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MAISTAS: a tool for automatic structural evaluation of alternative splicing products

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ABSTRACT

Motivation: Analysis of the human genome revealed that the amount of transcribed sequence is an order of magnitude greater than the number of predicted and well-characterized genes. A sizeable fraction of these transcripts is related to alternatively spliced forms of known protein coding genes. Inspection of the alternatively spliced transcripts identified in the pilot phase of the ENCODE project has clearly shown that often their structure might substantially differ from that of other isoforms of the same gene, and therefore that they might perform unrelated functions, or that they might even not correspond to a functional protein. Identifying these cases is obviously relevant for the functional assignment of gene products and for the interpretation of the effect of variations in the corresponding proteins.

Results: Here we describe a publicly available tool that, given a gene or a protein, retrieves and analyses all its annotated isoforms, provides users with three-dimensional models of the isoform(s) of his/her interest whenever possible and automatically assesses whether homology derived structural models correspond to plausible structures. This information is clearly relevant. When the homology model of some isoforms of a gene does not seem structurally plausible, the implications are that either they assume a structure unrelated to that of the other isoforms of the same gene, or that most of them might not give rise to proteins structurally and/or functionally related to the other isoforms of the same genes or be the result of aberrant splicing events giving rise to non-functional proteins (Tress et al., 2007).

Indeed, comparison of the putative proteins encoded by the alternatively spliced transcripts with the main isoform showed that most of them lacked an active site, key trans-membrane segments, essential signalling regions and post-transcriptionally modified sites. Most importantly, models of their putative three-dimensional structures did not seem to correspond to plausible folds (Tress et al., 2007).

This observation was confirmed by Moult and co-workers (Melanì and Moult, 2009a, b) who, using a completely different dataset of alternative splicing variants, found that the vast majority of them resulted in putatively unstable protein conformations.

Recently, some of us manually analysed the putative structures of isoforms of the human genome, the existence of which had been confirmed by mass-spectrometry and of isoforms of the same genes for which no evidence exists in proteomic databases reaching essentially the same conclusions (Leonì et al., 2011).

These observations suggest that we might be observing the effects of noisy selection of splice sites by the splicing machinery and/or that alternatively spliced products of a gene might assume unrelated conformations.

These findings raise several interesting questions, but also a few practical issues. First of all, the careful manual analysis performed by the BioSapiens consortium on 1% of the genome needs to be scaled up to the whole genome and therefore automated. Secondly, analysis tools should be available to biologists performing experiments in a user-friendly manner.

At present, there are a few systems that partially satisfy this need. For example, the ProSas database (Birzele et al., 2008) (http://www.bio.ifi.lmu.de/forschung/structural-bioinformatics/prosas) stores structures and models (provided the target proteins shares at least 40% sequence identity with a known template) for the alternative isoforms annotated in Ensembl (Hubbard et al., 2002).

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and Swiss-Prot (Bairoch et al., 2004) and allows the visualization of
the exon boundaries in the context of the three-dimensional
structures, but there is no provision for automatic analysis of
the plausibility or completeness of the resulting structures and models.
The same is true for AS-ALPS (Shionyu et al., 2009) (http://as-
alps.nagahama-i-bio.ac.jp/), a server that provides information
about the putative effect of alternative splicing on human and mouse
proteins, provided that at least one of the isoforms has an
experimentally solved structure.

Here, we describe a system named Modelling and Assessment of
ISoforms Through Automated Server (MAISTAS) that, given the
accession codes of one or more genes or proteins, collects all their
putative spliced isoforms annotated in the Ensembl genome database
(Hubbard et al., 2002), builds, whenever possible, comparative models
for their structures, analyses their features and provides an
estimate of the likelihood that the isoforms correspond to potentially
stable and structurally plausible proteins in the absence of major
conformational rearrangements.

Alternative splicing isoforms can also be uploaded in the
FASTA format in order to allow the user to analyse data
from more comprehensive and specialized databases such as
Aceview (http://www.ncbi.nlm.nih.gov/IEB/Research/Acembly/)
(Tierry-Mieg and Tierry-Mieg, 2006) or ASPicDB (http://as.caspur.
.it/ASPicDB/) (Martelli et al., 2010).

Model assessment is performed by analysing the quality of the
packing in the core of the structure and/or model, the extent of
exposed hydrophobic surface and the putative effect of deletions
and insertions. These properties are compared to those observed in
known protein structures and in the closest homology of the known
structure. The system is freely available as a Web server.

2 METHODS

The input data can be a set of sequences in the FASTA format or one
or more of the following codes: Ensembl Gene ID(s), Ensembl Transcript
ID(s), Ensembl protein ID(s) (Flicek et al., EMBL ID(s) (Leinonen et al.,
2011), EntrezGene ID(s) (Maglott et al., 2011), GO ID(s) (Ashburner et al.,
2000), HGNX automatic gene name, HGNC curated gene name
(Seal et al., 2011), UniProt/IEBM Accession(s), UniProt/Swissprot ID(s),
UniProt/Swissprot Accession(s) (The UniProt Consortium, 2008), VEGA
transcript ID(s), HAVANA transcript ID(s) (Wilm et al., 2008).

The collection of all putative splicing isoforms corresponding to the
input gene (or to the gene encoding for the protein when a protein accession
code is used) is achieved by taking advantage of a locally stored version of the
Ensembl database (release 58) (Flicek et al., 2011). Users can select accession
codes for more than 30 different organisms.

The HHsearch 1.1.5 (Söding, 2005) is used to search for possible structural
templates (E-value lower than 10−5, sequence coverage of at least 90%,
global alignment mode, all other parameters set at their default values) and
for obtaining the sequence alignment between the target and its templates.
Model building is performed using a local version of Modeller9v9/8 (Sali and

The selected parameters ensure that the quality of the produced models is
sufficiently high to be able to reliably measure properties described below as
demonstrated by the last CASP experiment (http://predictioncenter.org/
CASP9).

POPS (Cavallo et al., 2003) is used to calculate the accessibility to the
solvent of each residue of the models. The OS software (Pattabiraman
et al., 1995; Fleming and Richards, 2000) is used for computing infrong
environment of residues. Finally, the ‘packing-eff’ method from the
NUPROTP package (Voss and Gerstein, 2005) is used for estimating how
well packed the protein is.

The thresholds for POPS, Packing-eff and OS tools were derived by
running the programs on 7908 monomeric proteins solved by X-ray
crystallography at a resolution better than 2.5 Å. The chosen thresholds,
20.1 for POPS values, 17.8% for Packing-eff values and 0.54 for OS values,
correspond to two standard deviations from the average (data not shown).

Residues are considered exposed if their mean solvent accessibility—
calculating considered three residues on each side of them—is larger than
5 Å2.

The average response time for a typical request (three to four isoforms,
a few hundreds amino acid long) is <1 h, the time limiting factor being the
construction of the HMMs and of the corresponding models. The entire
pipeline was built using python scripts and the interface is PHP-based.

In order to verify that the system can be applied to a substantial fraction
of cases and that is able to recognize translated proteins, we ran it on
protein isoforms whose existence is unambiguously identified by mass
spectrometry. We used the May 2010 human build (http://www.peptideatlas.
org/builds/human/201005APD, Hs, all fasta) containing 72,396 different
peptides ranging in size from 6 to 66 (mean 17) (Deutsch et al., 2008). Of
these, 19,513 could be unambiguously mapped to 2972 isoform products
annotated in Ensembl (release 58). We also compared the results of
MAISTAS with those obtained by a manual analysis of human transcript
products described in Leoni et al. (2011).

3 RESULTS

The automatic analysis performed by MAISTAS requires that the
user inputs one or more protein/gene accession codes from the
common public databases (see Section 2) or a set of sequences in the
FASTA format. In all but the last case, the sequence(s)
corresponding to the user query is retrieved and mapped back to
the appropriate genome database by using a local installation of the
Biomart database (Durinck et al., 2005). The peptide sequences of
all isoforms of the target gene, as annotated in Ensembl, are
retrieved.

If the input is a set of amino acid sequences in the FASTA format,
they are assumed to be different isoforms of the same gene.

The user can supply an email address (optional) to which the
results will be sent or bookmark the result page. The initial query
page of MAISTAS provides a link to an example result page, which
allows the user to inspect a typical output (Fig. 1).

In the first step, the tool evaluates whether a structure exists
for any of the isoforms or, lacking this, whether a comparative
model can be built. In the latter case, the template is identified
using the HHsearch program, which builds a Hidden Markov Model
(HMM) of the target protein family and compares it to the HMMs
representing a set of non-redundant families of proteins of known
structure (sequence identity between any pair below 70%). This
strategy has been shown in blind tests to be one of the most sensitive
for finding structural templates (Battey et al., 2007).

The target sequence, the template(s) and the alignment obtained by
the HHsearch are automatically analysed. Only models based
on template structures solved by X-ray crystallography or an NMR
are considered. They are inspected to detect any possible gaps in the
coordinate set (for example, because of the absence of electron
density in X-ray structures). If these regions are present at the N-
or C-terminus of the protein they are trimmed, otherwise a warning is
issued. A warning is also issued if the alignment includes insertions
larger than 50 residues that might correspond to an inserted domain
or deletions larger than 20 residues.
Fig. 1. Snapshots of the MAISTAS output page. (A) Summary table for the modelled isoforms. The following data are shown: gene ID (gene identification code), isoform ID (isoform identification code), isoform length (number of residues of each isoform), first aa, last aa (the first and last modelled or solved amino acid), template ID (the PDB code of the template protein used for modelling or the PDB code of the known isoform structure), isoform/template % seq. ID (sequence identity between the splicing isoform and the sequence of the selected template), fraction of isoform modelled (percentage of the splicing isoform sequence modelled), summary (assessment of the plausibility of the structure). (B) Snapshot of the isoform section showing results of the analysis for each isoform, its final assessment and the modelled structure in a small Jmol window. Different links in the section allow the user to download the coordinates of all the models and, if desired, all the intermediate data used in the procedure. The next section of the output page describes the detailed results for each modelled isoform and reports (see Section 2 for details):

- The sequence identity and coverage of the template and its PDB code.
- The packing efficiency of the model and of its template together with their comparison with the expected value.
- The extent of the exposed hydrophobic area of the model and of its template together with their comparison with the expected value.
- The packing environment of residues in the model and the template together with their comparison with the expected value.
- The assessment of whether insertions and deletions (if any) can be easily accommodated into the model.
- The modelled or experimental structure in a Jmol window.
- The option to inspect the multiple sequence alignment via a JALVIEW applet (Waterhouse et al., 2009).
- The option to visualize and analyse the models via a Jmol applet (http://www.jmol.org/).
- A final remark about the plausibility/completeness of the predicted structure.

The alignment is used to build the model using a local installation of Modeller (Sali and Blundell, 1993). Once the model has been built, the system computes the model hydrophobic solvent accessible area and packing efficiency.

If the modelled isoform presents deletions with respect to the template, the Euclidean distance between the Cα residues before and after the deletion(s) is recorded. If insertions are present, the surface exposed to the solvent of the amino acids surrounding them and the number of inserted amino acids is computed.

The tool informs the user that the model might not correspond to a complete or plausible structure if the distance between the two residues on either side of a deletion is >15 Å and/or if there are more than three residues inserted in the core of the protein and/or if the hydrophobic solvent accessible area of the model is larger than a set threshold (see Section 2). In assessing the results, the system takes into account the corresponding values for the template used for modelling.

The output of MAISTAS is shown in Figure 1 and includes a summary table, where all the data regarding the modelled isoforms are reported. These can also be downloaded as a csv file. The user can download the coordinates of all the models and, if desired, all the intermediate data used in the procedure. The next section of the output page describes the detailed results for each modelled isoform and reports (see Section 2 for details):

- The sequence identity and coverage of the template and its PDB code.
- The packing efficiency of the model and of its template together with their comparison with the expected value.
- The extent of the exposed hydrophobic area of the model and of its template together with their comparison with the expected value.
- The packing environment of residues in the model and the template together with their comparison with the expected value.
- The assessment of whether insertions and deletions (if any) can be easily accommodated into the model.
- The modelled or experimental structure in a Jmol window.
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- The option to visualize and analyse the models via a Jmol applet (http://www.jmol.org/).
- A final remark about the plausibility/completeness of the predicted structure.

MAISTAS depends on the availability of structural templates to predict the three-dimensional structure of the isoforms by comparative modelling. If no structural templates are available, a ‘No template satisfying all parameters’ warning is issued. When MAISTAS is unable to provide a reasonable structural model (e.g. when very large insertions are present) the system will return the message ‘Maistas is having trouble modelling or assessing this isoform’.

The online result pages are accessible via the URL sent either by e-mail or via the ‘Retrieve results by job identifier or by email’ window, using the provided job identification code or the e-mail address.
As an example of the use of MAISTAS, we describe the results of our analysis in a local database unless the user requests them to be kept private. This implies that a user might be able to immediately retrieve the results on the gene(s) of interest if they were already been produced in a previous run of the system. The entries of the database are time stamped and presented to the user together with an option to repeat the analysis, which is advisable if major updates of the genome or structure database have taken place since the previous analysis was performed.

We ran the system on all human alternatively spliced isoform whose existence at the protein level could be unambiguously verified by mass spectrometry, i.e. of those protein isoforms for which a peptide that unambiguously identifies them has been detected with high reliability by mass spectrometry. The server was able to produce and analyse models in 30% of the cases (890 out of 2972). In 2082 of them (70%), the model could not be built because there is no template satisfying all parameters. This had to be expected since we use rather stringent parameters to select the template (E-value better than 10^{-5}, template coverage >50%, X-ray resolution <2.5 Å or solved by the NMR). Out of the modelled isoforms, 712 (80%) were assessed as structurally plausible (see http://www.bioinformatica.crs4.org/maistas/pub/dataset.xls). In the majority of the remaining cases, (160 out of 176) the model showed a large hydrophobic surface exposed to the solvent. In these cases, the protein might indeed represent an incomplete and therefore not plausible structure, but also simply be a subunit of a larger complex.

We compared the results obtained by MAISTAS with those derived from a manual analysis of the isoforms of genes for which at least one isoform had been detected in mass-spectrometry experiments [and unambiguously identified by the presence of a peptide in the PeptideAtlas database (Deutsch et al., 2008) and at least one had not (Leoni et al., 2011)]. The results obtained automatically using MAISTAS are consistent with those reported in Leoni et al. (2011). In particular, MAISTAS was able to model 30% of the 555 proteins for which there is an evidence of translation (to be compared with the 26.4% obtained in the manual analysis), 85% of which were assessed as structurally plausible. The difference in coverage between the manual and automatic analyses is due to the increased size of the protein sequence and structure databases. Models were also produced for 181 out of 555 isoforms for which there is no evidence of translation in PeptideAtlas. Only 44% of these isoforms were reported as complete and plausible by the automatic pipeline. The corresponding numbers for manual analysis are 145 isoforms (26%) modelled and 48% classified as structurally consistent.

3.1 Application example

As an example of the use of MAISTAS, we describe the results obtained using the gene coding as input for the voltage-dependent anion channel 3 (VDAC3) (Ensembl gene identification code: ENSG00000078668), a protein that forms a channel through anion channel 3 (VDAC3) (Ensembl gene identification code: ENSG00000078668), a protein that forms a channel through anion channel 3 (VDAC3) (Ensembl gene identification code: ENSG00000078668), a protein that forms a channel through anion channel 3 (VDAC3) (Ensembl gene identification code: ENSG00000078668), a protein that forms a channel through anion channel 3 (VDAC3) (Ensembl gene identification code: ENSG00000078668), a protein that forms a channel through anion channel 3 (VDAC3) (Ensembl gene identification code: ENSG00000078668). Although four peptides mapping to the putative products are present in the PeptideAtlas database (PeptideAtlas IDs: PAp00006999; PAp00007806; PAp00007714; and PAp00423732), they cannot be used to unambiguously identify specific isoforms of the gene since they fall in the exons present in all the isoforms.

Decker et al. (Decker and Craigen, 2000) used specific anti-VDAC3 antibody and demonstrated the existence of the ENSP00000428845 and ENSP0000022615 isoforms. The only difference between these two alternatively spliced isoforms is the insertion of a single methionine at position 39 of the ENSP00000428845 sequence.

ENSP00000022615 is also annotated in the CCDS database, a resource that centralizes the identification of well-supported, consistently annotated, protein-coding regions (Pruitt et al., 2009). MAISTAS was able to provide a plausible structural model for isoforms ENSP00000428845 and ENSP0000022615 (Fig. 2A and F), while models of ENSP00000428519, ENSP00000428977, ENSP00000429006 and ENSP00000428029 were considered unlikely or incomplete (Fig. 2B-E). Inspection of the HHpred alignment used for building the ENSP00000428519, ENSP00000428977, ENSP00000429006 and ENSP00000428029 isoform models does not highlight any specific problem with the alignment (data not shown); however, the VDAC3 beta-barrel domain architecture is completely disrupted in the models of ENSP00000428845, ENSP00000428977, ENSP00000429006 and
We thank Loredana Le Pera, Andrea Sbardellati, Alejandro Giorgetti and Francesca Camilli for valuable feedback. We also thank Gianmauro Cuccuru, Michele Miggieri and Carlo Podda of the CRS4 High Performance Computing Group for their technical advice. We thank all the kinds that kindly provided us with databases and binaries or source codes of the software installed and interfaced in this pipeline.

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4 CONCLUSION

The more detailed is the analysis of the genomes of higher eukaryotes, the more complex they are revealed to be. For example, it is becoming clear that alternative splicing events do not simply result in a modulation of the function of the gene products, for example, by removing or adding structurally compact domains, or by modifying the sequence of specific regions of the encoded protein, but that they can either have a profound effect on the structure and function of the products of the same gene or give rise to non-functional products (Melamud and Moult, 2009a; b; Tress et al., 2007).

The latter can nevertheless have a relevant biological function. For example, Poliseno et al. demonstrated that transcripts may also function by competing for microRNA binding, a biological activity independent of the translation of the protein they encode (Poliseno et al., 2010). It is impossible for any currently available method, including ours, to assess which is the case.

The method described here is able to correctly classify as plausible a large fraction of the experimentally characterized isoforms, and to highlight dubious cases. Our aim is to provide easy access to a computational tool able to draw the attention of the life science community to them. Consequently, we took special care to convey the results of the analysis, although based on rather sophisticated tools, in an easy and understandable fashion. MAISTAS provides access to all the intermediate data used to generate the results, but it describes them in a human readable form. We believe that MAISTAS represents a step in the direction of using the knowledge accumulated in structural bioinformatics as well as the maturity of the tools available for applications related to the interpretation of genomic data and that it can be effectively used as a first step in characterizing novel proteins as well as a support for selecting interesting and intriguing cases for structural and functional studies.

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