Creating a database and developing a website:

ReproMine

Summary

I. ReproMine's project

II. ReproMine's database

III. ReproMine's website

I. ReproMine's project

 Gather raw data on reproductive diseases and re-normalize for comparison

 Analyze these data to identify individual mRNAs related conditions or stages of disease development

 Create a list of molecular pathways, constituting each set of disease and development associated with mRNA transcript identified in the previous step

•Create a database to facilitate data access to users

Why generate this database?

 Microarray technologies allow tens of thousands of genes to be analysed simultaneously

Microarrays have been applied extensively to developmental and reproductive disease

•There is a realisation that more biological meaning can be obtained from microarray data when it is analysed <u>at the level of pathways and gene sets</u>

•There is also a realisation that <u>concordant data</u> <u>from several separate microarray studies</u> is more reliable than data from a single study

An example of bringing microarray data from several different studies together: Oncomine

Welcome to Oncomine 4.3 Research Edition

Upgrade to the Onconine Research Prenium Edition: advanced features for cutting edge cancer research

Multi-gene search

Searching has never been easier.

With Oncomine Research Premium Edition any number of genes, a concept, and countless filters can be added to your search in order to compare the expression of multiple genes at once and understand the relationships between multiple genes in a sample.

With the smart search box, when you type two characters, a list of options appears with terms from genes to tissue types.



What data is there to put into this database? Many microarray studies of reproduction and development have been performed over the last ten years



number

Based on these studies, there are now signficant amounts of microarray data available for several reproductive diseases



II. ReproMine's database

- •Demand Analysis: definition of user needs, simple database, easily accessible, which they can easily find the data that the user would need, to contain all relevant information
- •Solution Design: Conceptual Data Model (CDM)
- •Physical design: realization of the database
- Database Client server

II. ReproMine's database



III. ReproMine's website

Tools:

WampServer (Windows Apache MySQL PHP) platform for web development Windows

Php: interpreted language, mainly used for producing dynamic web pages, it allows to enter data in the database, create the website, and the interaction between the website and database

HTML: markup language, for writing the hypertext, to format the pages to include multimedia resources such as images, entry forms, and programmable elements

Mysql management system database, which allows sorting, filtering and data processing

An example of using this database: the disease endometriosis

What is endometriosis?

•A disease where endometrium (the lining of the uterus) gets into the wrong place

It causes severe pain and also infertility

It is thought to require several processes including cell proliferation and an immune response

An example of an endometriotic lesion seen in a women's abdomen through an endoscope



When you compare endometriosis to normal endometrium lining the uterus, what genes appear to be regulated in common in 7 studies?

Querry

- Endometriosis meta-analysis endometriosis vs endometrium
- Hever endometriosis vs endometrium
- Hever Reanalysis 500 endometriosis vs endometrium
- □ Hever Reanalysis 1057 endometriosis vs endometrium
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- Hull reanalysis 500 endometriosis vs endometrium
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Only 8 genes in common between all studies! endometrium lining the uterus, what <u>biologically coherent gene sets</u> (from the Gene Ontology database) appear to be regulated in common in 7 studies?

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17 biologically coherent gene sets, especially related to inflammation and immune response

Interestingly, inflammation and immune response are known to play important roles in this disease, and many drugs used to treat this disease act by blocking inflammation and immune response endometrium lining the uterus, what <u>sets of</u> <u>transcription factor targets</u> (from the Transfac database) appear to be regulated in common in 7 studies?

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21 sets of transcription factor targets are co-regulated in multiple studies, e.g. E2F1, SMAD3, STAT5A

E2F1 (which drives cell division), SMAD3 (response to TGF beta growth factors) and STAT5A (response to IL2, IL&, GMCSF) are all known to play a role in endometriosis

Key results from the endometriosis search

•Very few genes (8) are regulated in all studies, this is not unusual and reflects different experimental protocols

Despite this, the genes regulated in all studies share common themes - they are significantly enriched for 17 biologically coherent gene sets (e.g. immune response, which is known to be important for endometriosis)

•The genes regulated in the various studies are also significantly enriched for 21 <u>common transcription factor</u> <u>motifs in their promoters</u>, which appear to be related to what is known about this disease (e.g. cell division, response to growth factors, immune response)

The future

•Repromine will be maintained and expanded

It will be able to incorporate RNA-seq data as well as data of other types such as genetic data and miRNA data

.lt will be continued as a collaboration
France-NZ!!!

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