

vtpnet: variant-transcription factor-phenotype networks

VJ Carey

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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\\n\\nspondylitis", "Asthma",  
+ "Celiac\\n\\ndisease", "Crohn's\\n\\ndisease",  
+ "Multiple\\n\\nsclerosis", "Primary\\n\\nbiliary\\n\\ncirrhosis",  
+ "Psoriasis", "Rheumatoid\\n\\narthritis",  
+ "Systemic\\n\\nlupus\\n\\nerythematosus",  
+ "Systemic\\n\\nsclerosis", "Type 1\\n\\ndiabetes",
```

```

+       "Ulcerative\\ncolitis"
+ )
> 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)))

```

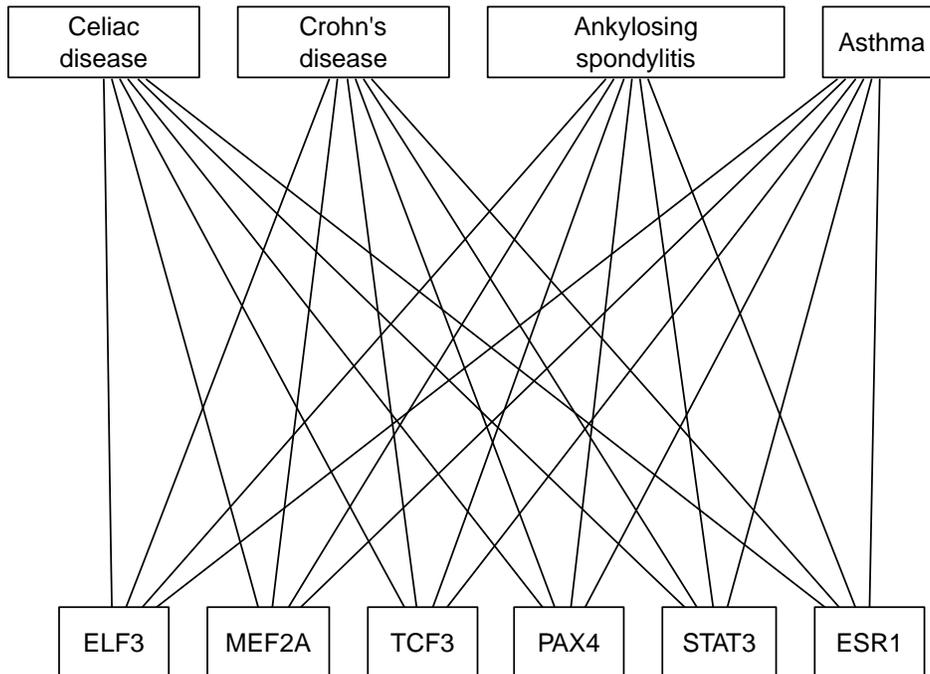


Figure 1: A complete bipartite graph for arbitrarily selected subsets of the autoimmune disorders and TFs found in Figure 4A of Maurano et al.

```
[1] 1862156
```

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

```
GRanges object with 4 ranges and 8 metadata columns:
```

| | seqnames | ranges | strand | source | type | score |
|-----|-------------------------|------------------------|-------------|-----------------------|------------------|-----------|
| | <Rle> | <IRanges> | <Rle> | <factor> | <factor> | <numeric> |
| [1] | chr1 | 10273-10302 | + | fimo nucleotide_motif | nucleotide_motif | 999.917 |
| [2] | chr1 | 10279-10308 | + | fimo nucleotide_motif | nucleotide_motif | 999.962 |
| [3] | chr1 | 11703-11732 | - | fimo nucleotide_motif | nucleotide_motif | 999.999 |
| [4] | chr1 | 11704-11733 | - | fimo nucleotide_motif | nucleotide_motif | 999.955 |
| | phase | Name | pvalue | qvalue | | |
| | <integer> | <character> | <character> | <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("gwascat")
> load(system.file("legacy/gwrngs19.rda", package="gwascat"))
> 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> |
| 15145 | http://www.ncbi.nlm... Loci on 7p12.2, 10q2.. Acute lymphoblastic .. | | |
| 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",
+ hgpacK = "BSgenome.Hsapiens.UCSC.hg19",
+ faElFun = function(x) sub("%%TAG%%", x, "alt%%TAG%%chr"),
+ faTargFun = function(x)
+   sub("%%TAG%%", x, "alt%%TAG%%_hg19.fa")) {
+   require(slpacK, character.only=TRUE)
+   require(hgpacK, 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 4.5.2 (2025-10-31)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.3 LTS

```

```
Matrix products: default
```

```
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p-r0.3.26.so; LAPACK ver
```

```
locale:
```

```

[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

```

```
time zone: Etc/UTC
```

```
tzcode source: system (glibc)
```

```
attached base packages:
```

```

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

```

```
other attached packages:
```

```

[1] vtpnet_0.51.0 doParallel_1.0.17 iterators_1.0.14
[4] foreach_1.5.2 gwascat_2.43.2 GenomicRanges_1.63.1
[7] Seqinfo_1.1.0 IRanges_2.45.0 S4Vectors_0.49.0
[10] Rgraphviz_2.55.0 graph_1.89.1 BiocGenerics_0.57.0
[13] generics_0.1.4

```

loaded via a namespace (and not attached):

| | |
|-------------------------------|-----------------------------|
| [1] tidyselect_1.2.1 | dplyr_1.2.0 |
| [3] blob_1.3.0 | filelock_1.0.3 |
| [5] Biostrings_2.79.4 | bitops_1.0-9 |
| [7] fastmap_1.2.0 | RCurl_1.98-1.17 |
| [9] BiocFileCache_3.1.0 | VariantAnnotation_1.57.1 |
| [11] GenomicAlignments_1.47.0 | XML_3.99-0.22 |
| [13] lifecycle_1.0.5 | survival_3.8-6 |
| [15] KEGGREST_1.51.1 | RSQLite_2.4.6 |
| [17] magrittr_2.0.4 | compiler_4.5.2 |
| [19] rlang_1.1.7 | tools_4.5.2 |
| [21] yaml_2.3.12 | data.table_1.18.2.1 |
| [23] rtracklayer_1.71.3 | knitr_1.51 |
| [25] S4Arrays_1.11.1 | bit_4.6.0 |
| [27] curl_7.0.0 | DelayedArray_0.37.0 |
| [29] abind_1.4-8 | BiocParallel_1.45.0 |
| [31] sys_3.4.3 | SummarizedExperiment_1.41.1 |
| [33] cli_3.6.5 | crayon_1.5.3 |
| [35] httr_1.4.8 | rjson_0.2.23 |
| [37] DBI_1.2.3 | cachem_1.1.0 |
| [39] splines_4.5.2 | AnnotationDbi_1.73.0 |
| [41] XVector_0.51.0 | restfulr_0.0.16 |
| [43] matrixStats_1.5.0 | vctrs_0.7.1 |
| [45] Matrix_1.7-4 | jsonlite_2.0.0 |
| [47] bit64_4.6.0-1 | GenomicFeatures_1.63.1 |
| [49] maketools_1.3.2 | snpStats_1.61.0 |
| [51] glue_1.8.0 | codetools_0.2-20 |
| [53] GenomeInfoDb_1.47.2 | BiocIO_1.21.0 |
| [55] UCSC.utils_1.7.1 | tibble_3.3.1 |
| [57] pillar_1.11.1 | rappdirs_0.3.4 |
| [59] BSgenome_1.79.1 | R6_2.6.1 |
| [61] dbplyr_2.5.2 | httr2_1.2.2 |
| [63] evaluate_1.0.5 | lattice_0.22-9 |
| [65] Biobase_2.71.0 | png_0.1-8 |
| [67] Rsamtools_2.27.0 | cigarillo_1.1.0 |
| [69] memoise_2.0.1 | SparseArray_1.11.10 |
| [71] xfun_0.56 | MatrixGenerics_1.23.0 |
| [73] buildtools_1.0.0 | pkgconfig_2.0.3 |

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 Kutuyavin, Sandra Stehling-Sun, Audra K Johnson, Theresa K Canfield, Erika Giste, Morgan Diegel, Daniel Bates, R Scott Hansen, Shane Neph, Peter J Sabo, Shelly Heimfeld, 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.