

AMOD: A morpholino oligonucleotide selection tool

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1 Introduction.

AMOD is a web-based program that aids in the functional evaluation of nucleotide sequences through sequence characterization and antisense morpholino oligonucleotide (target site) selection. Submitted nucleotide sequences are analyzed by translation initiation site prediction algorithms and sequence-to-sequence comparisons; results are used to characterize sequence features required for morpholino design. Within a defined subsequence, base composition and homodimerizations values are computed for all putative morpholino oligonucleotides. Using these properties morpholino candidates are selected and compared to genomic and transcriptome databases with the goal to identify target specific enriched morpholinos. AMOD has been used at the University of Minnesota to design approximately two hundred morpholinos for a functional proteomics screen in zebrafish. The AMOD web server and a tutorial are freely available to both academic and commercial users at <http://www.secretomes.umn.edu/AMOD/>.

2 Materials and Methods

AMOD is written in PERL (<http://www.perl.org/>) and uses HTML and JavaScript for the user interface. BioPerl modules [1] are used for BLAST parsing and nucleotide-to-protein sequence translation. Translational initiation site predictions are made using the ATGpr web server [2]. Sequence to sequence comparisons are performed using a local installation of NCBI BLAST Version 2.1.2. Sequence comparisons may be made against vertebrate RefSeq proteins and the Ensembl zebrafish genomic sequence set, housed in the Vertebrate Secretome and CTT-ome database (<http://www.secretomes.umn.edu/>).

3 Results and Discussion

The AMOD design process consists of six steps separated into two phases, as shown in Figure 1. Phase one includes steps to characterize the nucleotide sequence and aid users in identifying key sequence features, including the translational initiation site and intron-exon splice sites. Phase two of the AMOD process entails the selection of a morpholino oligonucleotide, within the defined gene subsequence that possesses biochemical properties conducive to effective application. An

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exhaustive list of putative morpholino oligonucleotides 25 bases long is created; the oligonucleotide length may be modified but is set to the size known for optimal morpholino performance [3, 4].

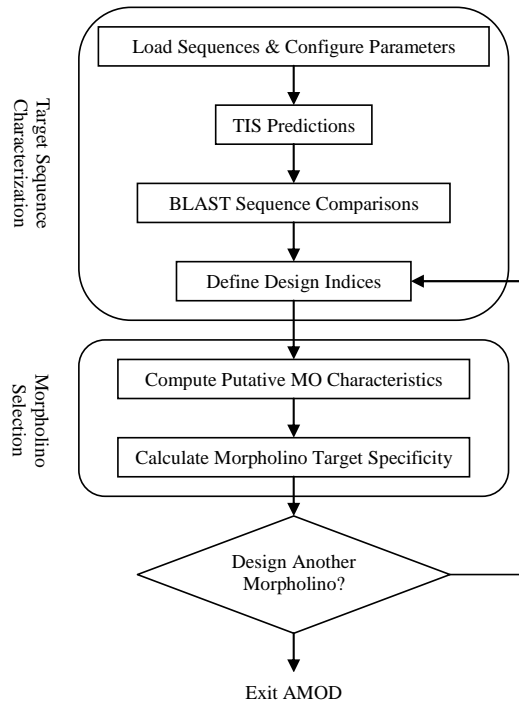


Figure 1: Process flow chart for AMOD.

4 Future Developments and Conclusions

The AMOD web server is a tool for selecting oligonucleotides for the construction of antisense morpholinos against target nucleotide sequences. Planned additions to the server include the incorporation of intron-exon splice site predictions, entropy calculations and a ranking system for putative morpholino designs. AMOD is a valuable addition to the computational resources available to the bioinformatics community.

5 References

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