

Creation of *Arabidopsis thaliana* response to drought pathway using the text mining tool PESCADOR

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INTRODUCTION

Kegg Pathway database has been initiated in 1995 with biochemical pathways. Hitherto, the database covers several biological phenomena. The propagation of information to all organisms comprised by the database allows its use in automated analyzes of new sequenced genomes. Using the text mining tool PESCADOR, we processed a total of 1686 abstracts sorted by significance with the software PubMed Ranker. PESCADOR has labeled 235 genes involved in 722 biointeractions.

METHODS AND RESULTS

Medline Ranker | about | query page | tutorial page | contact | CBDM group page

Abstracts selection

The query topic (the training set) is defined by:

- the following PubMed query
- all the following MeSH terms (tree top)
- the following list of PMIDs

one per line

Short documentation

The training set is a set of scientific articles related to the same topic. You can write a PubMed query to build automatically a training set. Alternatively, you can use biomedical terms from the Medical Subject Headings (MeSH). Please input only exact terms. These terms can be found in the MeSH Browser or hierarchical tree. The procedure is detailed in the tutorial section. The training set can be also defined with your own list of articles (identified by PubMed identifiers, e.g. PMIDs). You can get a list of PMIDs in few clicks from the PubMed interface: go to the PubMed page, make a query, select 'UI List' in the Display menu, and Send to file. Please see the related tutorial.

For demo: click on one of the following training set, and then on the 'Rank it' button:

- Mitochondria
- Host-Pathogen Interactions
- Alternative Splicing
- Cardiovascular Diseases and Smoking
- Phosphorylation and Protein Binding
- Phosphorylation-dependent molecular processes
- Neoplasms and Stem Cells
- Up-Regulation of physiological processes in Alzheimer Disease
- Computational Biology

The reference (the background set) is defined by:

- the whole Medline database
- the following list of PMIDs

one per line

The abstracts to be ranked (the test set) are defined by:

The test set defines abstracts which will be ranked by the MedlineRanker program. Ranking all the medline abstracts of the last months or years may be long. The processing speed is approximately: 1 Million abstracts (~2 years old abstracts) per minute after initialization steps.



PESCADOR

Platform for Exploration of Significant Concepts Associated to co-Occurrences Relationships.

Results for ID 128320463: [Summary](#) | [Terms](#) | [Concepts](#) | [Abstracts](#) | [Network](#) | [Validations](#) | [Help](#) | [Home](#)

Selected PubMed ID: 16714312

Sentence 1: Overexpression of the regulator of G-protein signalling protein enhances ABA-mediated inhibition of root elongation and DROUGHT tolerance in Arabidopsis.

Sentence 2: Regulator of G-protein signalling (RGS) proteins identified recently in Arabidopsis have been involved in the regulation of several physiological processes, but largely nothing is known about their roles at both the physiological and the molecular level.

Sentence 3: In the experiments reported here, the overexpression approach was used to present evidence that RGS1 protein plays critical roles in PLANT development and in modulating abscisic acid (ABA) and DROUGHT stress signal transduction.

Sentence 4: RGS1 affected the shapes of leaves, the development of floral buds, the elongation of stems, siliques, and hypocotyls, and the time of flowering.

Sentence 5: Post-germination growth was inhibited by 1 microM ABA, and root growth was hypersensitive to ABA for 35S-RGS1 transgenic plants.

Sentence 6: RGS1 overexpression conferred more DROUGHT tolerance to transgenic plants, as compared with the wild type (Columbia).

Sentence 7: Reverse transcription-PCR (RT-PCR) results indicated that RGS1 overexpression significantly stimulated the expression of NCED and ABA2, that encode two key enzymes catalysing ABA biosynthesis.

Sentence 8: Furthermore, the expression of several stress-regulated genes was either up- or down-regulated in RGS1-overexpressing transgenic plants.

Sentence 9: Combining the results above with previous results, it is suggested that RGS1 exerted its effects on PLANT responsiveness to ABA and DROUGHT tolerance largely through changing the expression either of genes responsible for ABA biosynthesis, which leads to changes in endogenous ABA levels, or of stress-responsive genes.

Legend of colors:
 Target sentence(s):
 Biological terms:
 Biointeraction terms:
 Biological concept(s).

