Health Hack

PubMed

WHAT PUBMED SAID

Challenge presented to HealthHack Sydney 2014 by Dr Fabian Buske, Quek Xiu Cheng and Kenneth Sabir, of the Garvan Institute.

THE PROBLEM

“As a biomedical researcher it is difficult for me to digest the overwhelming amount of information there is on just one specific gene, let alone a group of them. I want a better way to see what makes a given large set of genes special. ”

Dr Fabian Buske,
The Garvan Institute

THE PROBLEM

"As a PhD student, it's hard to keep up with my experiments and what is happening in the literature. If only there was a way to summarize the all literature about my protein of interest."

Quek Xiu Chen
PhD Student

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1. Clonal Dominance With Retroviral Vector Insertions Near the ANGPT1 and ANGPT2 Genes in a Human Xenotransplant Mouse Model.
Haemmerle R, Phaltane R, Rothe M, Schröder S, Schambach A, Moritz T, Modlich U.
Mol Ther Nucleic Acids. 2014 Oct 7;3:e200. doi: 10.1038/mtna.2014.51.
PMID: 25291142 [PubMed]
Related citations

...niotic fluid cells have haematopoietic potential and engraft after autologous in ...tion.
...ll MP, Pipino C, Shangaris P, Maghsoudlou P, Ramachandra DL, Georgiades F, ... AJ, Porada CD, Almeida-Porada G, Cheng PJ, David AL, De Coppi P.
...o 3. doi: 10.1002/stem.1839. [Epub ahead of print]
...bMed - as supplied by publisher]

...d human hematopoietic stem cell maintenance is critical for acute myeloid ...

...ger G, Bakker B, Rozenveld-Geugien M, Jaques J, de Haan G, Schuringa JJ, ...bers H.
... 3. doi: 10.1038/leu.2014.259. [Epub ahead of print]
...bMed - as supplied by publisher]

...Treatment of One Graft in a Double Cord Blood Transplant Provides Early Platelet ...Contributing to Long-Term Engraftment in **NSG** Mice.
... van Hensbergen Y, Brand A, Slot MC, de Graaf-Dijkstra A, Mulder A, Watt SM, Zwaginga JJ.
Stem Cells Dev. 2014 Sep 29. [Epub ahead of print]
PMID: 25137252 [PubMed - as supplied by publisher]
Related citations

5. Ex vivo assays to study self-renewal, long-term expansion, and leukemic transformation of genetically modified human hematopoietic and patient-derived leukemic stem cells.
Sontakke P, Carretta M, Capala M, Schepers H, Schuringa JJ.

New feature
Try the new Display Settings option - **Sort by Relevance**

Related searches
cd34 nsg mice

Titles with your search terms
Human **CD34**+ CD133+ hematopoietic stem cells cultured with growth factors inc [PLoS One. 2011]
Human T cell development in the liver of humanized NOD/SCID/IL-2F [Clin Immunol. 2011]
Ex vivo rapamycin treatment of human cord blood **CD34**+ cells en [Blood Cells Mol Dis. 2011]
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35 free full-text articles in PubMed Central
Sustained Engraftment of Cryopreserved Human Bone Marrow **CD34**([Biores Open Access. 2014]
Analysis of the clonal growth and differentiation dynamics of primitive barcoded hum [Blood. 2013]
Fucosyltransferase VII improves the function of selectin ligands on cord bloo [Glycobiology. 2013]
See all (35)...

Got a paper in PubMed?

THE STATUS BEFORE HEALTH HACK...

- The Garvan Institute has processed more than 2 million full-text scientific articles on biological and medical sciences from Pubmed Central
- Extracted meaningful keywords and associated these with categories such as “disease”. The result is a DB of 6 billion data points
- Each human protein-coding gene is now mapped to every PubMed article it appears in along with every term found in these papers

THE CHALLENGE

The challenge is to create a tool that allows us to query the DB categories via:

- Visual presentation layer to convey the returned information and illustrate the connectivity between the discoveries
- Ranked recommendations via collaborative filtering or consensus via aggregations
- Link back to the original publications to enable further in-depth studies.

THE TEAM

L-R: Quek Xiu Cheng (PhD Research Student), Andy Zeng (Data Scientist), Chunxiao Kin (Software Engineer), Paul Joseph (Software Developer), Svetlana Filimonova (Software Developer), Dr Fabian Buske (Garvan Institute), Amanda Wise (UX)

THE DATA

Data is in human un-readable objects.

The team needed to find the description for each term in the DB and associate this back to the data. We added statistical enrichment analysis of terms on some groups over others.


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        "ENSP00000312606"
    ],
    "ensg_id": [
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        "ENSG00000117448"
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            "DOID:1432": 1,
            "DOID:1492": 1,
            "DOID:7": 6,
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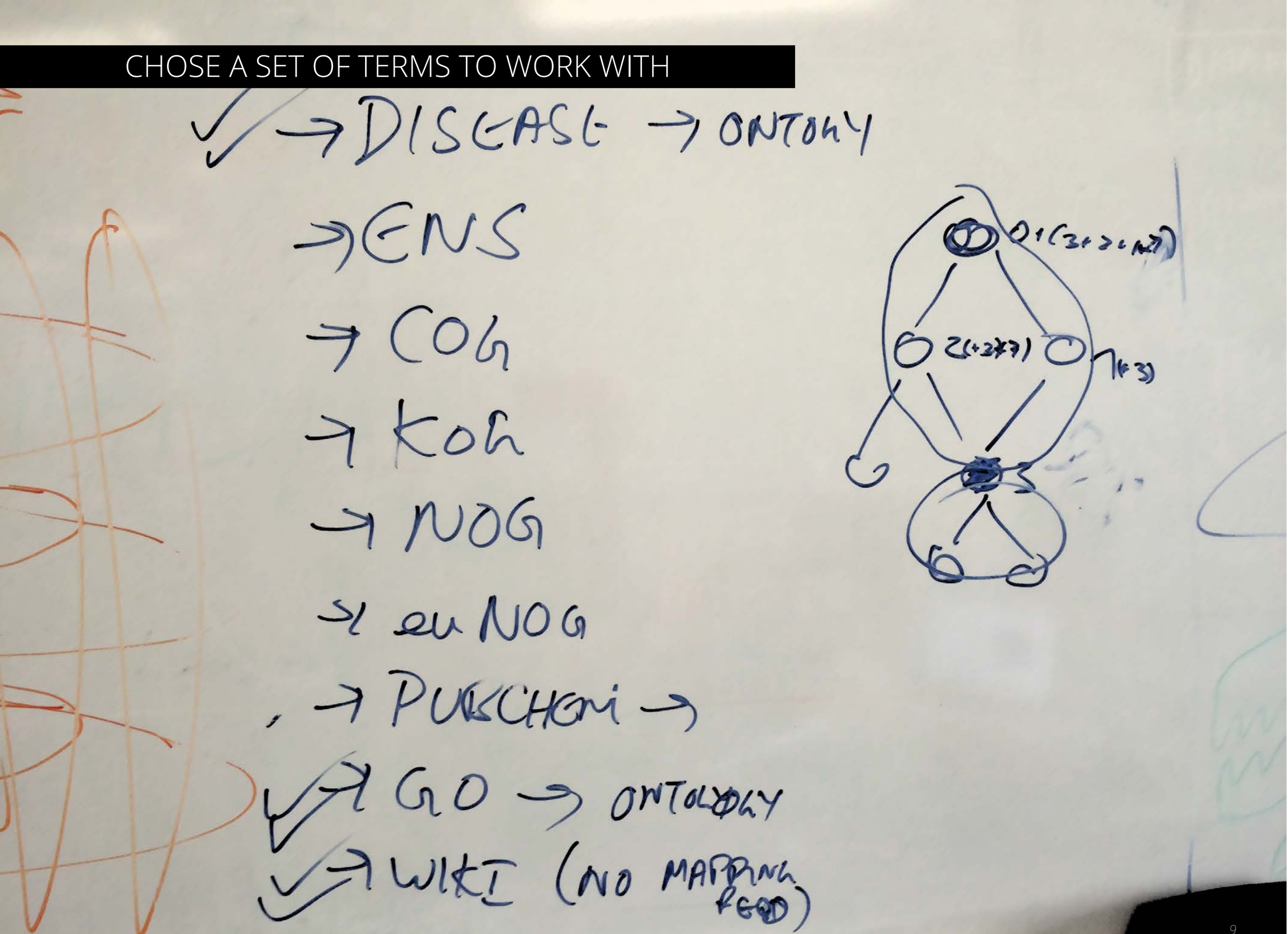
CHOSE A SET OF TERMS TO WORK WITH



THE DATA

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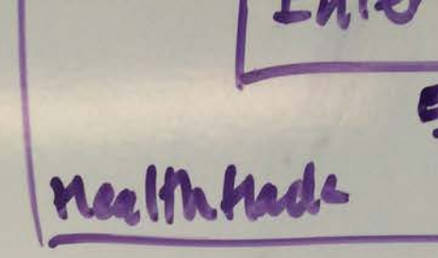
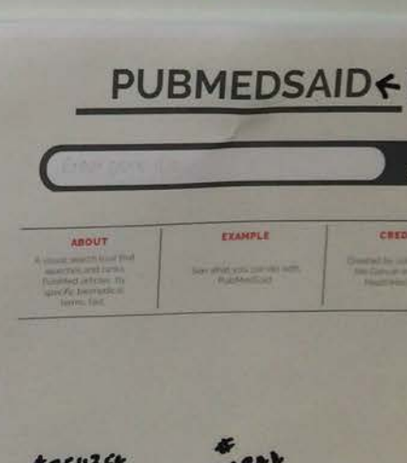
SKETCHBOARDS



Elevator pitch

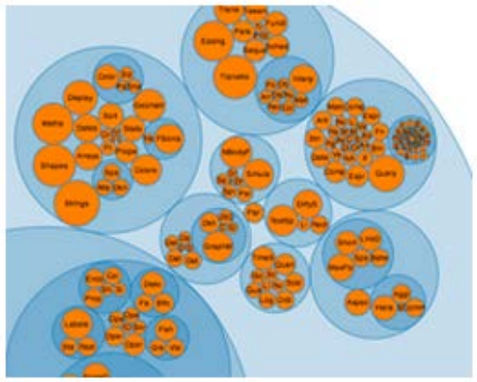
A visual search tool for biomedical researcher that enables search of PubMed & rank articles by specific biomedical terms, fa



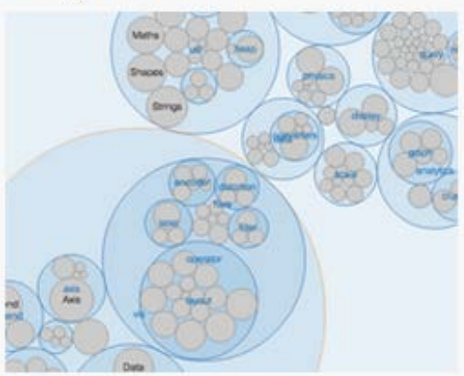
DISCUSSED WHICH SORT OF VISUALISATION WOULD COMMUNICATE BEST

Bubble Chart

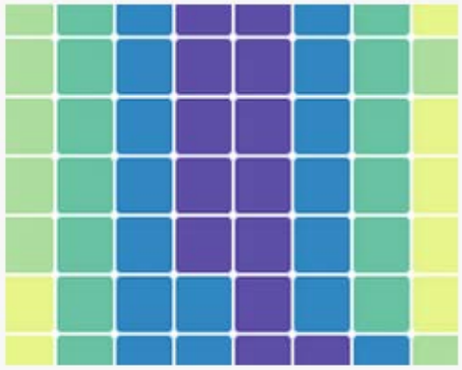
Circle Packing



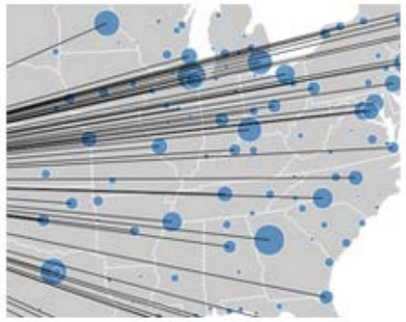
Layout



Trulia Trends

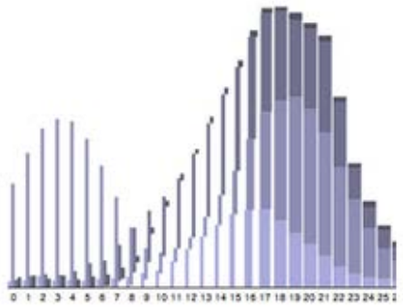


Symbol Map



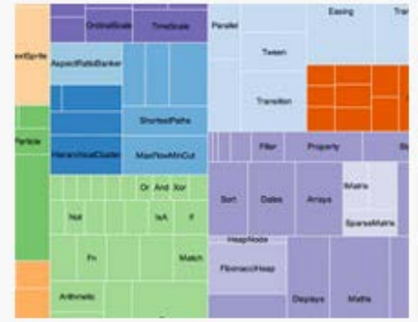
Site or blog concept browser

Stacked Bars

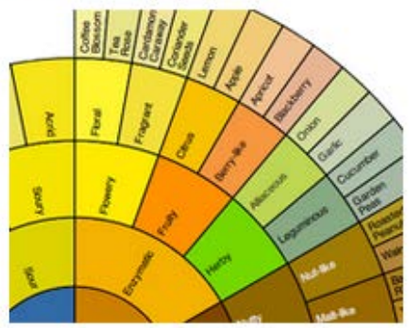


Gene Expression

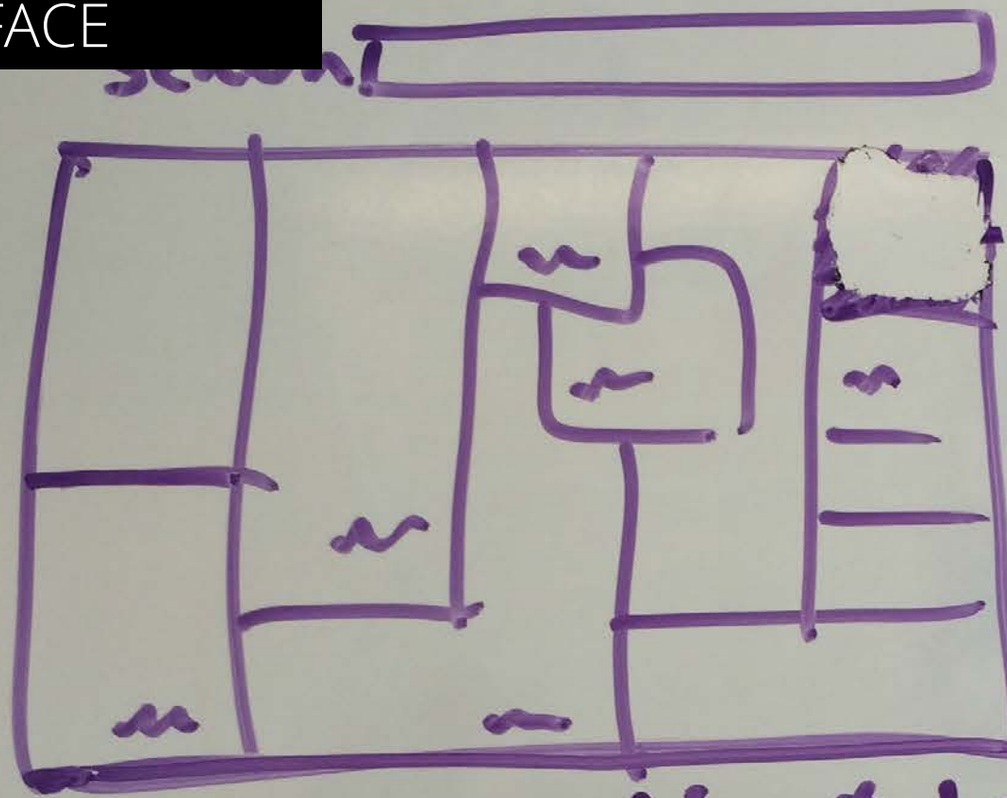
Zoomable Treemap



Zoomable Sunburst



USER INTERFACE

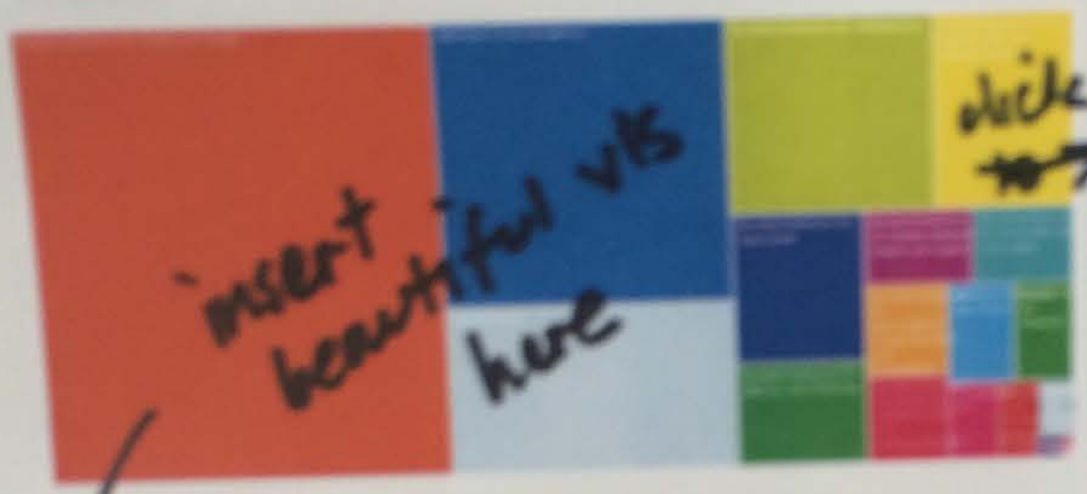


Title....
Year

- Terms proportionate to frequency in PubMed articles

WE DECIDED ON A ZOOMABLE TREEMAP

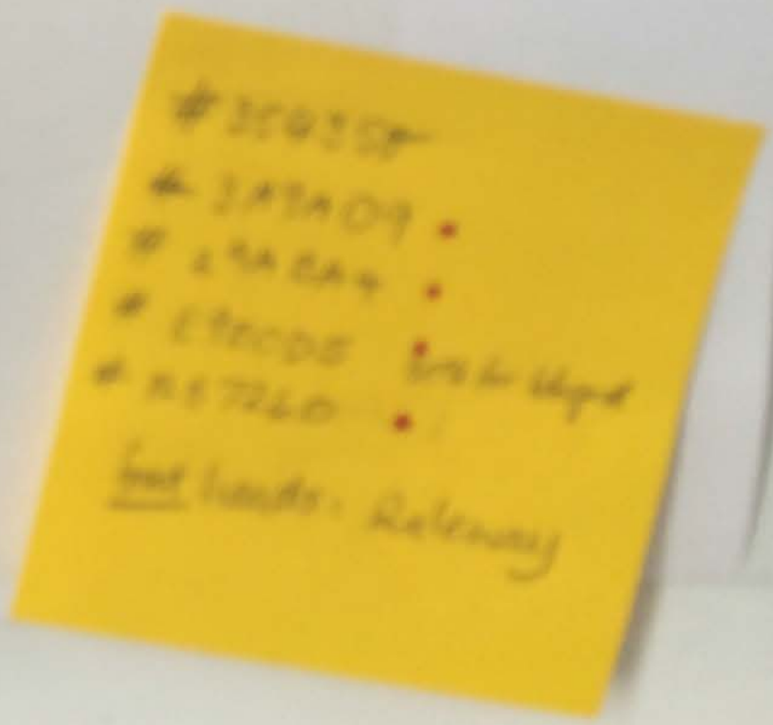
PUBMEDSAID



Rotating: title
• Light, Yr, Journal
▽ expand

mouse-over term label: definition

Need to play with article list at side or beneath

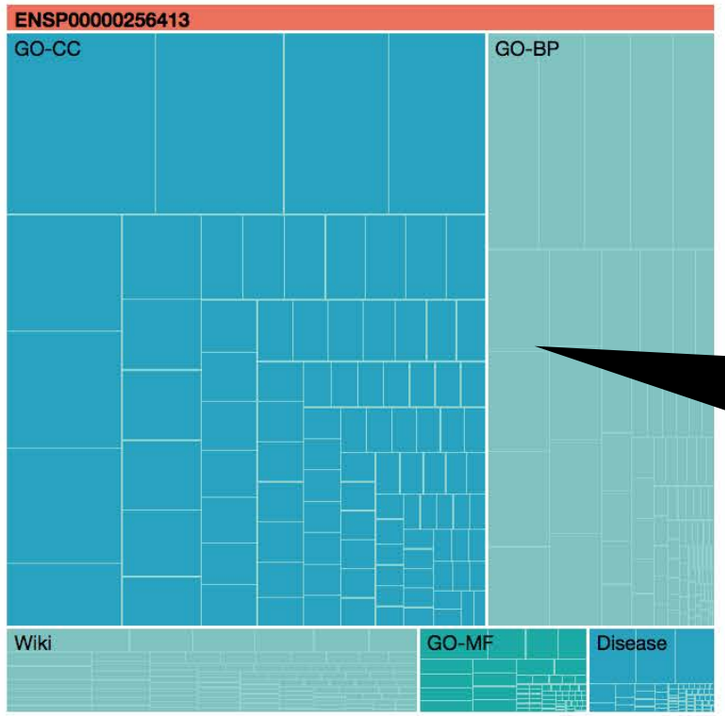


THE PROTOTYPE: http://svetixbot.github.io/pubmedsaid

- ENSP00000256413
- ENSP00000308318
- ENSP00000362705
- ENSP00000371690
- ENSP00000458989

PubMedSaid

Prototype presented by Dr Fabian Buske, Quek Xiu Cheng and Kenneth Sabir



Database sources – click to show frequency of terms within that DB

THE PROTOTYPE: http://svetixbot.github.io/pubmedsaid

- ENSP00000256413
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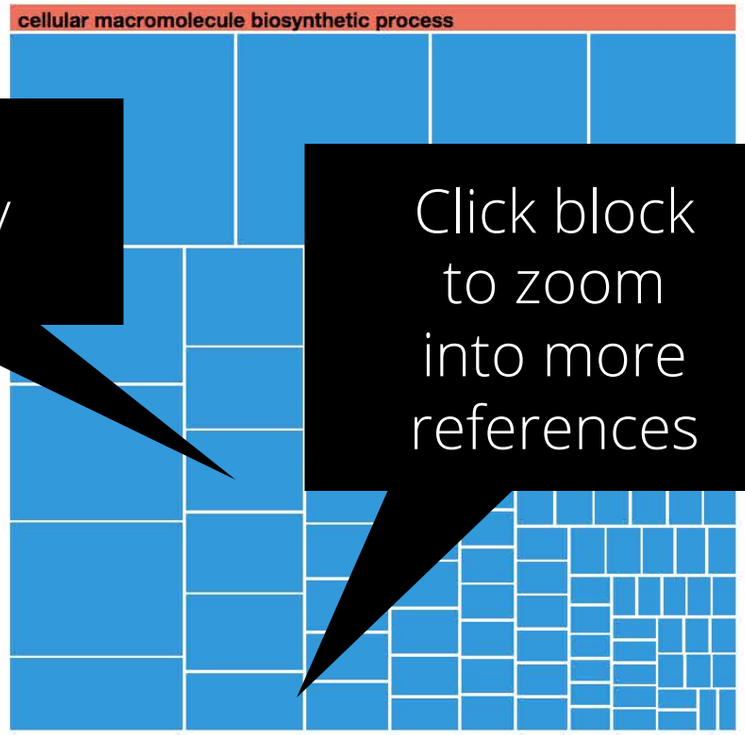
Data sets

PubMedSaid

Prototype presented by Dr Fabian Buske, Quek Xiu Cheng and Kenneth Sabir

Term and definition



Ranked frequency of terms

Click block to zoom into more references

cellular process

GO:0009987 "Any process that is carried out at the cellular level , but not necessarily restricted to a single cell. For example, c ell communication occurs among more than one cell, but occurs at the cellular level." [GOC:go_curators, GOC:isa_complete]

Found 357 articles

Articles ranked by date

- **FGFR1 mutations cause Hartsfield syndr… the unique association of holoprosen… and ectrodactyly.**

  Author: Simonis N,Migeotte I,Lambert N,Perazzolo C,de Silva DC,Dimitrov B,Heinrichs C,Janssens S,Kerr B,Mortier G,Van Vliet G,Lepage P,Casimir G,Abramowicz M,Smits G,Vilain C

  Journal: Journal of medical genetics

  Published: 2013 08

- **Tespa1 is a novel inositol 1,4,5-trisphosphate receptor binding protein in T and B lymphocytes.**

  Author: Matsuzaki H,Fujimoto T,Ota T,Ogawa M,Tsunoda T,Doi K,Hamabashiri M,Tanaka M,Shirasawa S

  Journal: FEBS open bio

  Published: 2013 05

- **Mutations in FGF17, IL17RD, DUSP6, SPRY4, and FLRT3 are identified in individuals with congenital hypogonadotropic hypogonadism.**

  Author: Miraoui H,Dwyer AA,Sykiotis GP,Plummer L,Chung W,Feng B,Beenken A,Clarke J,Pers TH,Dworzynski P,Keefe K,Niedziela M,Raivio T,Crowley WF,Seminara SB,Quinton R,Hughes VA,Kumanov P,Young J,Yialamas MA,Hall JE,Van Vliet G,Chanoine JP,Rubenstein J,Mohammadi M,Tsai PS,Sidis Y,Lage K,Pitteloud N

  Journal: American journal of human genetics

  Published: 2013 05

- **Defining regulatory and phosphoinositide-**

Article abstract

Congenital hypogonadotropic hypogonadism (CHH) and its anosmia-associated form (Kallmann syndrome [KS]) are genetically heterogeneous. Among the >15 genes implicated in these conditions, mutations in FGF8 and FGFR1 account for ~12% of cases; notably, KAL1 and HS6ST1 are also involved in FGFR1 signaling and can be e therefore hypothesized that mutations in genes encoding a broader s of the FGFR1 pathway might contribute to the genetics of CHH as mutations. Thus, we aimed to (1) investigate whether CHH individuals members of the so-called "FGF8 synexpression" group and (2) of a bioinformatics algorithm on the basis of protein-protein nteractome-based affiliation scoring [IBAS]) to identify high-quality n the basis of sequence homology, expression, and structural and ven genes were selected and sequenced in 386 unrelated CHH and 155 controls. Except for FGF18 and SPRY2, all other genes were found to be CHH individuals: FGF17 (n = 3 individuals), IL17RD (n = 8), DUSP6 (n = 5), SPRY4 (n = nd FLRT3 (n = 3). Independently, IBAS predicted FGF17 and IL17RD as the two top ndidates in the entire proteome on the basis of a statistical test of their protein-protein interaction patterns to proteins known to be altered in CHH. Most of the FGF17 and IL17RD mutations altered protein function in vitro. IL17RD mutations were found only in KS individuals and were strongly linked to hearing loss (6/8 individuals). Mutations in genes encoding components of the FGF pathway are associated with complex modes of CHH inheritance and act primarily as contributors to an oligogenic genetic architecture underlying CHH.

Presentation1.pptx | healthhack_logo_2014.png | images.jpeg | Show All

NEXT STEPS: UI ENHANCEMENTS

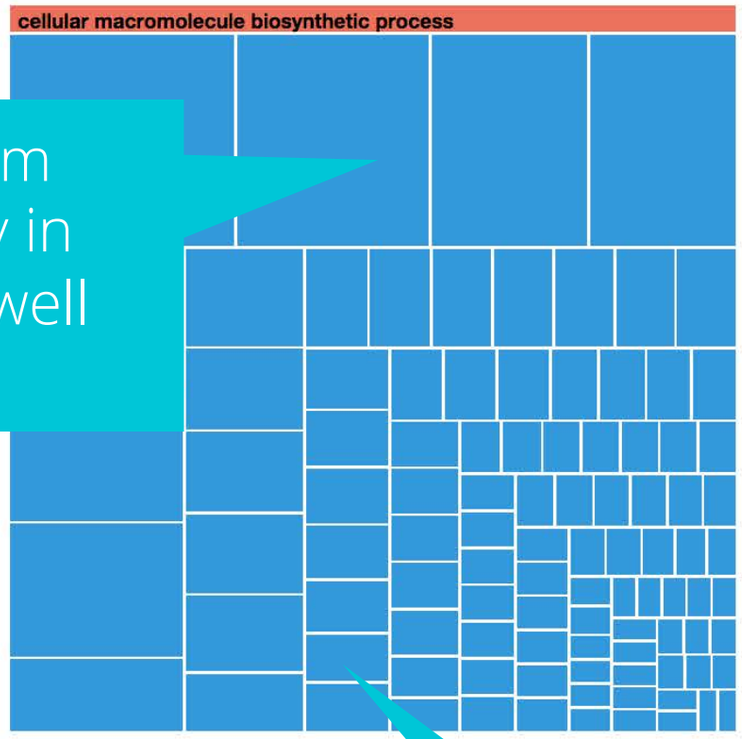
- ENSP00000256413
- ENSP00000308318
- ENSP00000362705
- ENSP00000371690
- ENSP00000458989

SEARCH FIELD

PubMedSaid

Presented by Dr Fabian Buske, Quek Xiu Cheng and Kenneth Sabir

Show term frequency in colour as well as size



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harbor mutations in members of the so-called "FGF8 syn
validate the ability of a bioinformatics algorithm on the ba
interactome data (interactome-based affiliation scoring [IB
candidate genes. On the basis of sequence homology, ex
functional data, seven genes were selected and sequence
individuals and 155 controls. Except for FGF18 and SPRY
to be mutated in CHH individuals: FGF17 (n = 3 individuals), IL17RD (n = 8), DUSP6 (n = 5), SPRY4 (n = 14), and FLRT3 (n = 3). Independently, IBAS predicted FGF17 and IL17RD as the two top candidates in the entire proteome on the basis of a statistical test of their protein-protein interaction patterns to proteins known to be altered in CHH. Most of the FGF17 and IL17RD mutations altered protein function in vitro. IL17RD mutations were found only in KS individuals and were strongly linked to hearing loss (6/8 individuals). Mutations in genes encoding components of the FGF pathway are associated with complex modes of CHH inheritance and act primarily as contributors to an oligogenic genetic architecture underlying CHH.

Term and definition on roll-over of each block

cellular process

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Layout of Article summary

Found 357 articles

- **FGFR1 mutations cause Hartsfield syndro the unique association of holoprosencepha and ectrodactyly.**

  Author: Simonis N,Migeotte I,Lambert N,Perazzolo C,de Silva DC,Dimitrov B,Heinrichs C,Janssens S,Kerr B,Mortier G,Van Vliet G,Lepage P,Cas G,Abramowicz M,Smits G,Vilain C

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  n bio

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  Author: Miraoui H,Dwyer AA,Sykiotis GP,Plummer L,Chung W,Feng B,Beenken A,Clarke J,Pers TH,Dworzynski P,Keefe K,Niedziela M,Raivio T,Crowley WF,Seminara SB,Quinton R,Hughes VA,Kumanov P,Young J,Yialamas MA,Hall JE,Van Vliet G,Chanoine JP,Rubenstein J,Mohammadi M,Tsai PS,Sidis Y,Lage K,Pitteloud N

  Journal: American journal of human genetics

  Published: 2013 05

- **Defining regulatory and phosphoinositide-**

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"Not being able to go after the answer at the opportune moment an idea strikes can stop new discoveries in its tracks.

Thus, a framework that can reveal the connections between distinct scientific fields or discoveries on the spot has the potential to facilitate future Eureka moments."