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Seventy-nine known regulons in *E. coli*, *B. subtilis*, *S. Cerevisiae*, and *D. melanogaster* were used to compare

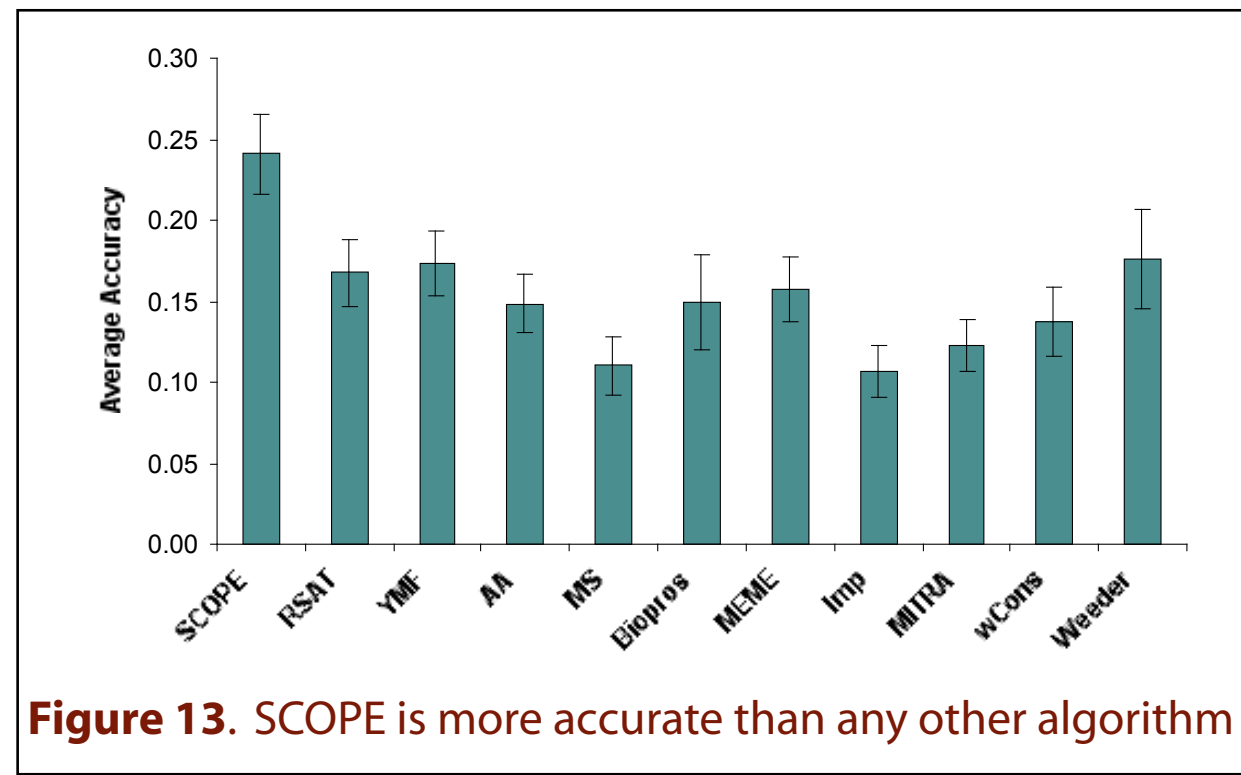


Figure 13. SCOPE is more accurate than any other algorithm

SCOPE to the 10 most popular and accurate motif finders. The results of that comparison are shown in **Figure 13**. Using the standard phi score accuracy metric, SCOPE clearly outperforms all other motif finders. Head-to-head comparisons are shown in **Figure 14**. *SCOPE wins 82% of these comparisons*. Thus, SCOPE presents a significant improvement in the ability to identify potential regula-

tory motifs in sets of genes. In addition to its improved accuracy, SCOPE is very robust to noisy

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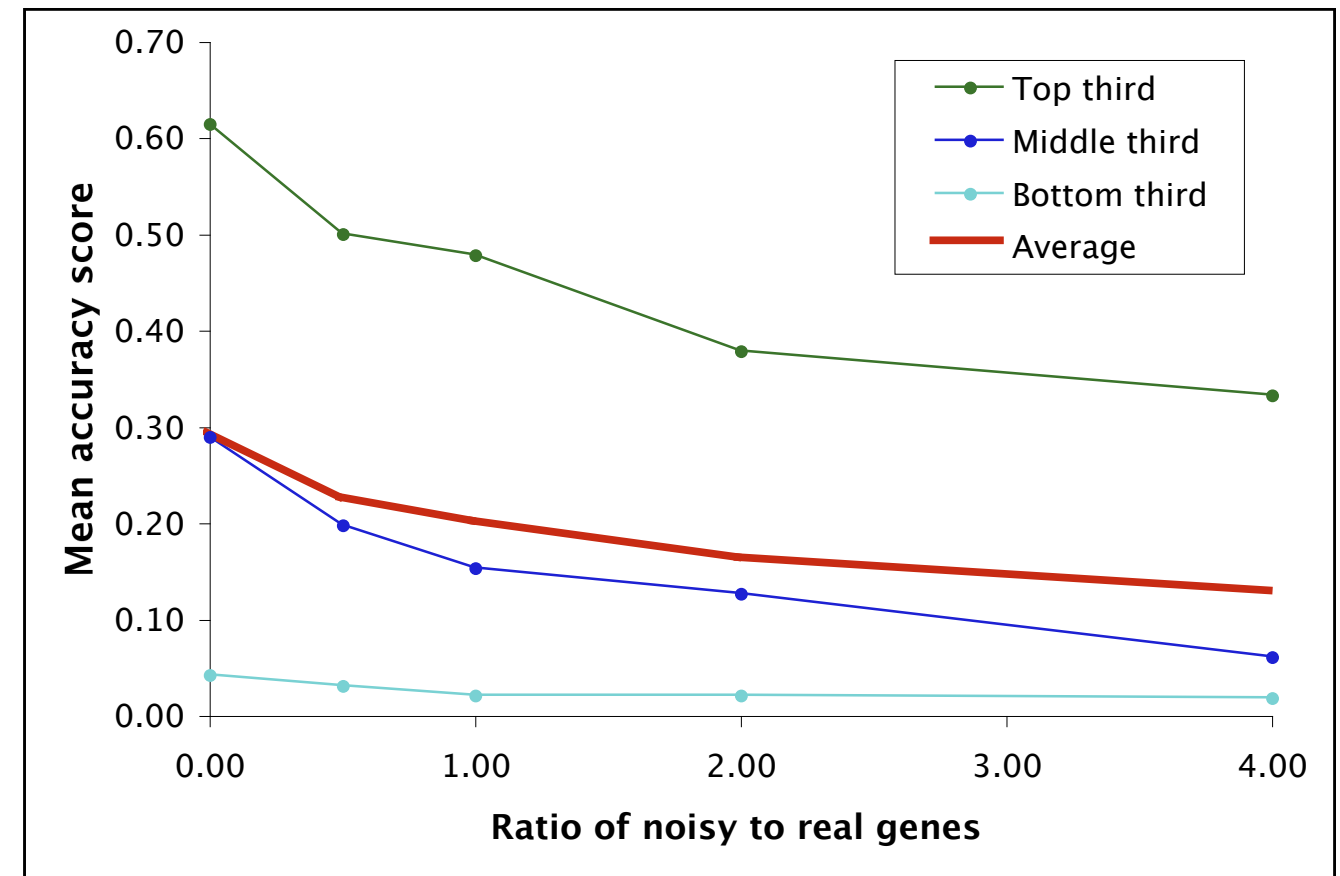


Figure 15. SCOPE is very resistant to noisy data

data (**Figure 15**). Even in the presence of 4-fold noise, it remains 50% as accurate as in the absence of noise. For comparison, Gibbs and MEME lose up to 90% accuracy in the presence of 0.5 noisy genes. This makes SCOPE an excellent choice for the analysis of microarray data, which is often noisy.

	SCOPE	RSAT	YMF	AA	MS	Biopros	MEME	Imp	MITRA	wCons	Weeder
Average	0.24	0.17	0.17	0.15	0.11	0.15	0.16	0.11	0.12	0.14	0.18
Stderr	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.03
Wins	19	5	3	5	2	2	11	3	6	13	3
scores >=0.50	8	4	7	6	3	2	5	3	0	5	4
scores >=0.33	21	12	14	10	5	9	12	6	9	10	11
scores >=0.20	39	24	22	22	14	12	23	14	18	24	13
Regulons returned	78	70	78	78	78	44	78	77	77	78	41
clear win for SCOPE vs	-	24	24	25	37	18	31	36	36	33	15
clear loss for SCOPE vs	-	8	6	6	3	1	13	5	4	13	3
t-test p-value	-	0.005	0.000	0.001	0.000	0.000	0.005	0.000	0.000	0.000	0.114

Figure 14. SCOPE is more accurate than any other algorithm

References

PRISM: Carson* JM, Chakravarty* A, Khetani RS, and Gross RH.; BMC Bioinformatics, 2006 May 15; 7(1):254.
 BEAM: Carlson* JM, Chakravarty* A, and Gross RH.;" Journal of Computational Biology, 2006; 13(3):686-701.