

TF input data and Logos from motif-finders are available at:
http://www.cs.cornell.edu/~ppn3/alico_suppl/alico_suppl.html

Table 1: Performance of individual motif finders

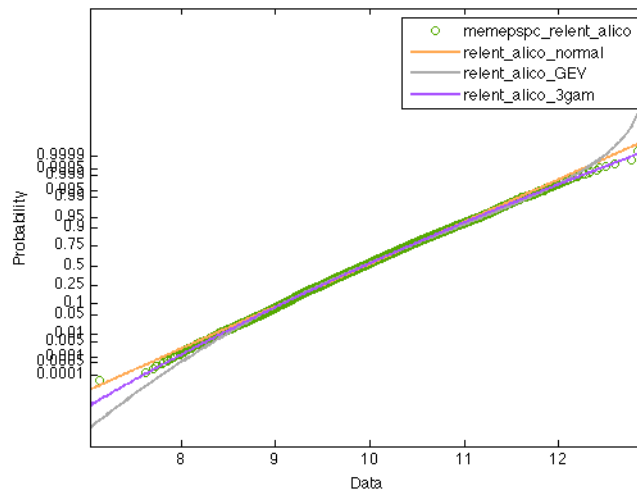
Finder	Width parameter	successes (out of 156)
PRIORITY- \mathcal{C}	8	66
PRIORITY- \mathcal{C}	13	63
PRIORITY- \mathcal{C}	18	52
MEME- \mathcal{C}	8	48
MEME- \mathcal{C}	13	45
MEME- \mathcal{C}	18	27
PhyloCon	N/A	37
GibbsMarkov	8	73
GibbsMarkov	13	73
GibbsMarkov	18	68

Table 2: Vertical constraint of 100 null sets from Drosophila (6 species)

Sequence pair	Template PID	ALICO samples (5%, median, 95%)	WAS (5%, median, 95%)
DroMel, DroSim	0.949261	0.948543, 0.948957, 0.949459	0.808509, 0.949348, 0.995377
DroMel, DroAna	0.746356	0.758876, 0.759838, 0.760745	0.571173, 0.743429, 0.858268
DroMel, DroSec	0.946809	0.945834, 0.946287, 0.946639	0.835395, 0.946660, 0.980406
DroMel, DroYak	0.885678	0.892422, 0.893157, 0.893819	0.672180, 0.887459, 0.964042
DroMel, DroEre	0.886409	0.888009, 0.888716, 0.889289	0.686341, 0.887382, 0.951092
DroSim, DroAna	0.751382	0.762772, 0.763617, 0.764654	0.571196, 0.747662, 0.861628
DroSim, DroSec	0.973060	0.971068, 0.971472, 0.971755	0.898480, 0.974964, 0.990406
DroSim, DroYak	0.891986	0.897740, 0.898350, 0.899283,	0.655130, 0.893729, 0.950000
DroSim, DroEre	0.892559	0.893347, 0.894021, 0.894467	0.668643, 0.887039, 0.976165
DroAna, DroSec	0.749012	0.761173, 0.761901, 0.762592	0.551982, 0.741673, 0.854913
DroAna, DroYak	0.743106	0.763832, 0.764539, 0.765426	0.569576, 0.752339, 0.850394
DroAna, DroEre	0.750019	0.762790, 0.763721, 0.764910	0.588965, 0.748346, 0.854052
DroSec, DroYak	0.889086	0.894996, 0.895355, 0.896240,	0.696892, 0.887326, 0.967195
DroSec, DroEre	0.889889	0.890688, 0.891252, 0.891965	0.671972, 0.884232, 0.954413
DroYak, DroEre	0.905828	0.913561, 0.913795, 0.914227	0.772598, 0.904078, 0.958388

Figure 1: Parametric fit for MEME-C null distribution. MEME-C was applied to 10,000 sets of ALICO and WAS resampled alignment-set with GAL4_YPD as template. The x-axis is the relative-entropy score returned by MEME.

(a) ALICO



(b) WAS

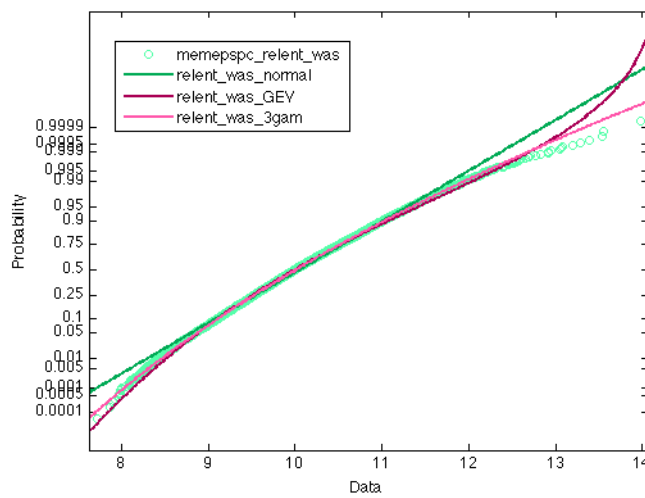
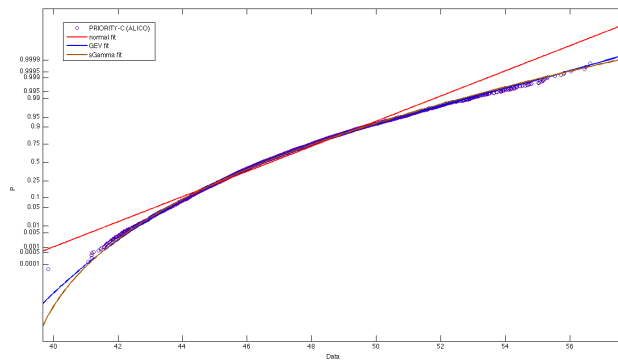


Figure 2: Parametric fit for PRIORITY-C null distribution. PRIORITY-C was applied to 10,000 sets of ALICO and WAS resampled alignment-set with GAL4_YPD as template. The x-axis is the score returned by PRIORITY-C.

(a) ALICO



(b) WAS

