

ENCODE DREAM Challenge

John Reid

```
## Joining, by = c("TF", "cell")
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##	TF	cell	split	true.blind	split.blind
## 1	ARID3A	HepG2	train	FALSE	train
## 2	ARID3A	K562	ladder	FALSE	ladder
## 3	ATF2	GM12878	train	FALSE	train
## 4	ATF2	H1-hESC	train	FALSE	train
## 5	ATF2	MCF-7	train	FALSE	train
## 6	ATF2	K562	ladder	TRUE	ladder.blind
## 7	ATF2	HepG2	submit	TRUE	submit
## 8	ATF3	HCT116	train	FALSE	train
## 9	ATF3	H1-hESC	train	FALSE	train
## 10	ATF3	HepG2	train	FALSE	train
## 11	ATF3	K562	train	FALSE	train
## 12	ATF3	liver	ladder	FALSE	ladder
## 13	ATF7	GM12878	train	FALSE	train
## 14	ATF7	HepG2	train	FALSE	train
## 15	ATF7	K562	train	FALSE	train
## 16	ATF7	MCF-7	ladder	TRUE	ladder.blind
## 17	CEBPB	A549	train	FALSE	train
## 18	CEBPB	H1-hESC	train	FALSE	train
## 19	CEBPB	HCT116	train	FALSE	train
## 20	CEBPB	HeLa-S3	train	FALSE	train
## 21	CEBPB	HepG2	train	FALSE	train
## 22	CEBPB	IMR-90	train	FALSE	train
## 23	CEBPB	K562	train	FALSE	train
## 24	CEBPB	MCF-7	ladder	FALSE	ladder
## 25	CREB1	GM12878	train	FALSE	train
## 26	CREB1	H1-hESC	train	FALSE	train
## 27	CREB1	HepG2	train	FALSE	train
## 28	CREB1	K562	train	FALSE	train
## 29	CREB1	MCF-7	ladder	TRUE	ladder.blind
## 30	CTCF	A549	train	FALSE	train
## 31	CTCF	H1-hESC	train	FALSE	train
## 32	CTCF	HeLa-S3	train	FALSE	train
## 33	CTCF	HepG2	train	FALSE	train
## 34	CTCF	IMR-90	train	FALSE	train
## 35	CTCF	K562	train	FALSE	train
## 36	CTCF	MCF-7	train	FALSE	train
## 37	CTCF	GM12878	ladder	FALSE	ladder
## 38	CTCF	PC-3	submit	TRUE	submit
## 39	CTCF	induced_pluripotent_stem_cell	submit	TRUE	submit
## 40	E2F1	GM12878	train	FALSE	train
## 41	E2F1	HeLa-S3	train	FALSE	train
## 42	E2F1	K562	submit	TRUE	submit
## 43	E2F6	A549	train	FALSE	train
## 44	E2F6	H1-hESC	train	FALSE	train
## 45	E2F6	HeLa-S3	train	FALSE	train
## 46	E2F6	K562	ladder	FALSE	ladder

## 47	EGR1	GM12878	train	FALSE	train
## 48	EGR1	H1-hESC	train	FALSE	train
## 49	EGR1	HCT116	train	FALSE	train
## 50	EGR1	MCF-7	train	FALSE	train
## 51	EGR1	K562	ladder	FALSE	ladder
## 52	EGR1	liver	submit	TRUE	submit
## 53	EP300	GM12878	train	FALSE	train
## 54	EP300	H1-hESC	train	FALSE	train
## 55	EP300	HeLa-S3	train	FALSE	train
## 56	EP300	HepG2	train	FALSE	train
## 57	EP300	K562	train	FALSE	train
## 58	EP300	SK-N-SH	train	FALSE	train
## 59	EP300	MCF-7	ladder	FALSE	ladder
## 60	FOXA1	HepG2	train	FALSE	train
## 61	FOXA1	MCF-7	ladder	TRUE	ladder.blind
## 62	FOXA1	liver	submit	TRUE	submit
## 63	FOXA2	HepG2	train	FALSE	train
## 64	FOXA2	liver	submit	TRUE	submit
## 65	GABPA	GM12878	train	FALSE	train
## 66	GABPA	H1-hESC	train	FALSE	train
## 67	GABPA	HeLa-S3	train	FALSE	train
## 68	GABPA	HepG2	train	FALSE	train
## 69	GABPA	MCF-7	train	FALSE	train
## 70	GABPA	SK-N-SH	train	FALSE	train
## 71	GABPA	K562	ladder	FALSE	ladder
## 72	GABPA	liver	submit	TRUE	submit
## 73	GATA3	A549	train	FALSE	train
## 74	GATA3	SK-N-SH	train	FALSE	train
## 75	GATA3	MCF-7	ladder	FALSE	ladder
## 76	HNF4A	HepG2	train	FALSE	train
## 77	HNF4A	liver	submit	TRUE	submit
## 78	JUND	HCT116	train	FALSE	train
## 79	JUND	HeLa-S3	train	FALSE	train
## 80	JUND	HepG2	train	FALSE	train
## 81	JUND	K562	train	FALSE	train
## 82	JUND	MCF-7	train	FALSE	train
## 83	JUND	SK-N-SH	train	FALSE	train
## 84	JUND	H1-hESC	ladder	FALSE	ladder
## 85	JUND	liver	submit	TRUE	submit
## 86	MAFK	GM12878	train	FALSE	train
## 87	MAFK	H1-hESC	train	FALSE	train
## 88	MAFK	HeLa-S3	train	FALSE	train
## 89	MAFK	HepG2	train	FALSE	train
## 90	MAFK	IMR-90	train	FALSE	train
## 91	MAFK	K562	ladder	FALSE	ladder
## 92	MAFK	MCF-7	ladder	FALSE	ladder
## 93	MAX	A549	train	FALSE	train
## 94	MAX	GM12878	train	FALSE	train
## 95	MAX	H1-hESC	train	FALSE	train
## 96	MAX	HCT116	train	FALSE	train
## 97	MAX	HeLa-S3	train	FALSE	train
## 98	MAX	HepG2	train	FALSE	train
## 99	MAX	K562	train	FALSE	train
## 100	MAX	SK-N-SH	train	FALSE	train

## 101	MAX	MCF-7	ladder	FALSE	ladder
## 102	MAX	liver	submit	TRUE	submit
## 103	MYC	A549	train	FALSE	train
## 104	MYC	HeLa-S3	train	FALSE	train
## 105	MYC	K562	train	FALSE	train
## 106	MYC	MCF-7	train	FALSE	train
## 107	MYC	HepG2	ladder	FALSE	ladder
## 108	NANOG	H1-hESC	train	FALSE	train
## 109	NANOG induced_pluripotent_stem_cell	submit		TRUE	submit
## 110	REST	H1-hESC	train	FALSE	train
## 111	REST	HeLa-S3	train	FALSE	train
## 112	REST	HepG2	train	FALSE	train
## 113	REST	MCF-7	train	FALSE	train
## 114	REST	Panc1	train	FALSE	train
## 115	REST	SK-N-SH	train	FALSE	train
## 116	REST	K562	ladder	FALSE	ladder
## 117	REST	liver	submit	TRUE	submit
## 118	RFX5	GM12878	train	FALSE	train
## 119	RFX5	HeLa-S3	train	FALSE	train
## 120	RFX5	MCF-7	train	FALSE	train
## 121	RFX5	SK-N-SH	train	FALSE	train
## 122	RFX5	HepG2	ladder	FALSE	ladder
## 123	SPI1	GM12878	train	FALSE	train
## 124	SPI1	K562	ladder	FALSE	ladder
## 125	SRF	GM12878	train	FALSE	train
## 126	SRF	H1-hESC	train	FALSE	train
## 127	SRF	HCT116	train	FALSE	train
## 128	SRF	HepG2	train	FALSE	train
## 129	SRF	K562	train	FALSE	train
## 130	SRF	MCF-7	ladder	FALSE	ladder
## 131	STAT3	HeLa-S3	train	FALSE	train
## 132	STAT3	GM12878	ladder	FALSE	ladder
## 133	TAF1	GM12878	train	FALSE	train
## 134	TAF1	H1-hESC	train	FALSE	train
## 135	TAF1	HeLa-S3	train	FALSE	train
## 136	TAF1	K562	train	FALSE	train
## 137	TAF1	SK-N-SH	train	FALSE	train
## 138	TAF1	HepG2	ladder	FALSE	ladder
## 139	TAF1	liver	submit	TRUE	submit
## 140	TCF12	GM12878	train	FALSE	train
## 141	TCF12	H1-hESC	train	FALSE	train
## 142	TCF12	MCF-7	train	FALSE	train
## 143	TCF12	SK-N-SH	train	FALSE	train
## 144	TCF12	K562	ladder	TRUE	ladder.blind
## 145	TCF7L2	HCT116	train	FALSE	train
## 146	TCF7L2	HeLa-S3	train	FALSE	train
## 147	TCF7L2	Panc1	train	FALSE	train
## 148	TCF7L2	MCF-7	ladder	FALSE	ladder
## 149	TEAD4	A549	train	FALSE	train
## 150	TEAD4	H1-hESC	train	FALSE	train
## 151	TEAD4	HCT116	train	FALSE	train
## 152	TEAD4	HepG2	train	FALSE	train
## 153	TEAD4	K562	train	FALSE	train
## 154	TEAD4	SK-N-SH	train	FALSE	train

## 155	TEAD4	MCF-7	ladder	FALSE	ladder
## 156	YY1	GM12878	train	FALSE	train
## 157	YY1	H1-hESC	train	FALSE	train
## 158	YY1	HCT116	train	FALSE	train
## 159	YY1	HepG2	train	FALSE	train
## 160	YY1	SK-N-SH	train	FALSE	train
## 161	YY1	K562	ladder	FALSE	ladder
## 162	ZNF143	GM12878	train	FALSE	train
## 163	ZNF143	H1-hESC	train	FALSE	train
## 164	ZNF143	HeLa-S3	train	FALSE	train
## 165	ZNF143	HepG2	train	FALSE	train
## 166	ZNF143	K562	ladder	FALSE	ladder

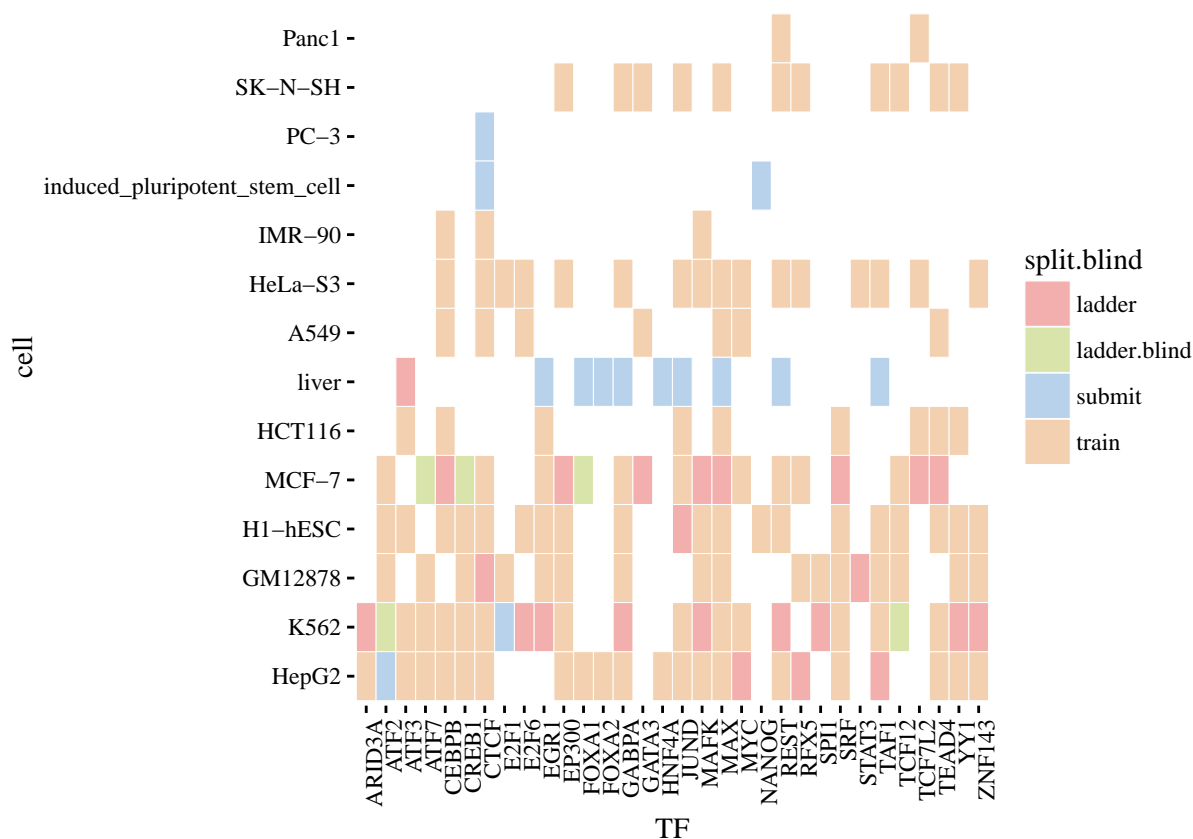
The ENCODE-DREAM challenge

The [challenge](#) is to predict cell-type specific binding of transcription factors (TFs) using four types of data:

- DNA sequence: a reference human genomic sequence
- *In-vitro* DNA shape: the physical shape of the genome in an *in-vitro* system
- DNase-seq: how open and accessible regions of the genome are
- RNA-seq: levels of gene expression

TF/cell-type combinations

TFs have different binding profiles in different cell types. 32 TFs and 14 cell types are represented in the data although not all combinations are present.



There are essentially three (two!?) prediction tasks:

- Held-out chromosomes: For each TF/cell-type combination, the ChIP-seq data will not be available for 3 chromosomes. Methods will be assessed by their predictive performance on these chromosomes.
- Across cell-type: Methods will be assessed by their performance on cell-types for which no training data has been made available (PC-3, induced pluripotent stem cells, liver).
- Within cell-type: Methods will be assessed on

Data

TF binding

TF binding is measured using the ChIP-seq protocol and converted to a binary score for sliding windows of 200bp. The windows slide by 50bp. For each 200bp location, binding is defined as bound (B), unbound (U) or ambiguous (A). In addition the challenge provides more detailed information from the ChIP-seq experiments including conservative and relaxed estimates of peaks and fold-control signals showing how enriched the ChIP-seq experiment was over a control background experiment. It is not clear how useful the extra information will be as it will obviously not be available on the held-out data.

DNA sequence

The human reference genome is over 3 billion base pairs long. Each base is represented as a character: adenine (A); cytosine (C); guanine (G) and thymine (T). The challenge is restricted to chromosomes 1-22 and chromosome X. All data in the challenge are defined with respect to release GRCh37/hg19. TFs tend to prefer to bind specific sequences. These preferences are summarised in binding motifs but these are not

known for all TFs. The only external data that is allowed to be used in this challenge are libraries of TF-DNA binding motifs. Obviously this data is not cell-type specific.

DNase-seq

Information on chromatin accessibility on a per-cell-type basis will be available in four formats:

- conservative peaks
- relaxed peaks
- filtered BAM alignment files
- fold-enrichment signal coverage tracks

The first two will be much easier to use as they summarise the last two.

DNA shape

Participants are encouraged to use the [DNAshapeR](#) to calculate DNA shape features across the genome. This information is not cell-type specific but has been shown to be predictive of TF-DNA binding. Note that DNAshapeR requires a version of R > 3.3.

Gene expression

Gene expression is regulated by TF binding and so should be useful indirectly to infer binding. The major difficulties are that - It is known which locations on the genome regulate which genes. Commonly TF binding sites regulate the closest gene but this is not always the case. - Several TFs can combine in an unknown way to regulate a gene. - There are other mechanisms of gene regulation that will confound the relationship.

Transcription factors

Motifs

- Hard to find motif for *TAF1*. Is *TBP* a good motif to use?