DAVID-WS: A Stateful Web Service to Facilitate Large Gene List Analysis

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DAVID: The Database for Annotation, Visualization and Integrated Discovery
http://david.niaid.nih.gov
Stateful DAVID web services

- Simple Object Access Protocol (SOAP), exchanges XML messages between client and the Service provider (Java, C, Perl, Python, etc...)

DAVID Web Services

http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_WebService.html

Available Operations:

(1) Upload
   • addList()

(2) Lookup
   • getAllAnnotationCategoryNames()
   • getAllListNames()
   • getAllPopulationNames()
   • getConversionTypes()
   • getCurrentList()
   • getCurrentPopulation()
   • getCurrentSpecies()
   • setDefaultCategoryNames()
   • getGeneReportCategories()
   • getListName()
   • getSpecies()

(3) Select
   • setCurrentList()
   • setCurrentPopulation()
   • setCurrentSpecies()
   • setCategories()

(4) Report
   • getChartReport()
   • getGeneClusterReport()
   • getListReport()
   • getSummaryReport()
   • getTableReport()
   • getTermClusterReport()
Load Testing

Conclusion

- Compared to the web-based interface and the current DAVID-API DAVID-Web Service is a more efficient and flexible interface for users to access DAVID and utilize the resources that DAVID provides to foster discovery.
- The client code provided by DAVID-WS can be easily integrated into programs, work flows and interactive analysis tools as computational components.
- Our simulation and performance testing show that it took about 5 to 9 seconds to generate the output for computationally intensive client tasks such as Gene Functional Classification or Functional Annotation Clustering with 2,000 genes.