**BIOL 367 Assignment: GenMAPP 2 Outline and Vocabulary List**

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**Vocabulary**

1. *Alternative splicing:* a process by which the exons of the RNA produced by transcription of a gene (a primary gene transcript or pre-mRNA) are reconnected in multiple ways during RNA splicing
2. *Exons:* a nucleic acid sequence that is represented in the mature form of an RNA molecule after either portions of a precursor RNA (introns) have been removed by cis-splicing or when two or more precursor RNA molecules have been ligated by trans-splicing.
3. *Gene expression:* the process by which information from a gene is used in the synthesis of a functional gene product. These products are often proteins, but in non-protein coding genes such as rRNA genes or tRNA genes, the product is a functional RNA.
4. *RNA interference:* a system within living cells that helps to control which genes are active and how active they are.
5. *Biological assays:* a type of scientific experiment typically conducted to measure the effects of a substance on a living organism. They are essential in the development of new drugs and in monitoring environmental pollutants.
6. *Polymorphisms:* occurs when two or more clearly different phenotypes exist in the same population of a species — in other words, the occurrence of more than one form or morph.
7. *Genomic amplifications:* a selective increase in the number of copies of a gene coding for a specific protein without a proportional increase in other genes.
8. *Homology:* any characteristic of organisms that is derived from a common ancestor.
9. *Proteomic:* of, or relating to, the study of proteins.
10. *Monoamine receptors:*membrane-bound receptors that are coupled to G-proteins. Upon stimulation by agonists, they initiate a cascade of intracellular events that guide biochemical reactions of the cell.

**Outline**

1. The purpose of GenMAPP 2, and its predecessor, is to improve the communicative and expressive power behind microarray data analysis in order to better empower and connect the scientific community
   1. GenMAPP stands for “Gene Map Annotator and Pathway Profiler”
   2. GenMAPP allows for pathway-based analysis of microarray data
2. GenMAPP is a response to biologist needs for clearer representation of genomic data
   1. Difficulties linking gene-level info to specific higher-level processes
   2. GenMAPP provides pathway-level information in an attempt to bridge the gap between the micro- and the macro-analysis
   3. In order to better serve the community, GenMAPP is free, open-source, and client-side software
3. Programmed in visual basic, binding GenMAPP to Windows platforms, but allows for several key components
   1. Records experimental data, gene databases, and pathways separately
   2. Distributed pathways are reviewed by the GenMAPP staff
4. GenMAPP 2 improves upon its predecessor in a variety of manners, addressing those most in demand by the community of biologists
   1. Major shortcoming of GenMAPP 1: limited species and gene expansion
      1. GenMAPP 2 provides a new database schema to provide unlimited species support and genomic expansion
      2. New additions to database including OMIM, GO, and PDB to provide better primary source connection
      3. Semi-autonomous database population using established database record tables such as from Uniprot and Ensembl
      4. Allows for custom gene database definition
   2. GenMAPP 1 did not allow for easy viewing of time-influenced changes at the genomic level; GenMAPP 2 improves upon this
      1. New version allows multiple defined color schemes to be viewed at the same time for swift juxtaposition
      2. Extends to easy viewing of RNA transcription and exon portions, allowing multi color scheme views all in one window
   3. MAPPed data made more portable to reach a wider audience by sporting a variety of new web-ready exports
      1. Exported maps retain their interactive nature, capable of linking to their respective components after compilation
      2. The level of responsiveness imbued in these exports is a unique feature of GenMAPP (unavailable in its peers’ features)
      3. Color schemes can be customized for export and visualization is highly malleable to maximize readability for a wider audience
   4. GenMAPP provides potent drawing utilities to link pathways in an individual-oriented focus for community curation
      1. Customizable layouts allows inter- and intra-linking of map entries for a truly expressive form of communication
      2. Already several efforts at community projects, including efforts at Johns Hopkins, the University of Bioinformatics, and even LMU!
   5. New support for homology maps that can serve as starting points for further mappings
      1. “Conversion” function in GenMAPP 2 adds homology information via communication between other databases and a specific map without altering the content of the map
      2. Allows for abstraction from the “top down”—human to new species—because human records are the most complete
   6. Challenge to extend existing pathways in an efficient manner while faced with the slower pace of pathway creation and curation
      1. New pathway extension includes additional genes into the preexisting pool to improve pathway coverage about 25%
      2. Gene ID’s extracted for one instance and are used as universal ID’s to query a multitude of other databases
5. The powerful data visualization afforded by GenMAPP 2 can be grasped by several illustrative examples displaying some features unique to this software
   1. One experiment was used to show the potential examination of whole-genome exon array data
      1. Unique to GenMAPP 2 is the viewing of identifiers to a related gene based on colored prioritization to provide a novel visual for analysis
      2. This strategy allows for clear representation of what tissues in which some genes are most significantly expressed
   2. Another experiment compared gene expression and proteomic data of mRNA and protein levels in yeast when exposed to changes in carbon source
      1. Physically concurrent coloring bands are used to clearly illustrate the time-effect data using GenMAPP’s color visualization
      2. Side-by-side comparisons of this nature are unique to GenMAPP and have very malleable implications as far as analysis is concerned
   3. A third example illustrates the streamline combination of genomic, phenotypic, and structural information of polymorphisms
      1. This feature grants a broad, predictive view of how various polymorphisms, and their proteomic distributions, can have an effect on greater biological systems
      2. Using this paradigm, GenMAPP adopts customizable displays to access multiple gene regulations at once
6. The future directions of GenMAPP development are primarily threefold:
   1. Focus on cross-platform adaption of the software
   2. Create dynamically updated gene databases to further automation
   3. Continue development of tools to quickly analyze high-throughput data
7. Main result: GenMAPP 2 provides powerful tools to visually interpret complex microarray data and pathway changes across a plethora of organisms, and then to share these results in the most efficient manner available