

Biosciences Bioinformatics Blog: New NCBI Interfaces and Requests for Input on Pathway Analysis

This article was featured in [Library Notes, #47 \(Spring 2008\)](#).

Well, spring is here and that means that new things are springing up all over. This includes new resources from the NCBI (National Center for Biotechnology Information). Recently NCBI introduced their new Sequence Viewer, which is replacing the old graphical view of a sequence accessed from the Entrez Nucleotide or Entrez Protein databases, though my favorite access point is from the Entrez Gene record for the gene I am viewing at any given time.

The screenshot displays the NCBI Sequence Viewer 2.0.β interface. At the top, the NCBI logo and navigation links (Home, PubMed, GenBank, BLAST) are visible. The main title is "Homo sapiens chromosome 21, reference assembly, complete sequence" with the accession number "gi|51511750|ref|NC_000021.7|NC_000021". The interface includes a search bar, a theme selector set to "NCBI Overview", and a genomic track showing the chromosome with a red vertical bar indicating the current position at approximately 26,340 K. Below the track, the "Main Features" section displays two gene models for APP: APP / NM_201414.1 (mRNA-amyloid beta (A4) precursor protein) and APP / NP_958817.1 (amyloid beta A4 protein precursor isoform c). The interface includes navigation tools, a position input field set to "26.16M 26.48M", and a theme selector set to "NCBI Details".

Practically everything in the new viewer is interactive: you can get a wide or narrow horizontal view of a chromosome with genes visible. You can view genes' isoforms, sequences and SNP profiles. Take a look at the [intro pages for Sequence Viewer](#).

For an overview of all the features of the new CDD, see the [help pages](#).

Finally, I'd like to get some input from the research community. I am looking at a number of pathway analysis software suites, such as Ingenuity Pathways Analysis and GeneGo Metacore. Many of these packages have features that allow users to integrate their own high-throughput data and to customize the pathway analysis. Take a look at some of these companies' products:

- Ingenuity Pathways Analysis <http://www.ingenuity.com/>
- GeneGo MetaCore <http://www.genego.com/metacore.php>

Please [e-mail me](#) or leave a comment to this blog entry and let me know if you need such software available for your research. With NU's new clinical and translational center and funding I suspect there will be increased demand for such packages, and I'd like to get some idea of what our need is here at Northwestern. Just send a quick note to me indicating if you would use pathway analysis tools and what package you would prefer, if any. You do not need to limit your preference to the two I listed above. They are there as examples for you to investigate.

Don't forget, I am available to provide instruction and assistance in the use of a variety of literature and molecular databases and tools. Please feel free to drop me a message any time you need to.

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