摘要：搜索基因组中CpxR潜在结合位点并用pssm打分。

生成pwm（Position-Weight Matrices）数据源：表格1

生成pssm（Position-Specific Scoring Matrices）：pseudocounts=0.5，log2，假定四种碱基背景概率相等。

PSSM信息：

打分矩阵见表格2。

mean = 10.78, standard deviation = 4.19

max = 19.11, min = -37.44

mean即相对熵

Searching for matches using the PSSM score：

基因组：NC\_000913.3（W3110） CP009273.1(BW25113)

threshold=6.58

结果说明：pos代表cpxR结合第一个碱基位置，“\_c”代表互补链，seq为序列。Score即以上打分，默认按照序列 位置排序，这样容易发现一个基因存在多个潜在结合位点的情况。也可以按照score自行排序，也可给定其它筛选阈值我来重新给出结果。Location代表潜在结合位点所在位置的基因信息。

表格1：CpxR结合位点数据源

|  |  |
| --- | --- |
| degP1 | GTAAAAATTTATTGT |
| skp | GTAAAACCTGGTAAG |
| ppiD1 | GTAAACTAAGCGTTG |
| ppiD2 | GTAAAGCACTGAAAG |
| ppiD3 | GTAAAGAGATCACCA |
| tomB | GTAATTTTTCGTAAT |
| aroG | GTAAAACCCCGTTTA |
| ldtD | GCAACTCCCTGAAAC |
| ompF1 | GTAACCAAAAGTAAA |
| yccA | GTAAAGATGGGTAAA |
| csgD-csgB1 | GAAATCAGATGTAAT |
| csgD-csgB2 | GTTACATTTAGTTAC |
| csgD-csgB4 | GTAACGCAGCGTTAA |
| csgD-csgB5 | GTAACTAAATGTAAC |
| csgD-csgB6 | GTAAAAAATTGTCCA |
| marR | GCAAGTATAAGTCAA |
| spy | GTAAAACAATGAAAG |
| yebE | GTATATCGAGACAAA |
| motA | GTAAAAAGACGTAAA |
| ftnB | GTAAAAATATATAAA |
| mdtA | GGAATCGTCTGAATG |
| ompC | GTAAAGAAGGGTAAA |
| rseD | GTAAAGTTCCGTAAC |
| ung | GCAAAAAAATGTAAA |
| bamE | GCAAAACGCCGTAAG |
| yqaE | GTAAATGAGAGTAAA |
| bacA | GTAAAGCGGCGAAAA |
| ppiA | GTAAAATTAGGTAAA |
| yidQ | GTAAAGCGGGGATAA |
| srkA | GTAAAAGCTTGTAAG |
| cpxR-cpxP1 | GTAAAACAACGTAAA |
| cpxR-cpxP2 | GCAAACATGCGTCAG |
| psd | GTAAAAACGCGTAAA |
| tsr | GTAAAGTAAGGTAAA |
| slt | GTAACGTGGCGTAAA |
| fabA | GTAGAAGAAGGCAAA |
| fabB | GTAAGGCTGCGCAAA |

表格2 Position-Specific Scoring Matrices

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| A: | -4.29 | -2.7 | 1.9 | 1.86 | 1.44 | 0.67 | 0.57 | 0.47 | 0.67 | -1.1 | -1.5 | -0.4 | 1.5 | 1.69 | 1.21 |
| C: | -4.29 | -0.8 | -4.3 | -4.3 | -0.58 | -0.8 | 0.36 | -0.83 | -0.6 | 0.36 | -2 | -1.5 | -1.1 | -2 | -1.1 |
| G: | 1.94 | -2.7 | -4.3 | -2.7 | -1.96 | 0.24 | -1.1 | -0.2 | 0.11 | -0 | 1.74 | -2.7 | -4.3 | -2.7 | -0.2 |
| T: | -4.29 | 1.65 | -2.7 | -2.7 | -1.48 | -0.6 | -0.4 | 0.24 | -0.6 | 0.36 | -4.3 | 1.44 | -0.6 | -1.5 | -1.5 |