












algorithm	original			detailed		
	error	FP	FN	error	FP	FN
pelt.n 	0.3	0.7	0.2	2.1	5.3	1.0
cghseg.k 	0.3	0.7	0.2	2.3	5.6	1.1
gada 	0.6	1.6	0.5	2.5	6.3	1.2
dnacopy.sd 	2.5	7.5	1.5	5.1	14.1	2.2
glad.lambdabreak 	6.4	2.1	7.3	8.0	7.1	7.2
flsa.norm 	1.2	3.0	0.8	8.7	19.5	4.9
flsa 	1.3	1.4	1.3	8.9	20.6	4.9
glad.haarseg 	9.0	1.6	10.5	9.5	6.0	9.0
pelt.default	8.0	42.2	1.1	13.9	59.0	1.0
dnacopy.alpha 	17.9	1.4	21.2	16.8	7.2	16.9
glad.MinBkpWeight 	19.7	0.7	23.6	18.4	4.6	19.4
dnacopy.prune 	25.9	2.8	30.5	23.6	8.9	24.1
glad.default	27.4	1.6	32.7	26.0	5.0	27.7
dnacopy.default	40.5	0.7	48.5	38.0	4.8	41.1
cghseg.mBIC	41.0	0.0	49.2	38.5	2.0	42.3
gada.default	80.7	0.0	96.9	82.7	0.1	92.1
cghFLasso	80.9	0.0	97.2	83.8	0.8	93.1