Saturn team write-up

We used `xgboost` (T. Chen and Guestrin 2016) to fit a gradient tree boosting model to a set of features derived from the called DNase peaks and a genome wide scan for known motifs and *de novo* motifs.

Features

We compiled a list of motifs that represented the binding specificities of all the TFs in the challenge from the following public motif databases:

- Human and Mouse high-throughput SELEX motifs from (Jolma et al. 2010)
- Human and Mouse HT-SELEX motifs from (Jolma et al. 2013)
- The Swiss Regulon human and mouse motifs (Pachkov et al. 2013)
- From (Zhao and Stormo 2011)
- JASPAR CORE (Mathelier et al. 2016)
- Direct and inferred motifs for *Homo sapiens* from (Weirauch et al. 2014)

We then perfomed a genome-wide scan of all these motifs using the `STEME` (Reid and Wernisch 2014) software to generate a set of putative binding sites. These were summarised as region-level features by the maximum of their log-odds ratio (Bayes factor?).

We used a discriminative motif finder, `DREME` (Bailey 2011), to find motifs that discriminated between the bound sequences and those that were unbound for each TF. In exactly the same way as for the known motifs, we perfomed a genome-wide scan and summarised the putative binding sites as region-level features on a per-TF basis.

We used `Wellington` (Piper et al. 2013), a DNase footprint detection algorithm to determine TF binding footprints in the DNase peaks. We used these to filter both the known motif binding sites and those the *de novo* sites.

Predictions

We applied a kernel smoothing method to the predictions. We adjusted the log odds ratio for each region using a Gaussian kernel. We used TF-specific

length-scales between 0 and 200 base pairs that we chose using cross-validation.

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