

Plus

1. DREME (Discriminative Regular Expression Motif Elicitation)

- **Purpose:** Identifies short, statistically significant **motifs** (usually 6-8 nucleotides long) that occur more frequently in an input set of sequences compared to a control set.
- **Method:**
 - Uses an **efficient heuristic algorithm** to find **regular expression-like motifs** that are overrepresented.
 - Employs **p-values** and **E-values** to rank motifs based on significance.
 - Faster than MEME, but **finds simpler motifs**.
- **Output:** Provides a list of **short motifs** with their occurrence frequency and **statistical significance**.

2. MEME (Multiple EM for Motif Elicitation)

- **Purpose:** Identifies **longer**, more complex **de novo motifs** in **unbiased** sequence data.
- **Method:**
 - Uses the **Expectation-Maximization (EM) algorithm** to iteratively refine motifs that best explain the observed sequences.
 - Can detect motifs in **three different modes**:
 - **OOPS (One Occurrence Per Sequence)** – assumes each sequence contains exactly **one** instance of the motif.
 - **ZOOPS (Zero or One Occurrence Per Sequence)** – assumes each sequence contains **zero or one** instance of the motif.
 - **TCM (Two-Component Mixture)** – assumes motifs can occur **multiple times** in a sequence.
- **Limitations:** Computationally expensive, so it is run on a **subset (600 sequences) of the input data** in MEME-ChIP.
- **Output:** Provides motifs as **position-specific probability matrices (PSPMs)**, along with **E-values** for statistical significance.

3. AME (Analysis of Motif Enrichment)

- **Purpose:** Determines whether known motifs (e.g., from the **JASPAR CORE database**) are statistically enriched in a given set of sequences.
- **Method:**
 - Takes an input motif **database (like JASPAR, TRANSFAC, etc.)** and compares it to the input sequences.
 - Uses **rank-based enrichment tests** to calculate **p-values** and **E-values** for each motif.
 - Can apply different scoring methods, such as **Wilcoxon rank-sum test**, **Fisher’s Exact Test**, or **Binomial Test**.
- **Output:** Lists **significantly enriched motifs** with **statistical scores**, helping determine which known transcription factor (TF) motifs are **most relevant** to the dataset.

Comparison Summary

Tool	Purpose	Motif Length	Algorithm	Output
DREME	Finds short, statistically overrepresented motifs	Short (6-8 bp)	Heuristic, p-value based	List of simple enriched motifs
MEME	Identifies de novo motifs in unbiased sequences	Variable (longer)	Expectation-Maximization (EM)	PSPMs , probability matrices

Tool	Purpose	Motif Length	Algorithm	Output
AME	Tests for statistical enrichment of known motifs	Uses known motifs	Rank-based statistical tests	List of enriched known motifs