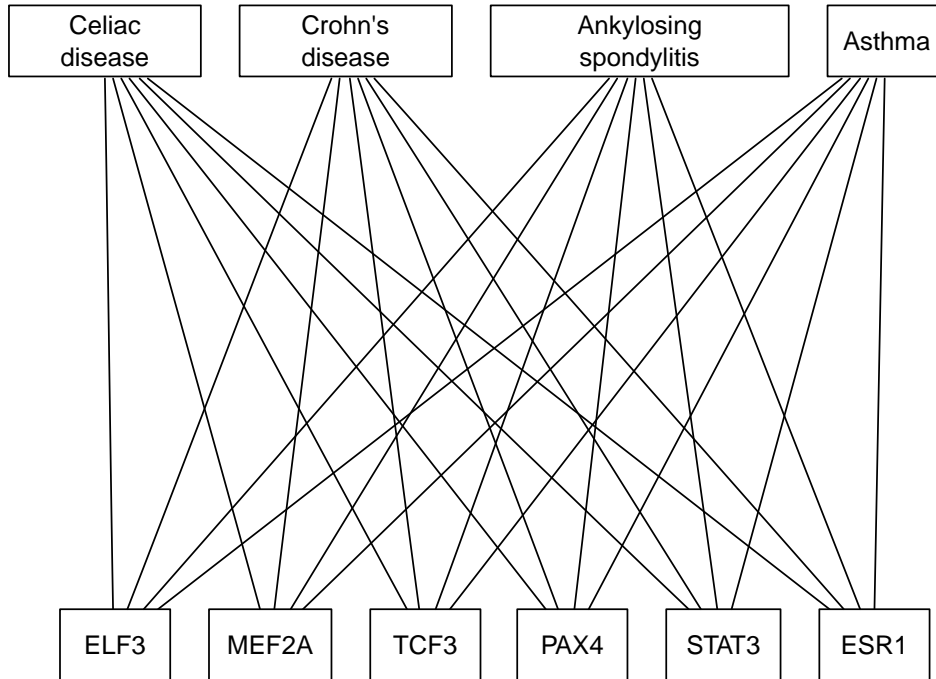


Figure 1: A complete bipartite graph for arbitrarily selected subsets of the autoimmune disorders and TFs found in Figure 4A of Maurano et al.

```
[1] 1862156
```

```
> pax4[1:4]
```

GRanges object with 4 ranges and 8 metadata columns:

	seqnames <Rle>	ranges <IRanges>	strand <Rle>	source <factor>	type <factor>	score <numeric>
[1]	chr1	10273-10302	+	fimo	nucleotide_motif	999.917
[2]	chr1	10279-10308	+	fimo	nucleotide_motif	999.962
[3]	chr1	11703-11732	-	fimo	nucleotide_motif	999.999
[4]	chr1	11704-11733	-	fimo	nucleotide_motif	999.955

	phase <integer>	Name <character>	pvalue <character>	qvalue <character>
[1]	<NA>	+Mmusculus-JASPAR_CO..	8.35e-05	0.396
[2]	<NA>	+Mmusculus-JASPAR_CO..	3.79e-05	0.361
[3]	<NA>	-Mmusculus-JASPAR_CO..	8.04e-07	0.194
[4]	<NA>	-Mmusculus-JASPAR_CO..	4.46e-05	0.368

	sequence <character>
[1]	TAACCCTAACCCCTAACCCCA..
[2]	TAACCCTAACCCCAACCCCA..
[3]	AAAAAAAATACACATGGCCAG..
[4]	TAAAAAAAATACACATGGCCA..

seqinfo: 92 sequences from an unspecified genome; no seqlengths

We can also generate our own motif-match ranges. Here is an example of a parallelized search against hg19 using `matchPWM`.

```
> library(foreach)
> library(doParallel)
> registerDoParallel(cores=12)
> library(BSgenome.Hsapiens.UCSC.hg19)
> library(MotifDb)
> sn = seqnames(Hsapiens)[1:24]
> pax4 = query(MotifDb, "pax4")[[1]]
> ans = foreach(i=1:24) %dopar% {
+   cat(i)
+   subj = Hsapiens[[ sn[i] ]]
+   matchPWM( pax4, subj, "75%" )
+ }
> pax4_75 =
+ do.call(c, lapply(1:length(ans), function(x)
```

```
+ {GRanges(sn[x], as(ans[[x]], "IRanges"))})
> save(pax4_75, file="pax4_75.rda")
```

Results of such searches retaining matches at scores of 85% and 75% of the maximum achievable score have been stored with this package.

5 Building a VTP network: one edge per phenotype

5.1 Raw matches

We can survey the entire GWAS catalog for intersection with putative PAX4 binding sites. First the two Bioconductor internal binding site sets.

```
> data(pax4_85)
> vp_pax4_85 = maurGWAS[ overlapsAny(maurGWAS, pax4_85) ]
> length(vp_pax4_85)
```

```
[1] 0
```

```
> data(pax4_75)
> vp_pax4_75 = maurGWAS[ overlapsAny(maurGWAS, pax4_75) ]
> length(vp_pax4_75)
```

```
[1] 54
```

Then the FIMO-based set.

```
> vp_pax4_fimo = maurGWAS[ overlapsAny(maurGWAS, pax4) ]
> length(vp_pax4_fimo)
```

```
[1] 67
```

The lengths reported here are the numbers of phenotypes linked to PAX4 in a VTP according to various motif matching schemes. For the two non-null results, we have

```
> u75 = unique(vp_pax4_75$disease_trait)
> ufimo = unique(vp_pax4_fimo$disease_trait)
> length(setdiff(u75, ufimo))
```

```
[1] 23
```

```
> length(setdiff(ufimo, u75))
```

```
[1] 28
```

Clearly the identification of TP links is sensitive to the approach used to locate binding sites. However, as noted in the Maurano paper, the use of matching to the reference genome without SNP injection is potentially problematic.

5.2 Filtering

It is useful to restrict the phenotypes of interest, and to map them to broader classes, and to include TFBS matching scores for the purpose of filtering edges. Here we will use the NHGRI GWAS catalog against FIMO-based (reference genome matching only) PAX4 calls.

```
> data(cancerMap)
> requireNamespace("gwascats")
> load(system.file("legacy/gwrngs19.rda", package="gwascats"))
> cangw = filterGWASbyMap( gwrngs19, cancerMap )
> getOneHits( pax4, cangw, "fimo" )
```

GRanges object with 8 ranges and 41 metadata columns:

	seqnames	ranges	strand	Date.Added.to.Catalog	PUBMEDID
	<Rle>	<IRanges>	<Rle>	<character>	<integer>
3475	chr8	129194641	*	09/12/2013	23535729
3480	chr11	65583066	*	09/12/2013	23535729
6963	chr2	26526419	*	01/25/2013	23144319
7155	chr6	143943314	*	01/15/2013	23108145
7480	chr20	32588095	*	11/30/2012	22976474
12585	chrX	37854727	*	11/15/2010	20932654
13650	chr12	14653867	*	07/12/2010	20543847
15145	chr10	63752159	*	09/04/2009	19684604
	First.Author	Date	Journal		
	<character>	<character>	<character>		
3475	Michailidou K	04/01/2013	Nat Genet		
3480	Michailidou K	04/01/2013	Nat Genet		
6963	Lee Y	11/08/2012	Carcinogenesis		
7155	Wang LE	10/29/2012	Cancer Res		
7480	Siddiq A	09/13/2012	Hum Mol Genet		
12585	Kerns SL	10/05/2010	Int J Radiat Oncol B..		
13650	Turnbull C	06/13/2010	Nat Genet		
15145	Papaemmanuil E	08/16/2009	Nat Genet		
	Link	Study	Disease.Trait		
	<character>	<character>	<character>		
3475	http://www.ncbi.nlm... Large-scale genotypi..		Breast cancer		
3480	http://www.ncbi.nlm... Large-scale genotypi..		Breast cancer		
6963	http://www.ncbi.nlm... Prognostic implicati..	Non-small cell lung ..			
7155	http://www.ncbi.nlm... Genome-wide associat..	Lung Cancer (DNA rep..			
7480	http://www.ncbi.nlm... A meta-analysis of g..	Breast cancer			
12585	http://www.ncbi.nlm... Genome-wide associat..	Erectile dysfunction..			
13650	http://www.ncbi.nlm... Variants near DMRT1,..	Testicular germ cell..			

Initial.Sample.Size	Replication.Sample.Size	Region	Chr_id
<character>	<character>	<character>	<character>
3475 10,052 European ance..	45,290 European ance..	8q24.21	8
3480 10,052 European ance..	45,290 European ance..	11q13.1	11
6963 348 Korean ancestry ..	NR	2p23.3	2
7155 914 European ancestr..	679 European ancestr..	6q24.2	6
7480 3,666 European ances..	562 European ancestr..	20q11.22	20
12585 27 African American ..	<NA>	Xp11.4	23
13650 979 European ancestr..	664 European ancestr..	12p13.1	12
15145 907 European ancestr..	<NA>	10q21.2	10

Chr_pos.hg38	Reported.Gene.s.	Mapped_gene
<numeric>	<character>	<character>
3475 128182395	MIR1208, MYC	MIR1208 - LINC01263
3480 65815595	DKFZp761E198, OVOL1,..	OVOL1-AS1 - SNX32
6963 26303551	GPR113	HADHB - GPR113
7155 143622177	PHACTR2	PHACTR2
7480 34000289	RALY, EIF2S2, ASIP	RALY
12585 37995474	SYTL5	CXorf27 - SYTL5
13650 14500933	ATF7IP	ATF7IP
15145 61992400	ARID5B	ARID5B

Upstream_gene_id	Downstream_gene_id	Snps_gene_ids	Upstream_gene_distance
<character>	<character>	<character>	<character>
3475 100302281	101927774		32.21
3480 101927828	254122		24.73
6963 3032	165082		13.09
7155 <NA>	<NA>	9749	<NA>
7480 <NA>	<NA>	22913	<NA>
12585 25763	94122		4.16
13650 <NA>	<NA>	55729	<NA>
15145 <NA>	<NA>	84159	<NA>

Downstream_gene_distance	Strongest.SNP.Risk.Allele	SNPs
<character>	<character>	<character>
3475 222.87	rs11780156-T	rs11780156
3480 18.24	rs3903072-G	rs3903072
6963 4.62	rs6753473-G	rs6753473
7155 <NA>	rs9390123-A	rs9390123
7480 <NA>	rs2284378-T	rs2284378
12585 11.11	rs872690-?	rs872690
13650 <NA>	rs2900333-C	rs2900333
15145 <NA>	rs7089424-C	rs7089424

Merged Snp_id_current	Context
	Intergenic

	<character>	<character>	<character>	<character>	
3475	0	11780156	Intergenic	1	
3480	0	3903072	Intergenic	1	
6963	0	6753473	Intergenic	1	
7155	0	9390123	intron	0	
7480	0	2284378	intron	0	
12585	0	872690	Intergenic	1	
13650	0	2900333	UTR-3	0	
15145	0	7089424	intron	0	
	Risk.Allele.Frequency	p.Value	Pvalue_mlog	p.Value..text.	OR.or.beta
	<character>	<numeric>	<numeric>	<character>	<numeric>
3475	0.16	3e-11	10.52288		1.07
3480	0.53	9e-12	11.04576		1.05
6963	0.052	4e-06	5.39794	(Additive model)	NA
7155	0.3957	7e-06	5.15490		NA
7480	0.31	1e-08	8.00000		1.16
12585	0.03	9e-06	5.04576		11.78
13650	0.62	6e-10	9.22185		1.27
15145	0.34	7e-19	18.15490		1.65
	X95..CI..text.	Platform..SNPs.passing.QC.		CNV	
	<character>	<character>	<character>		
3475	[1.04-1.10]	Illumina & Affymetri..		N	
3480	[1.04-1.08]	Illumina & Affymetri..		N	
6963	NR	Affymetrix [271,817]		N	
7155	NR	Illumina [303,669]		N	
7480	[1.10-1.22]	Illumina [2,608,509]..		N	
12585	[NR]	Affymetrix [512,497]		N	
13650	[1.12-1.44]	Illumina [298,782]		N	
15145	[1.54-1.76]	Illumina [291,473]		N	
	num.Risk.Allele.Frequency	dclass	score	tfstart	tfend
	<numeric>	<character>	<numeric>	<integer>	<integer>
3475	0.1600	Breast	999.985	129194621	129194650
3480	0.5300	Breast	999.952	65583065	65583094
6963	0.0520	Lung	999.987	26526415	26526444
7155	0.3957	Lung	999.939	143943292	143943321
7480	0.3100	Breast	999.928	32588075	32588104
12585	0.0300	Prostate	999.903	37854721	37854750
13650	0.6200	Testicular	999.990	14653848	14653877
15145	0.3400	ALL (ped)	999.962	63752142	63752171
	pvalue	qvalue			
	<numeric>	<numeric>			
3475	1.49e-05	0.318			

3480	4.83e-05	0.373
6963	1.25e-05	0.310
7155	6.13e-05	0.383
7480	7.16e-05	0.388
12585	9.72e-05	0.403
13650	1.05e-05	0.301
15145	3.79e-05	0.361

seqinfo: 23 sequences from hg19 genome

6 Appendix: generating the ALT-injected genome image

```
> altize = function(htag = "21",
+ #
+ # from sketch by Herve Pages, May 2013
+ #
+ slpack="SNPlocs.Hsapiens.dbSNP.20120608",
+ hgpak = "BSgenome.Hsapiens.UCSC.hg19",
+ faElFun = function(x) sub("%%TAG%%", x, "alt%%TAG%%chr"),
+ faTargFun = function(x)
+   sub("%%TAG%%", x, "alt%%TAG%%_hg19.fa")) {
+   require(slpak, character.only=TRUE)
+   require(hgpak, character.only=TRUE)
+   require("ShortRead", character.only=TRUE)
+   chk = grep("ch|chr", htag)
+   if (length(chk)>0) {
+     warning("clearing prefix ch or chr from htag")
+     htag = gsub("ch|chr", "", htag)
+   }
+   snpgettag = paste0("ch", htag)
+   ggettag = paste0("chr", htag)
+   cursnps = getSNPlocs(snpgettag, as.GRanges=TRUE)
+   curgenome = unmasked(Hsapiens[[ggettag]])
+   ref_allele =
+     strsplit(as.character(curgenome[start(cursnps)]),
+       NULL, fixed=TRUE)[[1L]]
+   all_alleles = IUPAC_CODE_MAP[cursnps$alleles_as_ambig]
+   alt_alleles = mapply( function(ref,all)
+     sub(ref, "", all, fixed=TRUE),
+     ref_allele, all_alleles, USE.NAMES=FALSE)
```

```

+   cursnps$ref_allele = ref_allele
+   cursnps$alt_alleles = alt_alleles
+   cursnps$one_alt = substr(cursnps$alt_alleles, 1, 1)
+   altg = list(replaceLetterAt(curgenome, start(cursnps),
+     cursnps$one_alt))
+   names(altg) = faElFun(htag)
+   writeFasta(DNAStringSet(altg), file=faTargFun(htag))
+ }

```

7 Session information

```
> sessionInfo()
```

R version 4.5.0 RC (2025-04-04 r88126)

Platform: aarch64-apple-darwin20

Running under: macOS Ventura 13.7.1

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRblas.0.dylib

LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRlapack.dylib

locale:

[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/New_York

tzcode source: internal

attached base packages:

```

[1] parallel stats4 grid stats graphics grDevices utils
[8] datasets methods base

```

other attached packages:

```

[1] vtpnet_0.48.0 doParallel_1.0.17 iterators_1.0.14
[4] foreach_1.5.2 gwascat_2.40.0 GenomicRanges_1.60.0
[7] GenomeInfoDb_1.44.0 IRanges_2.42.0 S4Vectors_0.46.0
[10] Rgraphviz_2.52.0 graph_1.86.0 BiocGenerics_0.54.0
[13] generics_0.1.3

```

loaded via a namespace (and not attached):

```

[1] KEGGREST_1.48.0 SummarizedExperiment_1.38.0
[3] rjson_0.2.23 Biobase_2.68.0
[5] lattice_0.22-7 vctrs_0.6.5

```

[7] tools_4.5.0	bitops_1.0-9
[9] curl_6.2.2	tibble_3.2.1
[11] AnnotationDbi_1.70.0	RSQLite_2.3.9
[13] blob_1.2.4	pkgconfig_2.0.3
[15] Matrix_1.7-3	data.table_1.17.0
[17] BSgenome_1.76.0	dbplyr_2.5.0
[19] lifecycle_1.0.4	GenomeInfoDbData_1.2.14
[21] compiler_4.5.0	Rsamtools_2.24.0
[23] Biostrings_2.76.0	codetools_0.2-20
[25] snpStats_1.58.0	yaml_2.3.10
[27] RCurl_1.98-1.17	pillar_1.10.2
[29] crayon_1.5.3	BiocParallel_1.42.0
[31] cachem_1.1.0	DelayedArray_0.34.0
[33] abind_1.4-8	tidyselect_1.2.1
[35] dplyr_1.1.4	restfulr_0.0.15
[37] VariantAnnotation_1.54.0	splines_4.5.0
[39] fastmap_1.2.0	cli_3.6.4
[41] SparseArray_1.8.0	magrittr_2.0.3
[43] S4Arrays_1.8.0	GenomicFeatures_1.60.0
[45] survival_3.8-3	XML_3.99-0.18
[47] filelock_1.0.3	UCSC.utils_1.4.0
[49] bit64_4.6.0-1	XVector_0.48.0
[51] httr_1.4.7	matrixStats_1.5.0
[53] bit_4.6.0	png_0.1-8
[55] memoise_2.0.1	BiocIO_1.18.0
[57] BiocFileCache_2.16.0	rtracklayer_1.68.0
[59] rlang_1.1.6	glue_1.8.0
[61] DBI_1.2.3	jsonlite_2.0.0
[63] R6_2.6.1	zlibbioc_1.54.0
[65] GenomicAlignments_1.44.0	MatrixGenerics_1.20.0

8 Bibliography

References

Charles E Grant, Timothy L Bailey, and William Stafford Noble. Fimo: scanning for occurrences of a given motif. *Bioinformatics (Oxford, England)*, 27(7):1017–8, Apr 2011. doi: 10.1093/bioinformatics/btr064.

Matthew T Maurano, Richard Humbert, Eric Rynes, Robert E Thurman, Eric Haugen, Hao Wang, Alex P Reynolds, Richard Sandstrom, Hongzhu Qu, Jennifer Brody, Anthony Shafer, Fidencio Neri, Kristen Lee, Tanya Kutayavin, Sandra Stehling-Sun,

Audra K Johnson, Theresa K Canfield, Erika Giste, Morgan Diegel, Daniel Bates, R Scott Hansen, Shane Neph, Peter J Sabo, Shelly Heinfeld, Antony Raubitschek, Steven Ziegler, Chris Cotsapas, Nona Sotoodehnia, Ian Glass, Shamil R Sunyaev, Rajinder Kaul, and John A Stamatoyannopoulos. Systematic localization of common disease-associated variation in regulatory dna. *Science*, 337(6099):1190–5, Sep 2012. doi: 10.1126/science.1222794.