

ASD: A Bioinformatics Resource on Alternative Splicing

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INTRODUCTION. Alternative splicing is widespread in mammalian gene expression, and variant splice patterns are often specific to different stages of development, particular tissues, or a disease state. There is a need to systematically collect data on alternatively spliced exons, introns and splice isoforms, and to annotate this data. The Alternative Splicing Database (ASD) consortium has been addressing this need, and is committed to maintaining and developing a value-added database of alternative splice events, and of experimentally verified regulatory mechanisms that mediate splice variants. In this poster we present three of the products from this project; namely a database of computationally delineated alternative splice events and isoform splice patterns as seen in alignments of EST/cDNA sequences with genome sequences, a database of alternatively spliced exons collected from literature, and a RNA splicing workbench. The reported splice events are from human and mouse genomes and are annotated for various biological features including expression states and cross-species conservation.

We present here three of the products from the ASD project³; namely

AltSplice : This is a value-added database of computationally delineated alternative splice events and transcript isoforms as seen in alignments of EST/mRNA sequences with genome sequences. The basal data includes alternatively spliced introns/exons, events, isoform splice patterns, and isoform peptide sequences. The data is annotated for various biological features including splice signals, expression states, SNP-mediated splicing and cross-species conservation.

Aedb: This is a manually curated (as collected from literature) database containing sequence and properties of alternatively spliced exons, functional enumeration of observed splice events, and characterisation of observed splice regulatory elements.

RNA workbench: The workbench enables users to carry out splice related analysis such as to (i) characterise an intron for various splice signals, (ii) locate splice regulatory elements on a given RNA sequence, (iii) identify putative coding regions and characterise, and (iv) locate putative exons (with the emphasis on predicting their exact boundaries).

The above different components are integrated to one another and are presented through user-friendly interfaces and visualisation tools. Integration has been implemented across the splice-related data from ASD, UniProt, and Ensembl. AltSplice data can be viewed as DAS resource on Ensembl gene view and contig view. The ASD resource is presented at our ASD web pages (<http://www.ebi.ac.uk/asd>).

a) Thanaraj T.A., Stamm S., Clark F., Riethoven J.J.M, Le Texier V., and Muili J. ASD: the Alternative Splicing Database. Nucl. Acids. Res. 32: D64-D69 (2004).

Screenshots from the AltSplice interface: features, splice patterns and peptide isoforms (above left), events, SNP mapping and information (above right)

Splice patterns from AltSplice can be viewed graphically on either the AltSplice Pattern Viewer (left) or as DAS tracks on the Ensembl Genome Browser (right).

STATISTICS. AltSplice database statistics. The current builds are based on Dec 2004 Releases of Ensembl gene sets.

	Confirmed		Genes with at least one confirmed		Extent of alternative splicing d/c
	Introns (a)	Exons (b)	Intron/exon (c)	Alternative event (d)	
AltSplice Human	137195	184731	16293	9945	61%
AltSplice Mouse	164321	123895	16391	8211	50%

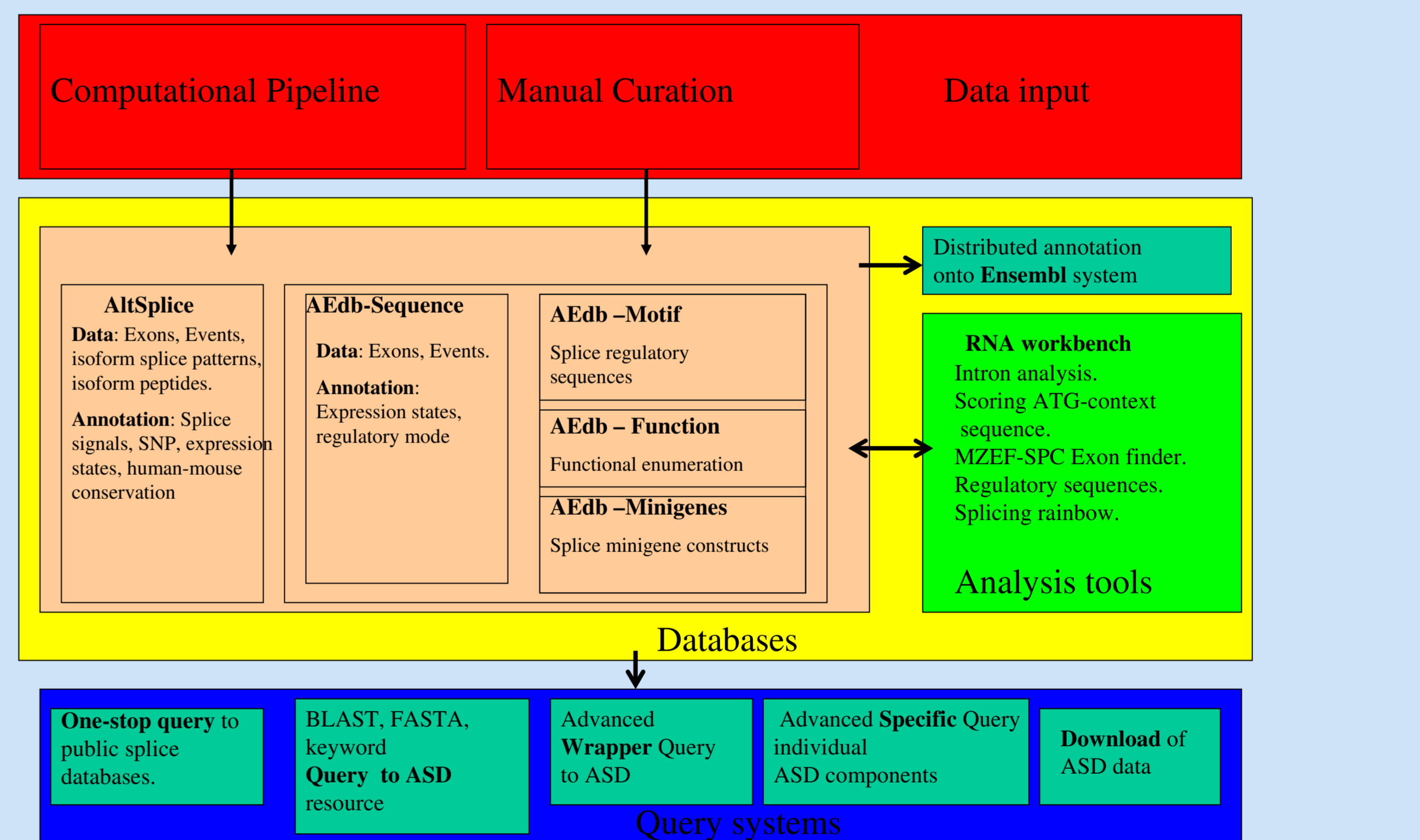
	Distribution of confirmed alternative events				
	Intron retention	Exon isoforms	Intron isoforms	Cassette exons	Mutual exclusive exons
AltSplice Human	5270	7575	13874	18815	1678
AltSplice Mouse	2900	5214	9668	10188	630

Aedb-sequence database statistics: 2256 records in Aedb-Sequence (Cassette exon = 1282; Mutually exclusive exon = 130; Alternate 3' splice site = 210; Alternate 5' splice site = 185; Intron retention = 154; Alternate poly-A = 71; unknown = 224).

Aedb-function database statistics: Number of Function entries: 355. Top Reported Functional changes: Protein interaction (137); Internal structure (119); Novel Carboxyl terminal (87); Disease association (81); Intra cellular location (76); Enzymatic activity (64); Channel activity (54); Novel amino terminal (38).

Aedb-motif database statistics: Number of Motif entries: 255

AEDB. Aedb is a manually curated database of alternative exons (as reported in literature) and their properties (Stamm, S., J. Zhu, K. Nalaj, P. Stelov, O. Stess, and M.Q. Zhang. An alternative exon database (AEDB) and its statistical analysis. DNA and Cell Biol., 19: 739-756 (2000).



INTEGRATION. The presented databases can be queried separately, but it is also possible to view the data in an integrated way.

ENDICES:				
Aedb associations:	o Exon level	o Event level	1306, 1308, 1310, 1324	
Human-Mouse Conservation:	o Intron/Exon level	o Event level	ENSMUSO0000009073	
Uniprot peptide isoforms:	View all the peptide isoform sequences from UniProt			
Ensembl transcript structures:	Ensembl predicts multiple transcript structures for this gene			

Gathering evidences for the reported alternative splicing is important.

ACKNOWLEDGEMENTS. AltSplice and Aedb are part of the ASD project (www.ebi.ac.uk/asd/asd-ec/) which has the following partners: Erlangen University (Stamm), EBI (Thanaraj), ExonHit (Bracco), EMBL (Bork), CRG (Valcarcel, Guigo), and Hebrew University Israel (Soreq).

This work is supported by a grant (QLRT-CT-2001-02062) from the European Commission. Andreas Kahari and Ewan Birney (EBI) are gratefully acknowledged for setting up a DAS server for the ASD data.

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