

Phylogenetic footprinting, a pipeline for motif identification in *Paramecium*

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Abstract

Author Summary

Introduction

Since Ohno first hypothesized the influence of Whole-Genome Duplications (WGD) (Ohno, 1970), scientists kept showing that a broad number of organisms experienced several rounds of WGD: *Saccharomyces cerevisiae* (Kellis et al., 2004), Angiosperms (Arrigo and Barker, 2012), Vertebrates (Dehal and Boore, 2005), Salmonids (Alexandrou et al., 2013), and many others. WGD are evolutionary event when the genome of a given individual is duplicated, meaning that the whole genome is in two copies, duplicated pairs of genes are called *paralogs*. WGD can also occur after two closely related species hybridize to avoid hybrid incompatibility issues.

WGDs may be involved in many evolutionary radiations (Alexandrou et al., 2013) as they provide the raw material to explore new evolutionary landscapes. A recent study on the horseshoe crab genome underlined that WGDs may be a more common phenomenon than stated. They showed that at least a WGD occurred in this conserved lineage, thus WGDs may not be evolutionary drivers.

Still, it seems that WGDs are widespread along the tree of life and since Ohno numerous models have been developed to explain the retention rate we observe between duplicate genes (reviewed in Innan and Kondrashov (2010)). Gene Balance Hypothesis is for example a well explored hypothesis in the literature, according to this hypothesis dosage-sensitive gene are more retained because of stoichiometry issues, it would thus explain the over retention of transcription factors and multi-complexes proteins.

To understand the consequences of WGDs we have been studying various *Paramecium* species (Beisson et al., 2010). *Paramecium* are a Ciliates group (See Fig. 1). Aury et al. showed that at least three round of WGDs occurred in the *Paramecium* genus (Aury et al., 2006), two of which occurred in the *aurelia* complex (see Fig. 2). This cryptic species complex of 13 reproductively isolated species is a great model to study the fate of duplicate genes (Catania et al. 2009, McGrath et al. 2014).

Recently, several studies unraveled the link between gene expression in gene retention after WGD in *Paramecium* (Gout et al. 2010, Arnaiz et al. 2010). Genes that are highly expressed are more likely to be retained than genes with a low expression. The COSTEX model proposed by the authors states that gene evolution is more constrained as gene expression is high. It explains well why highly expressed genes are more retained and why they evolve more slowly than other genes.

Having established this link between gene retention and expression level of the gene, it is normal to try to get better understanding of *Paramecium* regulatory sequences. The compactness of *Paramecium* genomes makes the study of regulatory elements easier than in other eukaryotic species (McGrath et al., 2014). *Paramecium* genomes have on average 250nt long inter-genic regions close to those of *Saccharomyces cerevisiae* (Chen et al., 2011). These short inter-genic regions are known, in *S. cerevisiae*, to regulate genes directly downstream of them. Transcription regulator is thus far easier to study as for each gene its *cis*-regulatory sequence is directly upstream of it and not hundreds of thousand bases away as it can be the case in mammalian genomes. Because *Paramecium* also have very short inter-genic regions, it is reasonable to assume that the promoters share the same mechanisms.

Various strategies to study regulatory elements evolution have been developed (Wittkopp and Kalay,

2012); the idea being that regulatory elements can be conserved along evolution, some tools can detect these more conserved regions and thus output putative motifs. Phylogenetic footprinting is one of the approaches developed when trying to detect motifs among several species (Zhang and Gerstein, 2003), the idea being that regulatory motifs tend to be conserved by purifying selection (Nelson and Wardle, 2013), while non-functional elements will accumulate mutation along evolution. The motifs are then weighted by the phylogenetical relationships of the given sequences, *id est*, if a motif is found in two closely related species it will have less weight than if it is detected between two distant species.

In this paper we develop a phylogenetic footprinting workflow to study the *cis*-regulatory elements among three *aurelia* species: *P. biaurelia*, *P. sexaurelia*, *P. tetraurelia* and a more basal species *P. caudatum*. The three *aurelia* experienced two specific rounds of WGD compared to *P. caudatum*, thus when studying orthology and paralogy groups between genes, they can contain up to 13 different genes: 1 from *P. caudatum* and 4 from each *aurelia* species. Using those groups we use our workflow to identify conserved motifs in the upstream regions in each group.

Methods

We set up a pipeline using Biopython (Cock et al., 2009) to make our analysis (Fig. 3), the code is available at <https://github.com/LynchLabGroup/para>

Genomes and Annotation

We used annotation and sequence from our previous analyses for *P. caudatum* & the species from the *aurelia* complex. (see McGrath et al. 2014)

Gene families

Looking at the phylogenetic tree of the *aurelia* species, two WGDs occurred at the root and affected three of our species. We have established some gene families from WGD2 using comparison, each family contains a set of orthologous genes between the four *aurelia* species studied, and eventually, the paralogous gene found in each species; at maximum the families contain 13 different genes. Those families were established previously in our team. For details in the method see (McGrath et al. 2014 & McGrath *et al.* in press)

Upstream sequences extraction

For each gene, we extracted 250nt upstream of the start codon. If the previous gene was less than 250nt away, we reduced the extracted region so that it includes only inter-genic region. If the region was less than 15nt long, we removed the gene from the family. Sequences were extracted so that the first nucleotide of each one was the nearest from the start codon.

Coding Sequences extraction and alignment

Phylogenetic footprinting requires a phylogenetic tree to weigh the evolutionary signal of given motifs (Zhang and Gerstein, 2003). A motif conserved between two close species will have less importance than a motif conserved in two distant species. Because we are focusing on the conservation of upstream sequences we chose not to use them to avoid circularity. Instead, corresponding coding sequences (CDS) were extracted and used to model phylogenetic trees for each family. We preferred to have a gene tree over species tree, to avoid eventual inconsistencies because of gene conversion (ref. needed). See Challenges section for explanations on the use of gene tree over species tree.

CDSs in each family were aligned using TranslatorX (Abascal et al., 2010) a protein-guided alignment software. The Maximum Likelihood (ML) tree was then computed using PhyML (Guindon et al., 2010) the HKY85 model.

Phylogenetic footprinting

We used a phylogenetic footprinting software BigFoot (Satija et al., 2009) to detect highly conserved motifs in upstream sequences. We used 10000 burn-in cycles and 20000 cycles with a sampling rate of 1000 for the Hidden Monte-Carlo Markov Chain (HMC MC) process. BigFoot aligns the given sequences with gaps and tries to identify conserved and non-conserved regions ; it models the evolution of those regions along the phylogenetic tree assuming conserved regions evolve more slowly than non-conserved ones. At the end of the analysis BigFoot outputs an alignment of sequences used to identify slow and fast evolving regions as well as, for each nucleotide in the alignment, the posterior probability of the alignment, higher values show higher confidence in the alignment, and the phylogenetic footprinting result, higher values indicating higher posterior probability of purifying selection.

Using a phylogenetic footprinting program means we have to use a phylogenetic tree and depending on the phylogenetic tree we are using, the evolutionary signal used in the footprinting is not identical.

The species tree (see Fig. 2) gives us the relation between all considered, accounting for the various splits between species along with WGDs. The problem is that, not all gene families follow this tree. Because of the high similarity between duplicates, gene conversion occurs, the paralogs may recombine in a "copy-paste" way, we do not know what is the tree in each family and have to compute it for each of them.

Transcription factor binding sites are known to be generally conserved but degenerate on certain positions. For example, Whitfield et al. 2012 showed that this motif was conserved in human promoters with several highly variable positions (Fig. 4). Thus, to seek biologically relevant motifs, we had to take into account that in the middle of motifs, the phylogenetic score could drop on several positions, before rising again.

BigFoot does not output directly identified motifs, instead it produces two files with an alignment of the sequences and associated phylogenetic and alignment scores, as explained above. Using these scores we detected motifs of at least 6 nucleotides long, alignment score over 0.8 and phylogenetic score over 0.9. Because of the known biological nature of Transcription Factor Binding Sites, we allowed for a "gap" in motifs of 2 nucleotide, so that the scores could drop under the thresholds in those gaps (see Fig. 5). (Still need to add scores distribution)

To answer this problem we use a sliding window method of 8 nucleotides in our analysis: for each family, we looked at the scores of 8 nucleotides at the time and slide along the sequences. If the window contained at least 6 bases with scores above our thresholds, we would retain this motif. Then, from this particular region we would try to extend the sequence by adding adjacent nucleotides with good scores.

Comparison with MEME

To check our predictions and assess the conservation of found motifs, we compared motifs prediction with those of MEME (Bailey et al., 2006), a widely used *ab initio* motif finding tools. It searches for statistically significant motifs, with a gap-less, local multi-alignment system.

MEME was shown to have a very high False Positive Rate of the discovery (Zia and Moses, 2012). That is why many studies combine multiple motif detection tools (Liseron-Monfils et al., 2013). In our case, MEME is of particular interest as it obtains motifs using a totally different method from BigFoot.

To assess the relevance of motifs found from BigFoot's outputs, we compared them to a well-known motif finding program: MEME. For each family we identified overlapping motifs between MEME and

BigFoot. We computed an overlapping index as follows:

$$0 \leq \frac{\text{nucleotides in common}}{\text{size of the smallest motif}} \leq 1 \quad (1)$$

if this index was over 0.9 we would then considered the motif as relevant.

Motif classification and data analysis

All the analyses were produced using R, scatter plots and graphs were produced using the R package ggplot2.

Results

From our orthologs and paralogs gene families we had 5751 families, only 5008 gene families had at least 4 genes. Among these 5008 families BigFoot found 811 motifs in 608 families. From these 811 motifs 117 matches with motifs found by MEME.

Future Directions

We identified motifs using an automated pipeline (Fig. 3), comparing motifs identified using phylogenetic footprinting and statistical enrichment methods. We were able to detect X motifs, associated with specific expression values and distance. Still, we plan to improve this pipeline in several ways.

After identifying motifs, we scan the entire *Paramecium* genomes to find associated genes, however we only search for perfect matches. Thus, we do not take into account degenerate motifs. Thus we can miss genes that have slightly different motifs. Recently XXX showed that looking exact matches during motif identification may miss most of the signal. Indeed we have increase evidence that real motifs are most of the time degenerate and that Transcription Factor binding mostly depends on the general DNA context.

After identifying motifs, one's might want to group the motifs by similarity. We generally think about motifs as families, having specific sequences with some variation. For the moment, in our pipeline, we do not cluster motifs using "supposed" family, we consider each exact motifs as unique. However, several clustering methods exist to measure the diversity among motifs. The small sizes of motifs (about 6nt to 15nt) make these methods complicated to develop. Several methods have been implemented, but still, are not adapted for motifs and do not output families of motifs.

Another way to think about the problem can be to cluster motifs according to features one can measure on them. For example, one can compute several statistical indexes on motifs to compare. Thus we do not need to implement a new algorithm to cluster motifs as other classical methods such as principal components analysis, hierarchal clustering or *k*-means clustering can be applied. Still, these methods rely on the indexes you choose to measure, the motifs you are studying have to have well-defined clusters using those variables. We tried to cluster the studied motifs with this hierarchal clustering method (Fig.).

Several other new methods have been proposed to cluster motifs as they are, considering the sequences and the variability along each nucleotide. Some of them rely on position-specific weight matrices (PSM) which are matrices of the abundances of each base at each position. In a future improvement of the pipeline we cool try to implement such methods to reduce the redundancy of our data.

It has been proven that most motif identification tools have a high false positive discovery rate, thus, we need ways to confirm the relevance of found motifs. One way used by [Liseron-Monfils et al. 2013](#) is to increase the number of tools used in the pipeline, in their analysis they used MEME, XXX and XXX and filtered out significant results and then only combined them. Here we used MEME and BigFoot but we could include other tools in our workflow.

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Figure Legends

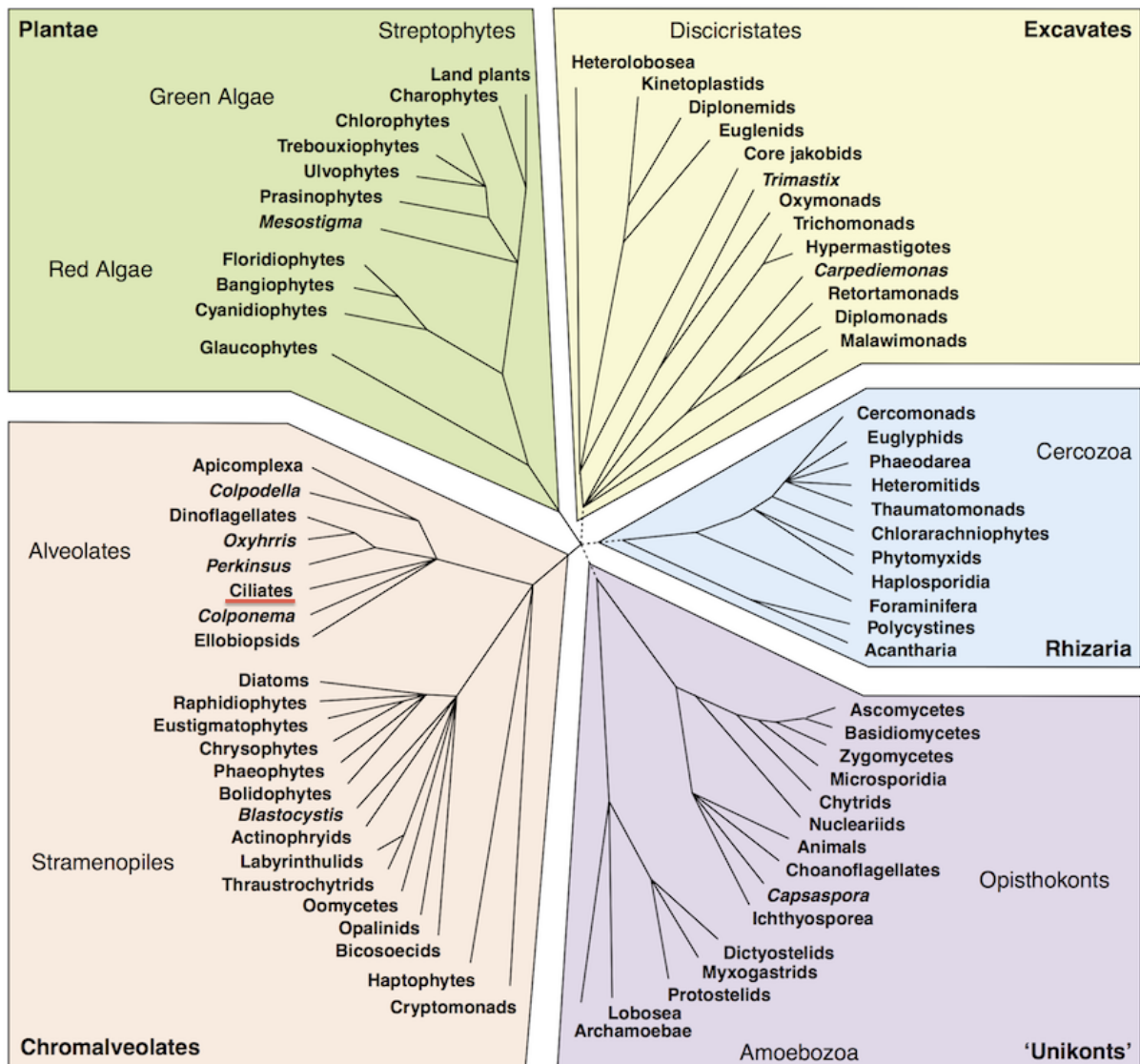


Figure 1. Phylogenetic tree of eukaryotes phylas. The *Ciliates* group, underlined in red in the figure, inside the Alveolates among the Chromoalveolates, it contains the *Paramecium* genus. While the Animals (Metazoa) belong to the Opisthokonts group. From (Keeling et al., 2005)

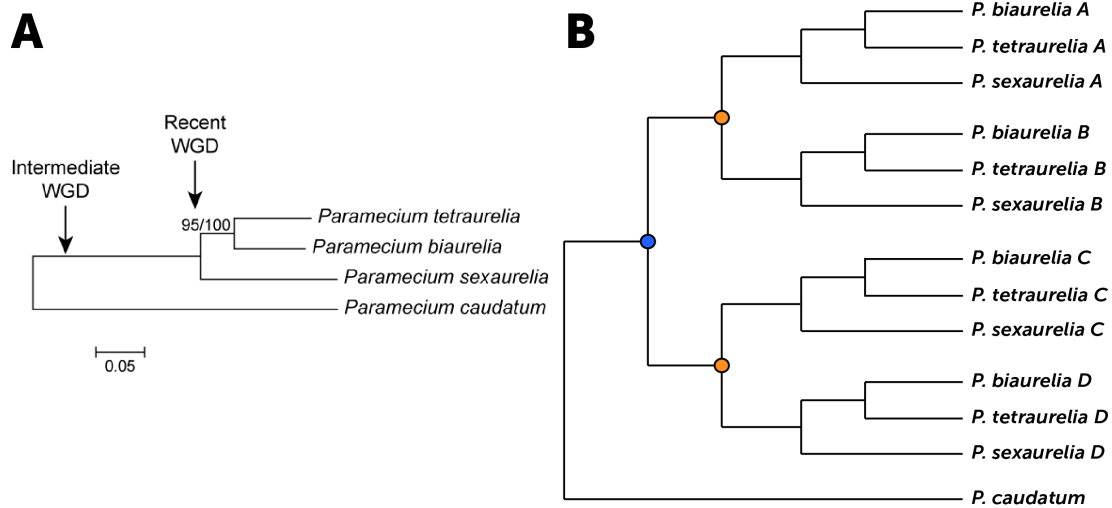


Figure 2. Phylogenetic trees of *Paramecium* and according gene tree. A: *Paramecium* species tree with WGD positions (Adapted from McGrath et al. 2014); B: An example of a family gene tree. A single *caudatum* gene and four genes for each *aurelia* species. *Legend:* blue circle, intermediary WGD; orange circle, more recent WGD; as dated by (Aury et al., 2006). (Adapted from McGrath et al. 2014)

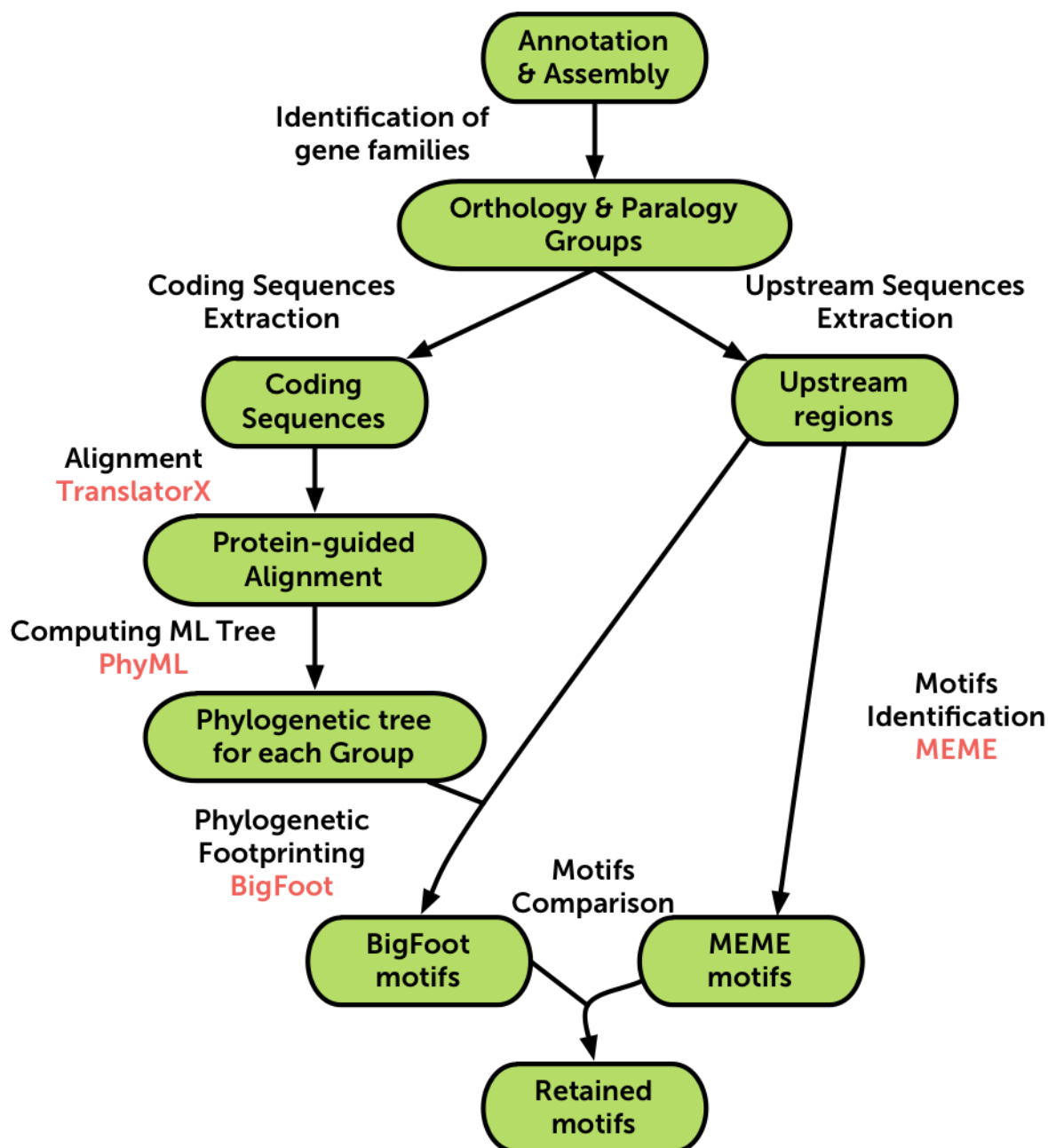


Figure 3. Flow chart of the whole pipeline. From the genome assembly and annotation of the four species, we used orthology and paralogy groups from (McGrath et al., 2014). For each of these families we extracted the coding sequences (CDS) as well as upstream regions from the start codon. We built a maximum likelihood phylogenetic tree using PhyML on pre-aligned CDS with TranslatorX (Abascal et al., 2010). On the one hand we computed the first fifth motifs of size of at least 4 nt using MEME on upstream regions (Bailey et al., 2006), while on the other hand using both the tree and the upstream sequences were used to detect motifs with a phylogenetic footprinting approach using BigFoot (Satija et al., 2009). We then retained only conserved motifs between MEME and BigFoot.



Figure 4. Degenerate Motif Example. This is a binding site from [Whitfield et al. 2012](#), in human promoters. Some positions are clearly conserved, like position 5 with T, while others are highly variable (positions 1 and 4). Transcription Factor Binding Sites are very conserved on some positions while highly variable on others.

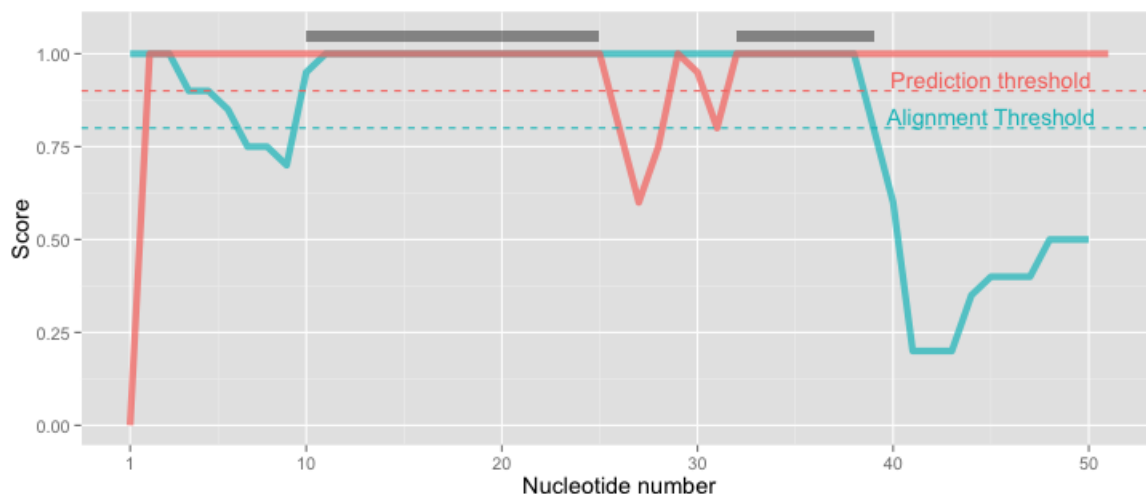


Figure 5. Motif detection from BigFoot example. BigFoot proceeds to phylogenetic prediction using an alignment technique, refer to ([Satija et al., 2009](#)) for more informations. For each position in the alignment, BigFoot assigns an alignment confidence score and phylogenetic footprinting, *i.e.* motif prediction, confidence score. In our analysis we used a detection technique to allow gaps in both the prediction and the alignment score. Curves: Red solid: Prediction score, Red dashed: Prediction threshold used, Blue solid: Alignment score, Blue dashed: Alignment threshold. Gray boxes: potential motifs detected in the sequence.

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