

About MAMA score

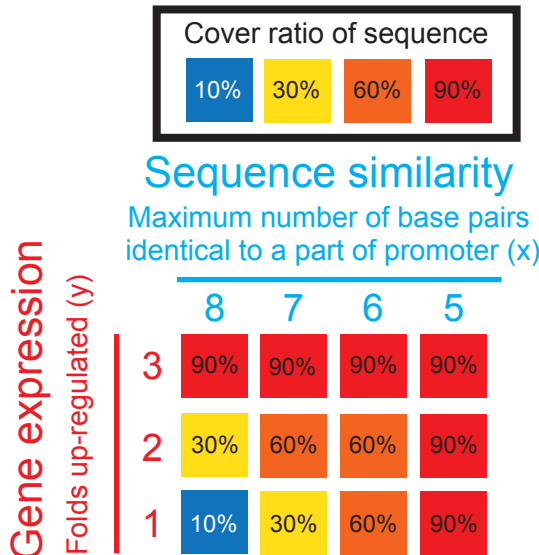
The MAMA score was calculated from gene expression and sequence similarities. The following examples will help clarify how this score is related to gene expression and sequence similarities.

How to calculate MAMA score

CR: Cover ratio

CR = $N(x|y)/N(y)$ $N(x|y)$: number of genes that have x bp of identical sequence to a candidate sequence and upregulated y -folds

$N(y)$: number of genes upregulated y -folds





$$\text{*MAMA score} = \frac{\sum(\text{CR} \cdot x \cdot y)}{\sum(\text{CR} \cdot x)}$$

* In the paper, x was replaced with h_score , y was replaced with r_score , and each gene (1/1) was used instead of the cover ratio.

$$\begin{aligned} & \{(0.9 \cdot 8 \cdot 3) + (0.9 \cdot 7 \cdot 3) + (0.9 \cdot 6 \cdot 3) + (0.9 \cdot 5 \cdot 3) \\ & + (0.3 \cdot 8 \cdot 2) + (0.6 \cdot 7 \cdot 2) + (0.6 \cdot 6 \cdot 2) + (0.9 \cdot 5 \cdot 2) \\ & + (0.1 \cdot 8 \cdot 1) + (0.3 \cdot 7 \cdot 1) + (0.6 \cdot 6 \cdot 1) + (0.9 \cdot 5 \cdot 1)\} \\ & / \{(0.9 \cdot 8) + (0.9 \cdot 7) + (0.9 \cdot 6) + (0.9 \cdot 5) \\ & + (0.3 \cdot 8) + (0.6 \cdot 7) + (0.6 \cdot 6) + (0.9 \cdot 5) \\ & + (0.1 \cdot 8) + (0.3 \cdot 7) + (0.6 \cdot 6) + (0.9 \cdot 5)\} = 2.25 \end{aligned}$$

MAMA score and examples

	Score	Exsample												
Candidate sequence A  <table border="1"> <tr><td>90%</td><td>90%</td><td>90%</td><td>90%</td></tr> <tr><td>90%</td><td>90%</td><td>90%</td><td>90%</td></tr> <tr><td>90%</td><td>90%</td><td>90%</td><td>90%</td></tr> </table>	90%	90%	90%	90%	90%	90%	90%	90%	90%	90%	90%	90%	2.0	Common sequence
90%	90%	90%	90%											
90%	90%	90%	90%											
90%	90%	90%	90%											
Candidate sequence B  <table border="1"> <tr><td>10%</td><td>30%</td><td>60%</td><td>90%</td></tr> <tr><td>10%</td><td>30%</td><td>60%</td><td>90%</td></tr> <tr><td>10%</td><td>30%</td><td>60%</td><td>90%</td></tr> </table>	10%	30%	60%	90%	10%	30%	60%	90%	10%	30%	60%	90%	2.0	Completely at random Sequences 8 bp identical are rare Sequences 5 bp identical are common
10%	30%	60%	90%											
10%	30%	60%	90%											
10%	30%	60%	90%											
Candidate sequence C  <table border="1"> <tr><td>30%</td><td>30%</td><td>60%</td><td>90%</td></tr> <tr><td>10%</td><td>30%</td><td>60%</td><td>90%</td></tr> <tr><td>10%</td><td>30%</td><td>60%</td><td>90%</td></tr> </table>	30%	30%	60%	90%	10%	30%	60%	90%	10%	30%	60%	90%	2.05	8 bp identical sequence is enriched in genes upregulated threefold when it is compared from that of onefold
30%	30%	60%	90%											
10%	30%	60%	90%											
10%	30%	60%	90%											
Candidate sequence D  <table border="1"> <tr><td>30%</td><td>60%</td><td>60%</td><td>60%</td></tr> <tr><td>10%</td><td>30%</td><td>30%</td><td>60%</td></tr> <tr><td>10%</td><td>10%</td><td>30%</td><td>60%</td></tr> </table>	30%	60%	60%	60%	10%	30%	30%	60%	10%	10%	30%	60%	2.25	8 bp identical sequence is enriched in genes upregulated threefold 7 bp identical sequence is enriched in genes upregulated two- and threefold 6 bp identical sequence is enriched in genes upregulated threefold
30%	60%	60%	60%											
10%	30%	30%	60%											
10%	10%	30%	60%											

MAMA scores become higher if identical sequences are enriched in upregulated genes.