Table 1: Performance of the programs in the set of original sequences
(from Burset and Guigó, *Genomics* 34, 353-367, 1997)

	sequences			nucleotide				exon					protein
				Sn	*Sp*	*AC*	(*CC*)	*Sn*	*Sp*	$\frac{(Sn+Sp)}{2}$	*ME*	*WE*	*%Sim*
FGENEH	all	569	22	0.77	0.88	0.78±0.26	0.80	0.61	0.64	0. 64±0.33	0.15	0.12	71%
	new	195	11	0.70	0.83	**0.70±0.27**	0.73	0.51	0.54	**0.54±0.30**	0.22	0.18	**62%**
GeneID	all	570	2	0.63	0.81	0.67±0.27	0.65	0.44	0.46	0.45±0.34	0.28	0.24	57%
	new	196	1	0.58	0.78	**0.62±0.27**	0.60	0.41	0.43	**0.42±0.30**	0.34	0.27	**52%**
GeneParser2	all	562		0.66	0.79	0.67±0.26	0.65	0.35	0.40	0.37±0.30	0.29	0.17	
	new	188		0.63	0.76	**0.63±0.25**	0.62	0.33	0.39	**0.36±0.27**	0.32	0.20	
GenLang	all	570	30	0.72	0.79	0.69±0.28	0.71	0.51	0.52	0.52±0.33	0.21	0.22	62%
	new	196	13	0.63	0.73	**0.60±0.29**	0.63	0.39	0.44	**0.43±0.29**	0.29	0.25	**53%**
GRAIL 2	all	570	23	0.72	0.87	0.75±0.21	0.76	0.36	0.43	0.40±0.27	0.25	0.11	(64%)
	new	196	6	0.69	0.85	**0.71±0.22**	0.72	0.34	0.41	**0.38±0.27**	0.30	0.13	**(61%)**
SORFIND	all	561		0.71	0.85	0.73±0.24	0.72	0.42	0.47	0.45±0.28	0.24	0.14	(61%)
	new	189		0.65	0.79	**0.66±0.25**	0.65	0.36	0.39	**0.38±0.27**	0.29	0.19	**(54%)**
Xpound	all	570	28	0.61	0.87	0.68±0.24	0.69	0.15	0.18	0.17±0.23	0.33	0.13	
	new	196	7	0.58	0.83	**0.64±0.25**	0.64	0.12	0.15	**0.14±0.20**	0.36	0.16	
GeneID+	all	478	1	0.91	0.91	0.88±0.16	0.88	0.73	0.70	0.71±0.29	0.07	0.13	84%
	new	143		0.88	0.87	**0.85±0.18**	0.84	0.68	0.64	**0.66±0.29**	0.10	0.15	**79%**
	new2	50		0.85	0.85	0.82±0.22	0.82	0.67	0.64	0.65±0.30	0.13	0.16	75%
GeneParser3	all	478		0.86	0.91	0.86±0.18	0.85	0.56	0.58	0.57±0.30	0.14	0.09	
	new	143		0.83	0.89	**0.82±0.18**	0.82	0.50	0.53	**0.51±0.33**	0.17	0.09	
	new2	50		0.83	0.91	0.84±0.15	0.84	0.51	0.56	0.53±0.34	0.17	0.07	

Table 1: Performance of the programs in the original (non-mutated) sequence test set. The measures of prediction accuracy discussed in *Materials and Methods* have been averaged over the set of sequences effectively analyzed. At the nucleotide level, *Sensitivity (Sn)*, *Specificity (Sp)*, and *Approximate Correlation (AC)* are given. For comparison purposes, the value of the *Correlation Coefficient (CC)* is also given. At the exon level, *Sensitivity Sn*, *Specificity Sp*, their average *(Sn+Sp)/2*, *Missing Exons (ME)*, and *Wrong Exons (WE)* are given. Finally at the protein level, the *Percentage Similarity (%Sim)* is given. %Sim is shown between parentheses for those programs that do not attempt to assemble genes, but that provide translational frame for the predicted exons. %Sim was assumed to be zero, when no prediction was made, all other measures were averaged only over those cases for which they are defined. Averages are given separately for all of the sequences in the test set, ALLSEQ, and for a subset unlikely to contain sequences similar to the sequences on which the programs were trained, NEWSEQ (results in bold face.) Standard Deviations are given for *AC* at the nucleotide level and *(Sn+Sp)/2* at the exon level. The table also gives (3rd column) the number of sequences effectively analyzed for each program (over a total of 570 sequences in ALLSEQ, and 196 in NEWSEQ), and the number of sequences among those analyzed for which no gene was predicted (4th column). Performance of the programs using amino acid similarity searches—GeneID+ and GeneParser3—is shown separately. In addition to performance in the ALLSEQ and NEWSEQ data sets, performance for such programs is also given in a third data set, NEWSEQ2, a test set in which the DNA sequences are unlikely to encode amino acid sequences included in the databases used by these programs.