

Gold Standard Alignments – 24 carat?

Steve Chien

`schien@cs.berkeley.edu`

Lawrence Ip

`lip@cs.berkeley.edu`

Goals

To determine

- How good are gold standard alignments?
- How good are scoring schemes for alignments?

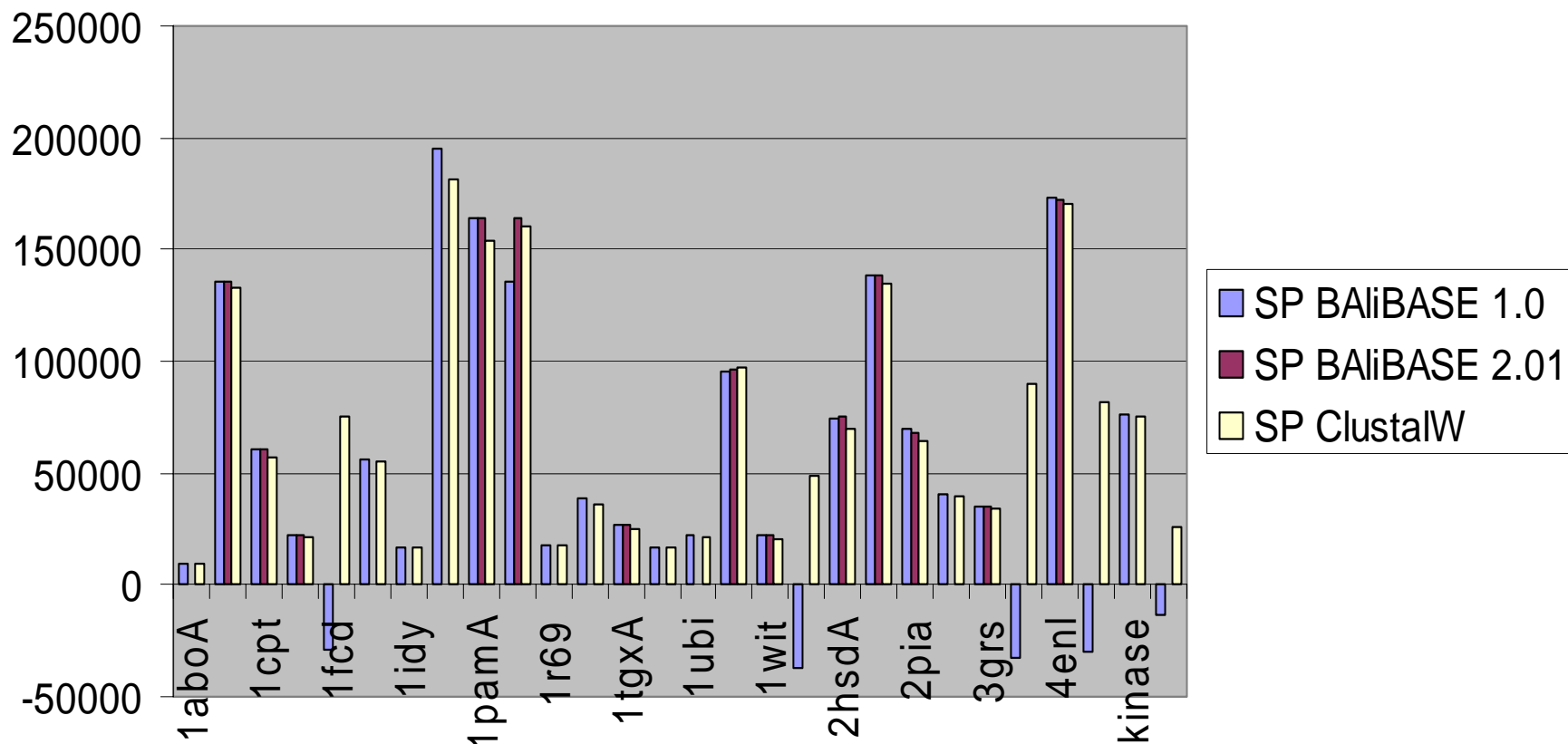
Findings

- BAliBASE alignments are not yet stable enough to serve as perfect benchmarks.
- Sum-of-pairs scoring is more effective than minimum entropy, though both are flawed.
- Differences b/w BAliBASE and ClustalW alignments can be explained in terms of treatment of “core” regions.

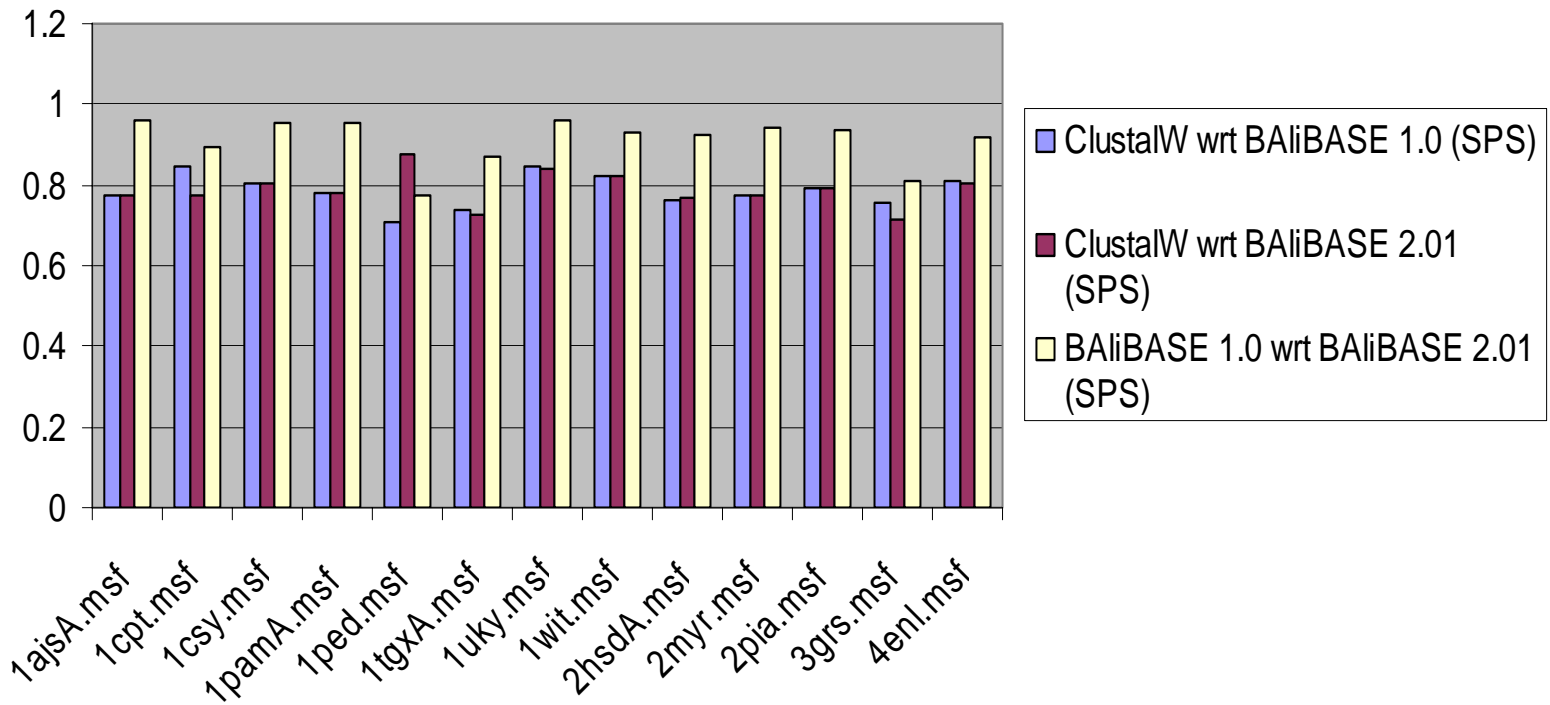
BAiBASE 1.0 vs 2.01

	v1=v2.01	different seqs	different alignments	CW>B1 (SP)	B2>B1 (SP)	CW<B1 (entropy)	B2<B1 (entropy)
ref1/test1	11	5	11	8	6	5	5
ref1/test2	14	1	12	9	11	3	9
ref1/test3	17	1	10	4	7	2	6
ref2	0	10	13	4	7	5	4
ref3	0	7	5	0	1	1	2
ref4	3	3	6	4	4	5	5
ref5	5	0	7	1	3	0	2
total	50	27	64	30	39	21	33
	35%	19%	45%	21%	28%	15%	23%
total number of alignments			141				

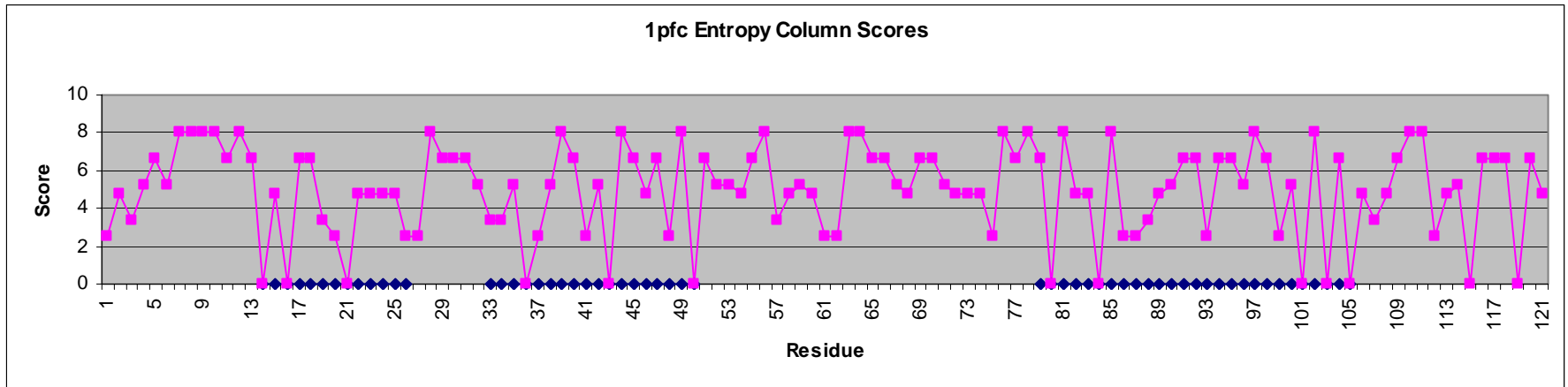
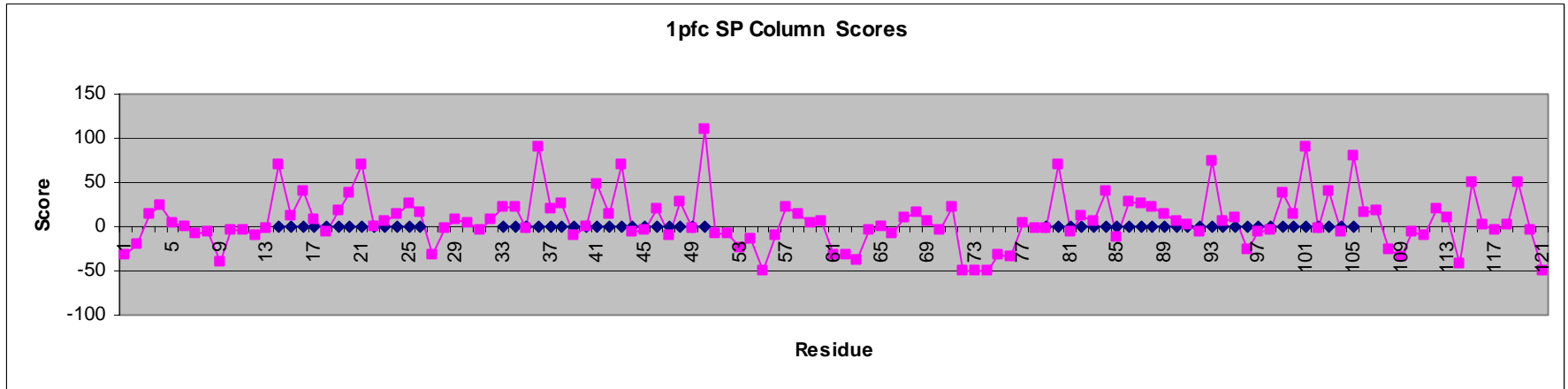
SP Scores BAliBASE vs ClustalW (Ref 2)



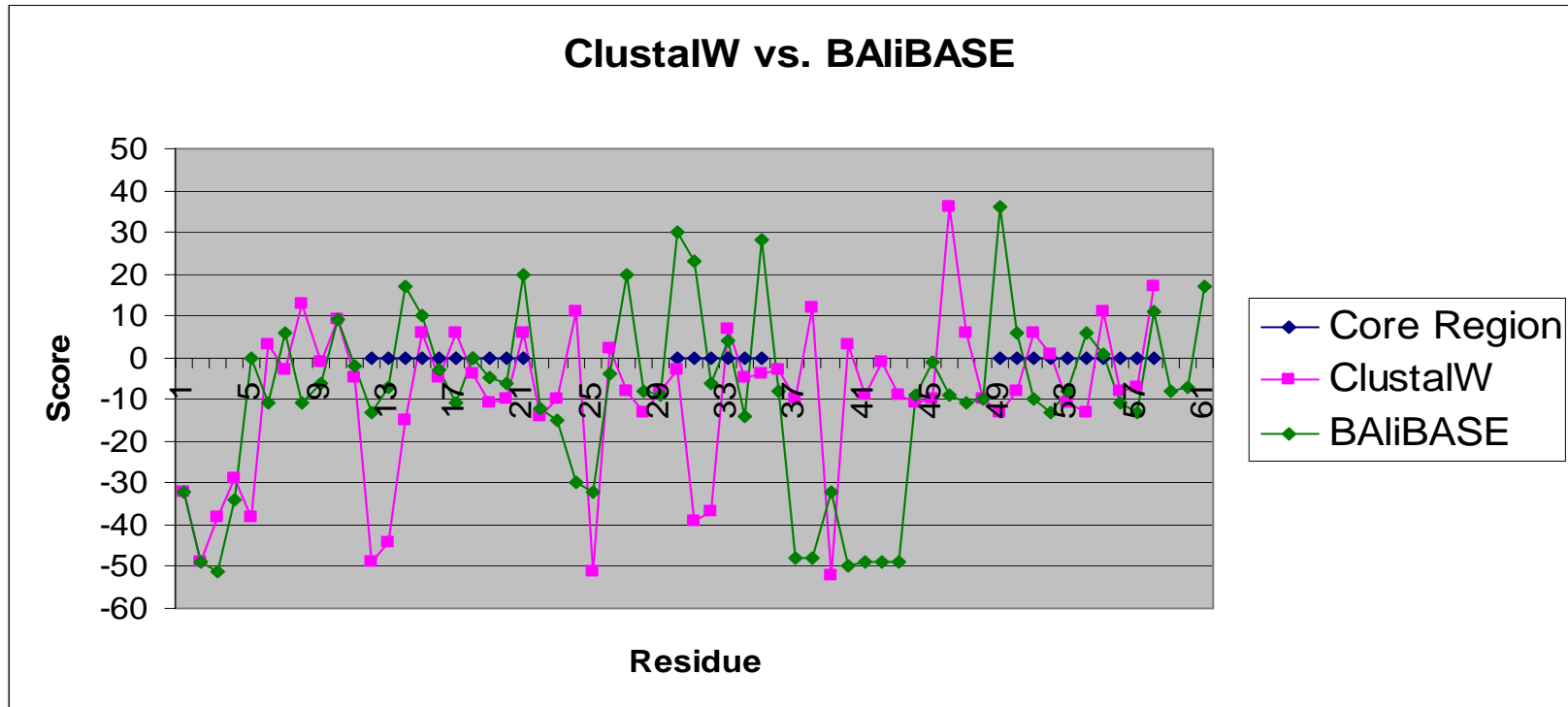
SPS Comparison of BALiBASE 1.0, BALiBASE 2.01 and ClustalW



SP vs. Entropy



ClustalW vs. BaliBase



BALiBASE concentrates on core regions and sacrifices the rest.

BALiBASE's variance is larger than ClustalW's on 70 of 80 sequences in Reference 1 test cases.

Lengths of Core Regions and Gaps

