A change-point model for identifying 3'UTR switching by next-generation RNA sequencing

Supplementary Table 1.

Significant Gene Ontology terms in analysis of the Ni2013 dataset at FDR=0.05.

GO TERM	*P Value*
CYTOPLASMIC_PART	3.64E-05
POSITIVE_REGULATION_OF_CELLULAR_PROCESS	6.55E-05
POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	1.18E-04
CYTOPLASM	1.69E-04
MITOCHONDRION	1.91E-04
REGULATION_OF_DEVELOPMENTAL_PROCESS	2.96E-04
LIPID_BINDING	4.19E-04
NEGATIVE_REGULATION_OF_APOPTOSIS	4.91E-04
ANTI_APOPTOSIS	5.11E-04

Supplementary Table 2.

Significant Gene Ontology terms in analysis of the Fu2011 dataset at FDR=0.05.

GO TERM	*P Value*
SIGNAL_SEQUENCE_BINDING	4.66E-05
ORGANELLE_PART	1.70E-04
CYTOPLASM	2.01E-04
MACROMOLECULAR_COMPLEX	2.12E-04
INTRACELLULAR_ORGANELLE_PART	2.24E-04
ENDOPLASMIC_RETICULUM	3.46E-04
PEPTIDE_BINDING	4.03E-04
CYTOPLASMIC_PART	4.50E-04

Supplementary Figure 1.

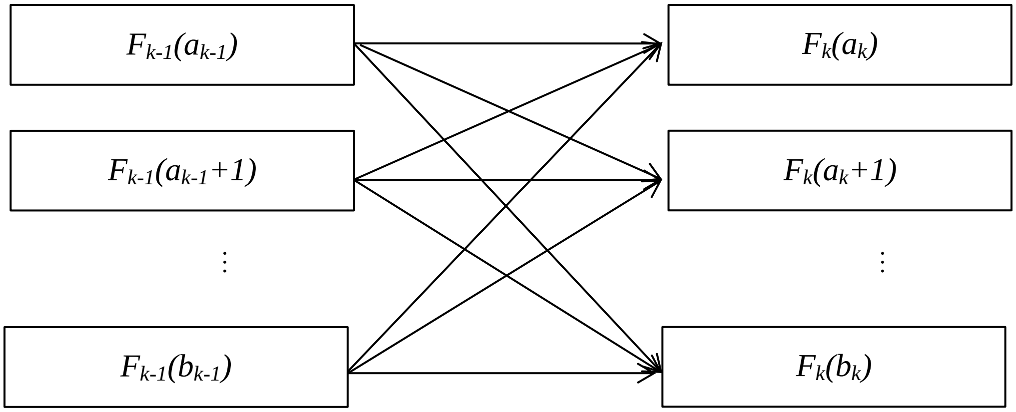

Figure S1. Implementation of the computation of the forward variable $F_k(v)$ in terms of a lattice of locations k, and legitimate values v *for* S_k.