Science Communication & Impact

What I think about

Steven B. Roberts
School of Aquatic and Fishery Sciences
University of Washington

robertslab.info
@sr320

Personal Learning Environments

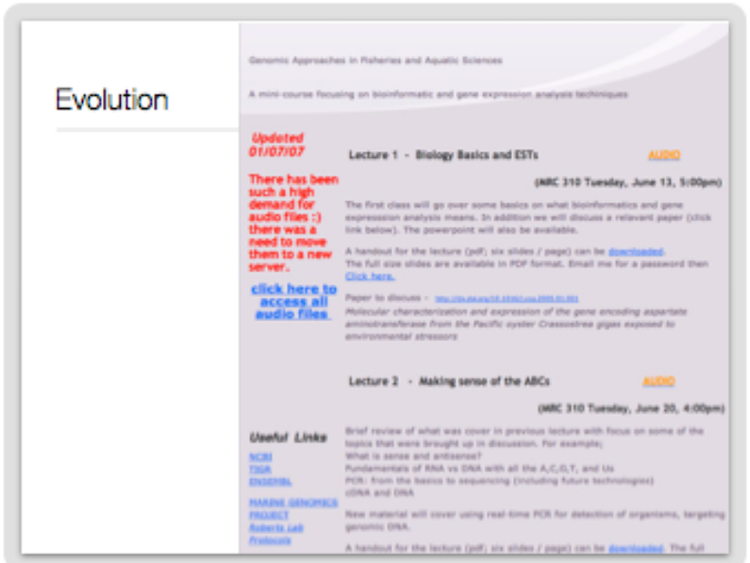
PLE in '*Conventional*' scientific cycle

What we do…

altmetrics

Backstory

4



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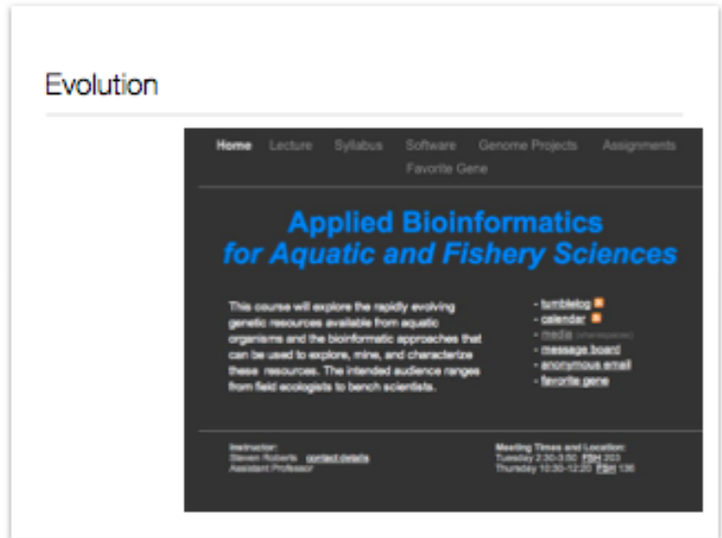

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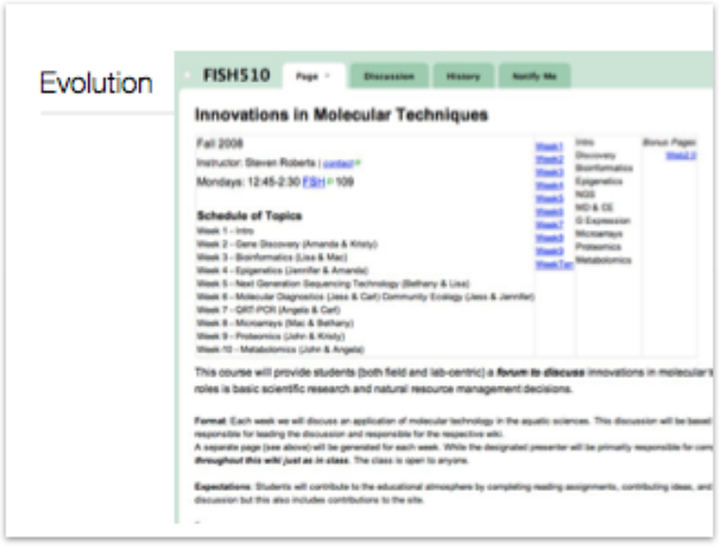

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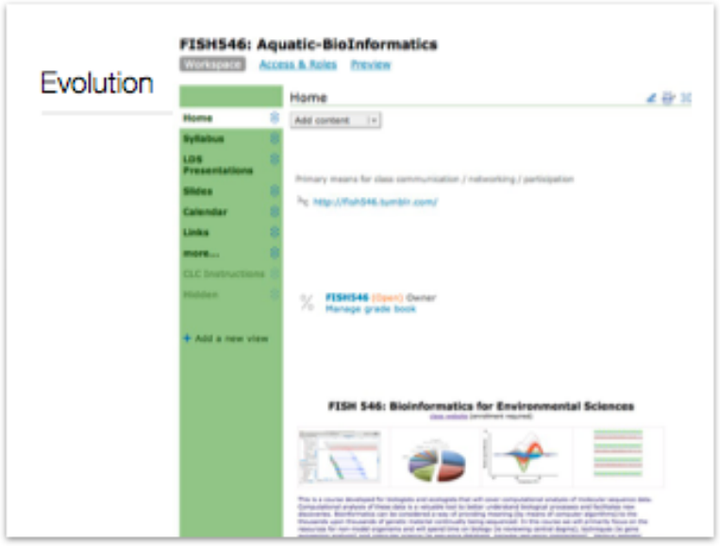


8

9

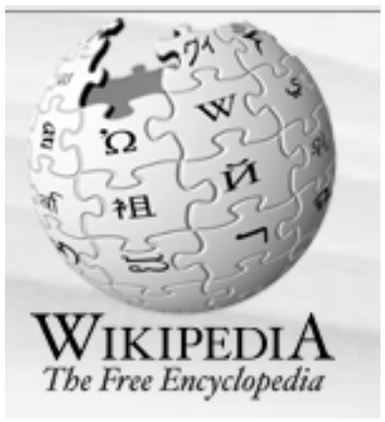
P L E

"**Personal Learning Environments** are systems that help learners take control of and manage their own learning. This includes providing support for learners to

- set their own learning goals
- manage their learning; managing both content and process
- communicate with others in the process of learning

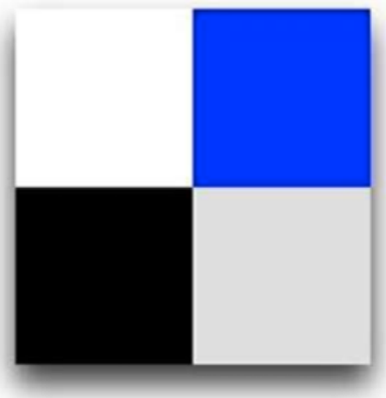
and thereby achieve learning goals.

A PLE may be composed of one or more subsystems: As such it may be a desktop application, or composed of one or more web-based services."[1]



P L E

Personal Learning Environments



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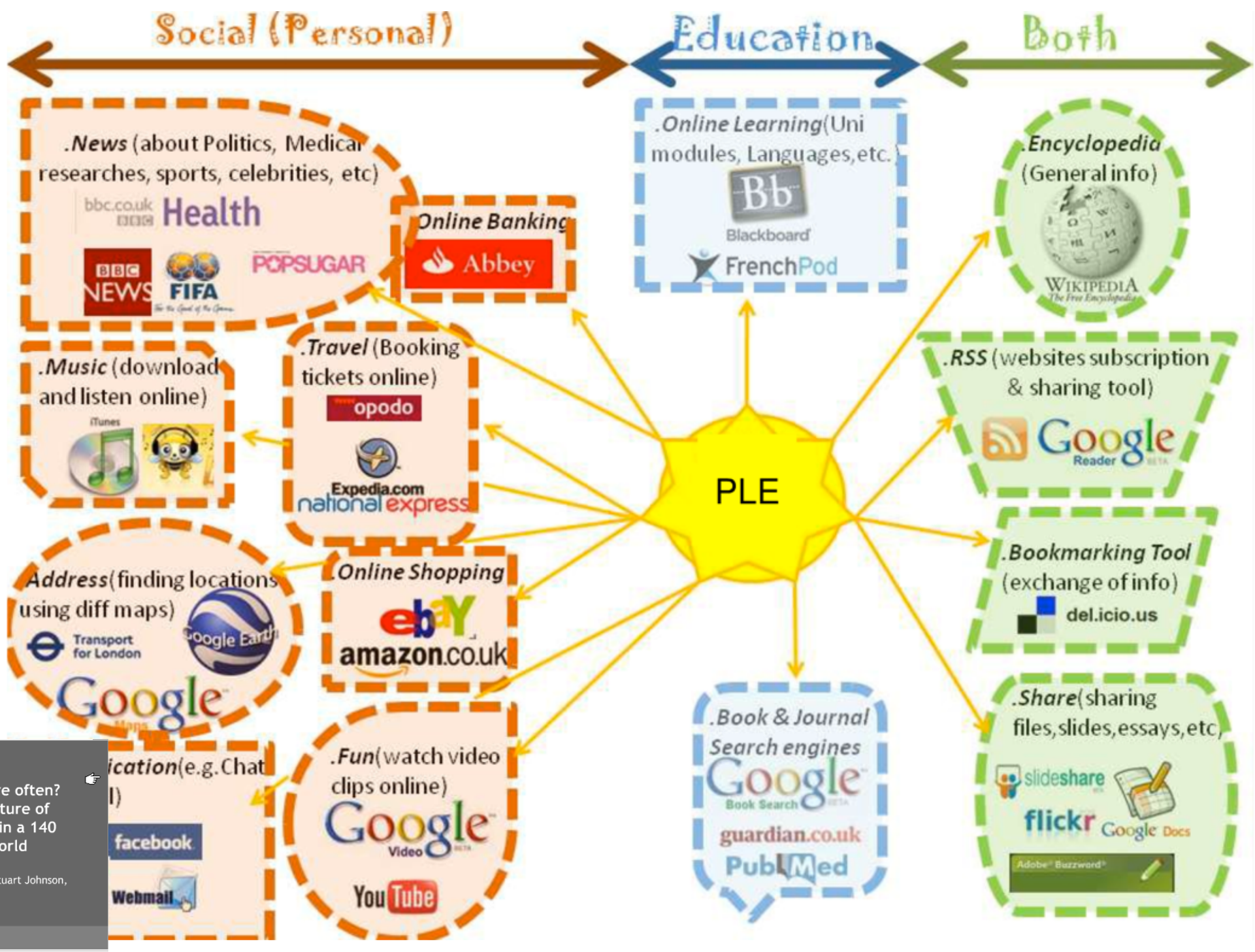
P L E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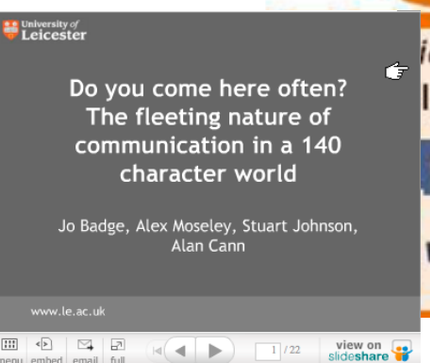
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Do you come here often? The fleeting nature of communication in a 140 character world
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P L E

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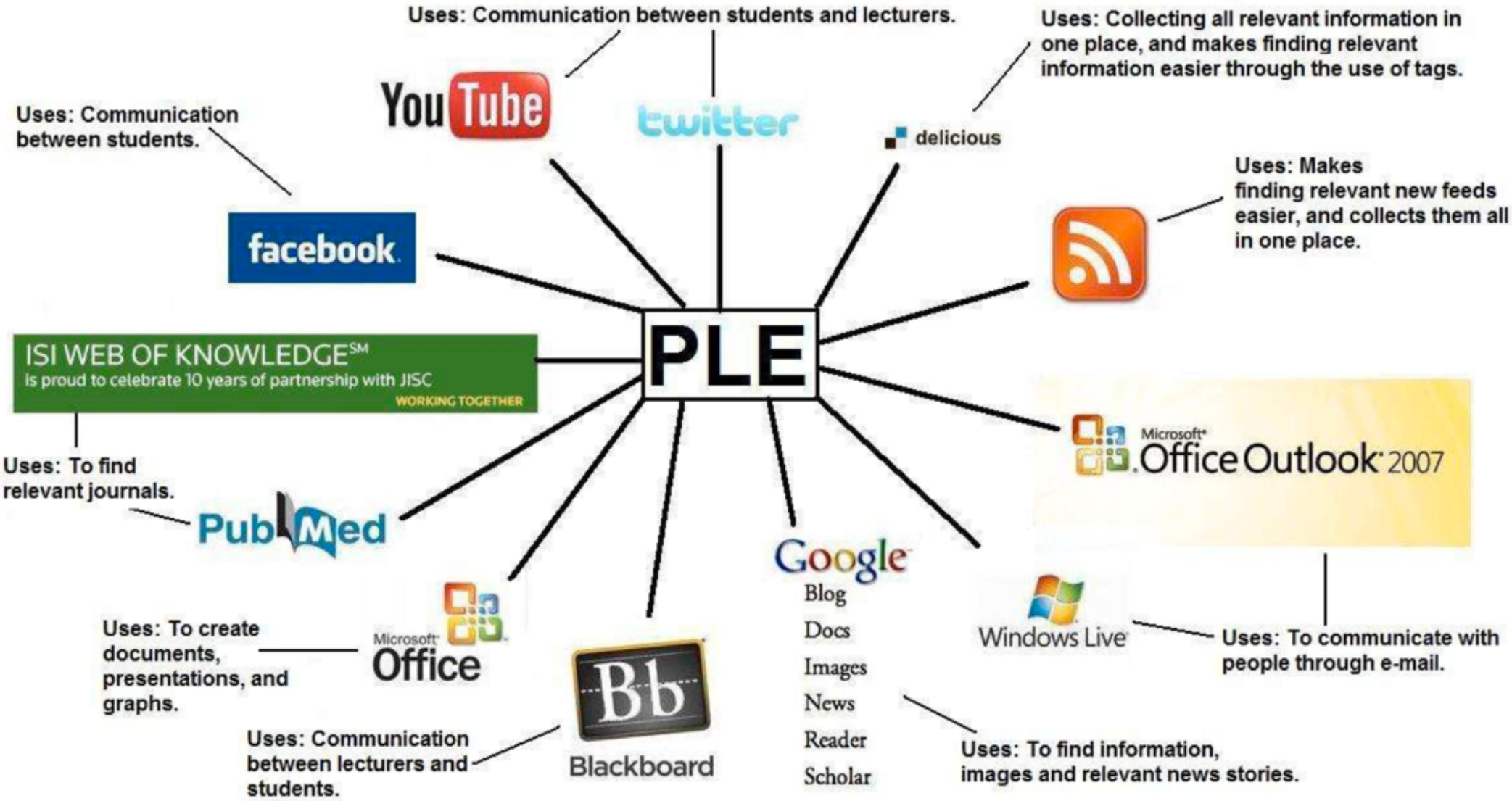

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Do you come here often? The fleeting nature of communication in a 140 character world

Jo Badge, Alex Moseley, Stuart Johnson, Alan Cann

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C L E

PLATFORM?

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SEPTEMBER 25, 2007

Manual sequence analysis - some common mistakes « Freelancing science

A gene network for navigating the literature

iHOP – Robert Hoffmann

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Roberts Lab Wiki

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delicious Home

Bioinformatics

Find info on your favorite gene(s)/pathway(s)

See some great example of some that already have.

Resources:

- NCBI

Video Tutorial. How to quickly use BLAST to find out more about an EST Blast tips [via NCBI]

- genomic_it (download)

Video Tutorial. How to use genomic_it [Hi-Res]

- iHOP
- Panther
- The Reactome Book: a textbook of biological pathways
- Gene Ontology

Video Tutorial. How to generate GO Pie Charts [Hi-Res]

- cGRASP (Salmonids only)
- KEGG

Identify Intron Location

- Spidey

Video Tutorial . How to find Intron location in genes [Hi-Res]

- Splign

Design Primers

Tools available include

- NCBI primer Blast
- Geneious
- IDT
- BiBiServ GF2 (I have not tested) - sr320 Sep 14, 2008 9:47 am

See also: post on approach for gene discovery in Vt

Align Sequences

- Geneious
- Blast
- NCBI BLINK

Video Tutorial: Sequence Alignments using BLINK and

TODAY

Idea Generation

Data Acquisition and Analysis

Publication

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Publication

Publication

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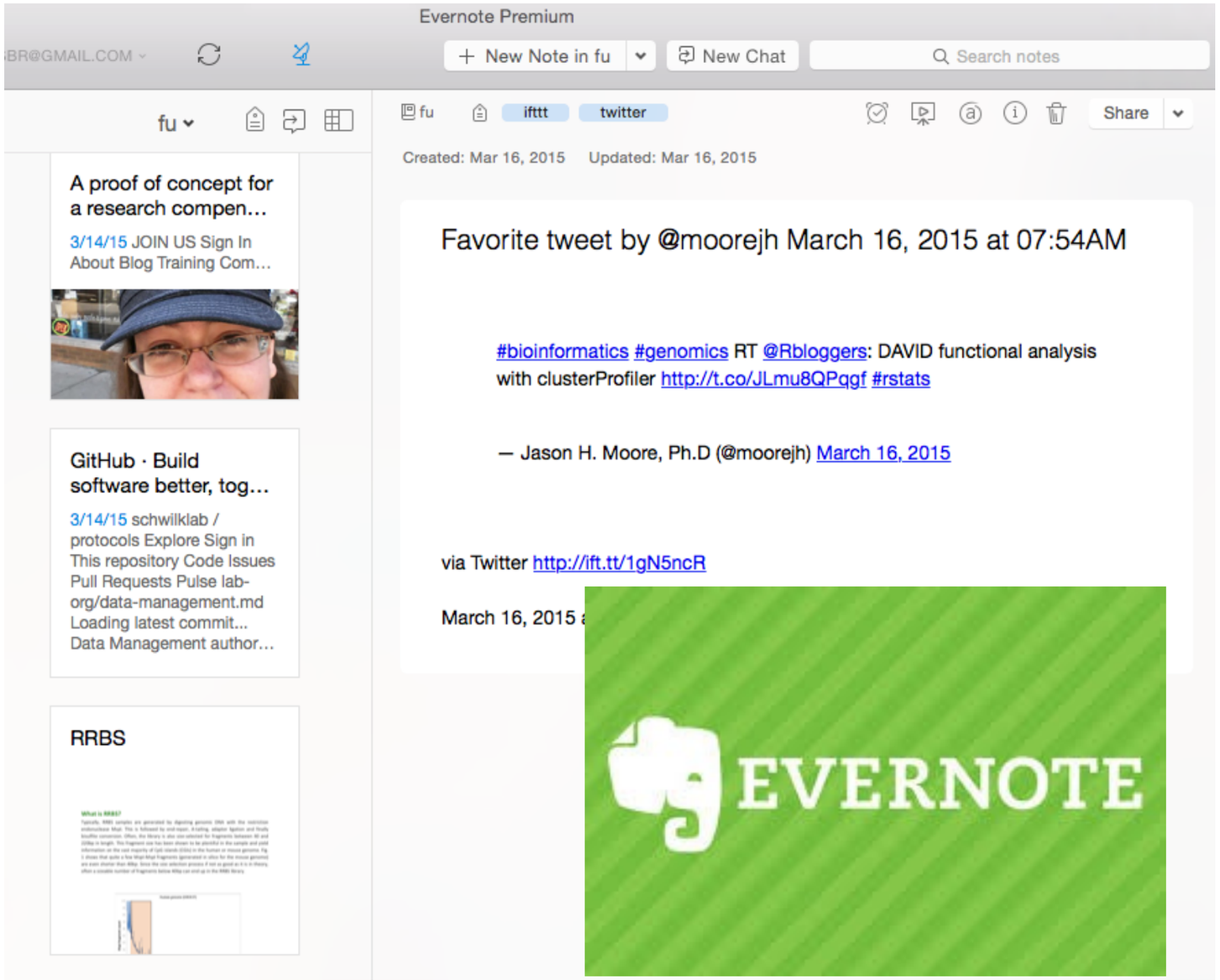

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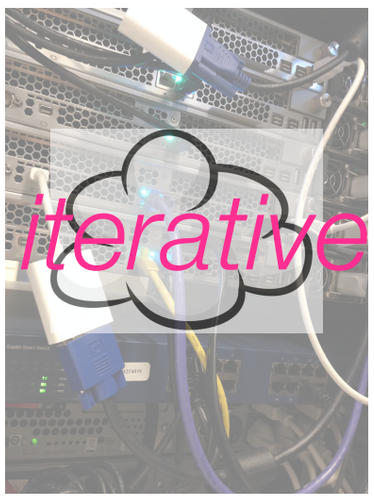

Open Notebook Science

lab notebooks

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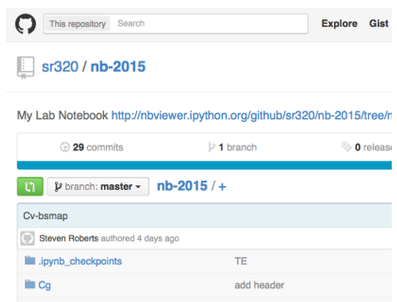
IP[y]: IPython
Interactive Computing



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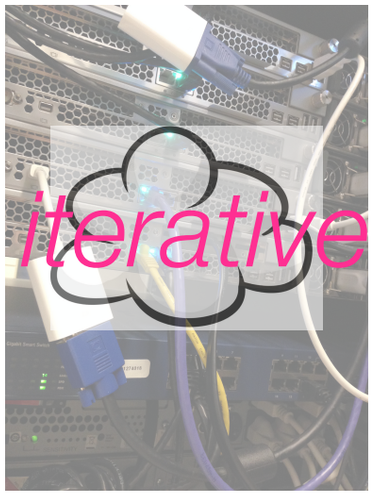

lab notebooks

wikispaces
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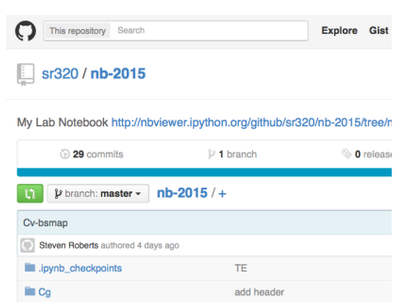
IP[y]: IPython
Interactive Computing



Automating a Workflow: Beyond Blast - to GO Slim

The concept is that you can take a fasta file in a working directory and end up with GO slim information all within a single notebook that is automated. Current
writing (and overwriting) as scracth file to SQLShare. Assumptions are that you are working in a directory with fasta file named `query.fa`. And blast algorithms a

```
In [13]: #allows plots to be shown inline
         %pylab inline

         Populating the interactive namespace from numpy and matplotlib

In [4]:  #Setting Working Directory
         wd="/Volumes/web/whale/fish546/qpx_go_val"
         #Setting directory of Blast Databases
         dbd="/Volumes/Bay3/Software/ncbi-blast-2.2.29\+/db/"
         #Database name
         dbn="uniprot_sprot_r2013_12"
         #Blast algorithim
         ba="blastx"
         #Location of SQLShare python tools: you can empty ("") if tools are in PATH
         spd="/Users/sr320/sqlshare-pythonclient/tools/"

In [5]:  cd {wd}

         /Volumes/web/whale/fish546/qpx_go_val

In [5]:  !{ba} -query query.fa -db {dbd}{dbn} -out {dbn}_{ba}_out.tab -evalue 1E-50 -num_threads 4 -max_hsps_per_

         BLAST Database error: No alias or index file found for protein database [/Volumes/Bay3/Software/ncbi-bla
         /db/uniprot_sprot_r2013_12] in search path [/Volumes/web/whale/fish546/pipeline_test_dir4::]

In [6]:  !head -1 {dbn}_{ba}_out.tab

         QPX_transcriptome_v1_Contig_2    sp|P52712|CBPX_ORYSJ    43.75    416    213    12    2095    869
         7    3e-98    326

In [17]: #Translate pipes to tab so SPID is in separate column for Joining
         !tr '|' "\t" <{dbn}_{ba}_out.tab> {dbn}_{ba}_out2.tab

In [18]: !head -1 {dbn}_{ba}_out2.tab

In [8]:  #Uploads formatted blast table to SQLshare; currently has generic name and meant to be temporary: Warnin
         !python {spd}singleupload.py -d scratchblast_out {dbn}_{ba}_out2.tab

         ...

In [9]:  !python {spd}fetchdata.py -s "SELECT * FROM [sr320@washington.edu].[scratchblast_out]blast Left Join [sr

In [10]: !head -2 {dbn}_join2goslim.txt

         ...

In [11]: !python {spd}singleupload.py -d scratchjoin_slim {dbn}_join2goslim.txt

         processing chunk line 0 to 18037 (0.0718240737915 s elapsed)
         pushing uniprot_sprot_r2013_12_join2goslim.txt...
         parsing 9A18D989...
         finished scratchjoin_slim

In [12]: #Sets GO aspect
         !python {spd}fetchdata.py -s "SELECT Distinct Column1 as query, Column3 as SPID, GOSlim_bin FROM [sr320@

In [13]: !head justslim.txt

         ...

In [15]: from pandas import *
```

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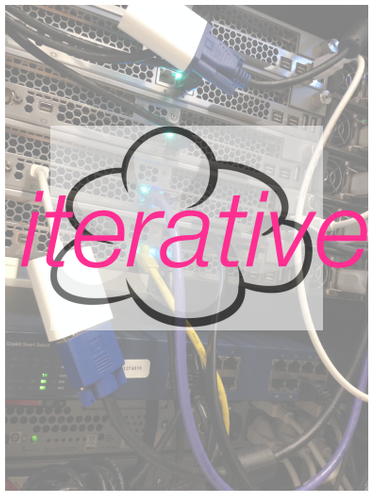

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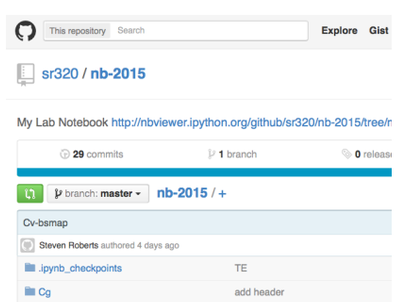
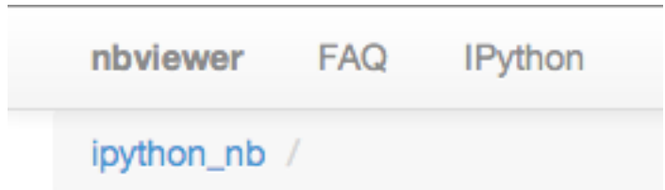
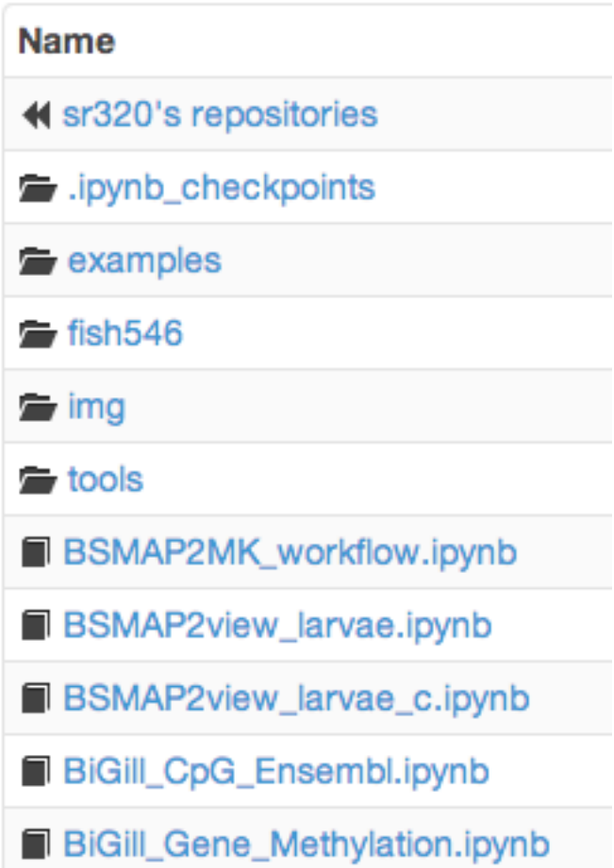


GitHub





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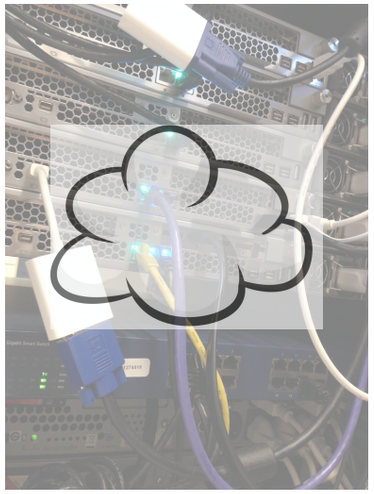

universal challenges

archiving

metadata

version control

simple sharing

data management

self-discoverability

provenance

collaboration

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Data Acquisition and Analysis

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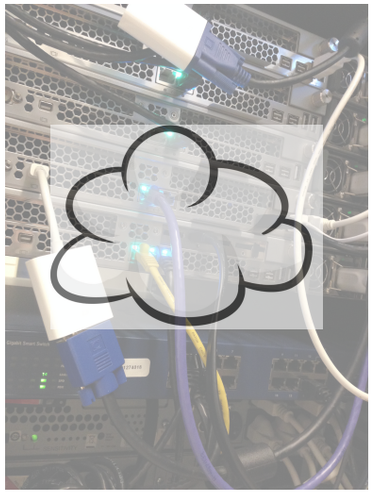
Publication

Publication

universal challenges



archiving

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version control

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collaboration

our current ~~solution~~ - analyses on local web server (NAS)

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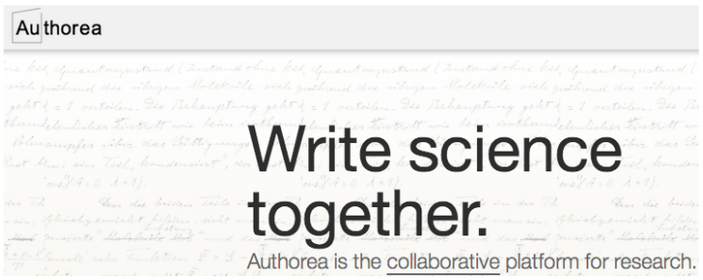

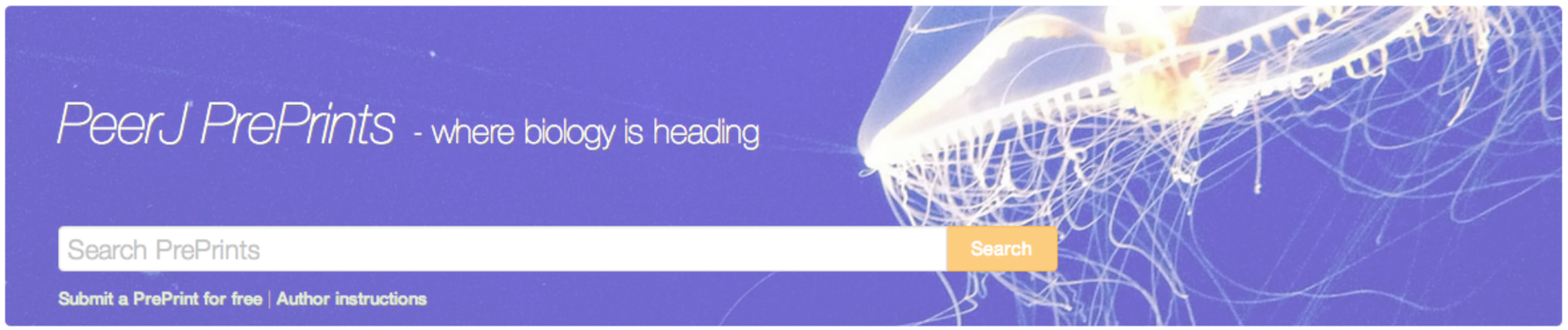

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JBLIC sr320 / qdod

Home

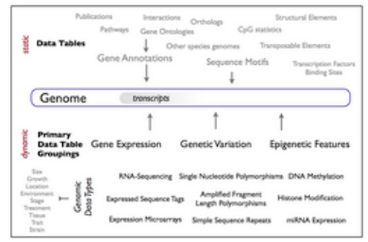
sr320 edited this page on Feb 7 · 23 revisions

This wiki serves as the *primary means for documentation* for project qdod: **querying disparate oyster datasets**.

In brief, data in the form of delimited text files is aggregated into SQLShare where they can be easily queried. The simplest way to start exploring the uses for this system is to interact with SQLShare using the simple web interface. All you need to get started is a Google account. Please see this page for a beginner's guide to SQLshare.

There is a python client for advanced users.

Below is schematic representation of the different types of datasets.



Reference Genome Sequence files are described on this page.

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Associate Professor in the School of Aquatic and Fishery Sciences at the University of Washington.

Impactstory Advisor

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A context dependent role for DNA methylation in bivalves

(2014) Gavery, Roberts. *Briefings in Functional Genomics*

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Steven Roberts

Associate Professor in the School of Aquatic and Fishery Sciences at the University of Washington.

Impactstory Advisor

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Does DNA methylation facilitate phenotypic plasticity in marine invertebrates?
(2014) *Slideshare.*
view slides
highly viewed

Crassostrea gigas high-throughput bisulfite sequencing (larvae and sperm tissues)
(2014) *figshare.*
highly viewed viewed

Key profile metrics

11.6k **views** on 57 articles

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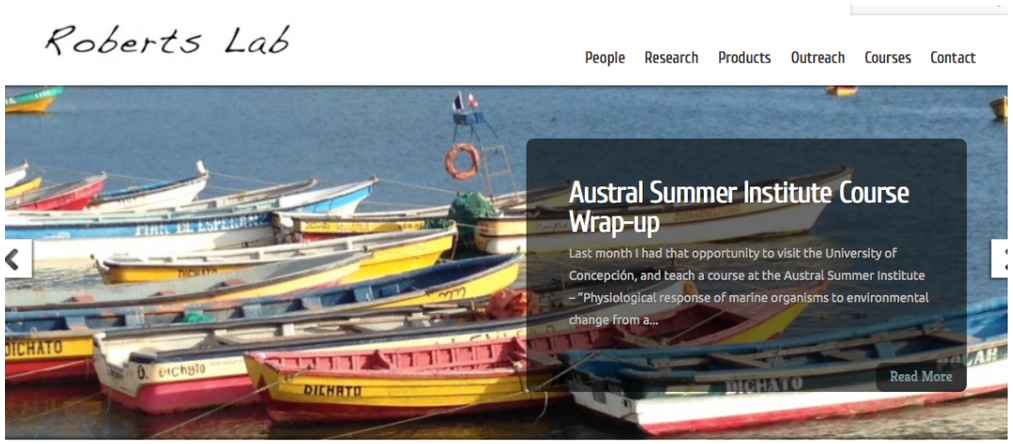
107 **views** on 3 peer reviews



Altmetric

Peer-Reviewed Publications

see also *preprints*

Timmins-Schiffman E, Coffey WD, Hua W, Nunn BL, Dickinson GH and Roberts SB. (**2014**). Shotgun proteomics reveals physiological res… acidification in *Crassostrea gigas* BMC Genomics 2014, 15:951 doi:10.1186/1471-2164-15-951 Altmetric 6

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Olson CE and Roberts SB. (**2014**). Genome-wide profiling of DNA methylation and gene expression in *Crassostrea gigas* male gametes … Physiology. 5:224. doi: 10.3389/fphys.2014.0022 Altmetric 5

Gavery MR and Roberts SB. (**2014**) A context specific role for DNA methylation in bivalves Briefings in Functional Genomics. doi:10.1093/bfgp/elt054 (pdf) Altmetric 3

Gavery MR and Roberts SB. (**2013**) Predominant intragenic methylati… a bivalve mollusc PeerJ 1:e215. doi:10.7717/peerj.215 Altmetric 6

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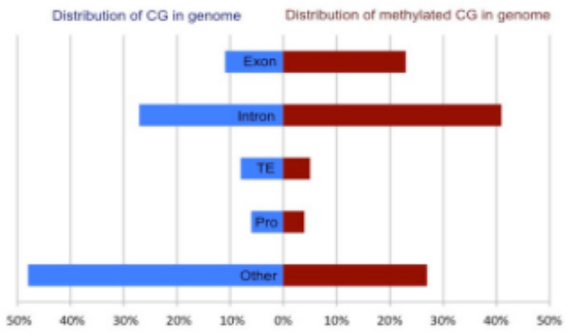

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Garcia-Vedrenne AE, Groner M, Page-Karjian A, Siegmund G-F, Singhal S, Sziklay J and Roberts SB. (**2013**) Development of Genomic Resources for a thraustochytrid Pathogen and Investig… LoS ONE 8(9): e74196. doi:10.1371/journal.pone.0074196 Altmetric 2

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Burge CA, Mouchka ME, Harvell CD and Roberts SB. (**2013**) Immune response of the Caribbean sea fan, Gorgonia ventalina, exposed to an *Aplanochytrium parasite* as revealed by transcriptome sequencing Frontiers in Physiology 4:180. doi:10.3389/fphys.2013.00180 Altmetric 15

Timmins-Schiffman EB, Nunn BL, Goodlett DR and Roberts SB. (**2013**) Shotgun proteomics as a viable approach for biological discovery in the Pacific oyster… Conservation Physiology. doi:10.1093/conphys/cot009 Altmetric 3

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## Peer-Reviewed Publications</a>

see also <a href="#preprint">*preprints*</a>

Timmins-Schiffman E, Coffey WD, Hua W, Nunn BL, Dickinson GH and Roberts SB. (**2014**). [Shotgun proteomics reveals physiological response to ocean acidification in *Crassostrea gigas*](http://www.biomedcentral.com/1471-2164/15/951/) BMC Genomics 2014, 15:951  doi:10.1186/1471-2164-15-951 <span data-badge-popover="right" data-badge-type="4" data-doi="10.1186/1471-2164-15-951" data-hide-no-mentions="true" class="altmetric-embed"></span>

Olson CE and Roberts SB. (**2014**). [Genome-wide profiling of DNA methylation and gene expression in _Crassostrea gigas_ male gametes](http://journal.frontiersin.org/Journal/10.3389/fphys.2014.00224/abstract) Frontiers in Physiology. 5:224. doi: 10.3389/fphys.2014.0022   <span data-badge-popover="right" data-badge-type="4" data-doi="10.3389/fphys.2014.00224" data-hide-no-mentions="true" class="altmetric-embed"></span>

Gavery MR and Roberts SB. (**2014**) [A context specific role for DNA methylation in bivalves](http://bfg.oxfordjournals.org/content/13/3/217) Briefings in Functional Genomics. doi:10.1093/bfgp/elt054 ([pdf](http://eagle.fish.washington.edu/cnidarian/Briefings%20in%20Functional%20Genomics-2014-Gavery-217-22.pdf))   <span data-badge-popover="right" data-badge-type="4" data-doi="10.1093/bfgp/elt054" data-hide-no-mentions="true" class="altmetric-embed"></span>

Gavery MR and Roberts SB. (**2013**) [Predominant intragenic methylation is associated with gene expression characteristics in a bivalve mollusc](https://peerj.com/articles/215/) PeerJ 1:e215. doi:10.7717/peerj.215   <span data-badge-popover="right" data-badge-type="4" data-doi="10.7717/peerj.215" data-hide-no-mentions="true" class="altmetric-embed"></span>


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Garcia-Vedrenne AE, Groner M, Page-Karjian A, Siegmund G-F, Singhal S, Sziklay J and Roberts SB. (**2013**) [Development of Genomic Resources for a thraustochytrid Pathogen and Investigation of Temperature Influences on Gene Expression](http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0074196) PLoS ONE 8(9): e74196. doi:10.1371/journal.pone.0074196 <span data-badge-popover="right" data-badge-type="4" data-doi="10.1371/journal.pone.0074196" data-hide-no-mentions="true" class="altmetric-embed"></span>

Storer CS, Quinn TP and Roberts SB. (**2013**) [Quantitative PCR analysis used to characterize physiological changes in brain tissue of senescent sockeye salmon](http://link.springer.com/article/10.1007/s10522-013-9448-1) Biogerontology. doi:10.1007/s10522-013-9448-1 ([pdf](https://dl.dropboxusercontent.com/u/115356/docs/Storer2013.pdf))   <span data-badge-popover="right" data-badge-type="4" data-doi="10.1007/s10522-013-9448-1" data-hide-no-mentions="true" class="altmetric-embed"></span>

Burge CA, Mouchka ME, Harvell CD and Roberts SB. (**2013**) [Immune response of the Caribbean sea fan, Gorgonia ventalina, exposed to an _Aplanochytrium parasite_ as revealed by transcriptome sequencing](http://www.frontiersin.org/invertebrate_physiology/10.3389/fphys.2013.00180/abstract) Frontiers in Physiology 4:180. doi:10.3389/fphys.2013.00180   <span data-badge-popover="right" data-badge-type="4" data-doi="10.3389/fphys.2013.00180" data-hide-no-mentions="true" class="altmetric-embed"></span>

Timmins-Schiffman EB, Nunn BL, Goodlett DR and Roberts SB. (**2013**) [Shotgun proteomics as a viable approach for biological discovery in the Pacific oyster](http://conphys.oxfordjournals.org/content/1/1/cot009.full.pdf+html) Conservation Physiology. doi:10.1093/conphys/cot009   <span data-badge-popover="right" data-badge-type="4" data-doi="10.1093/conphys/cot009" data-hide-no-
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Peer-Reviewed Publications

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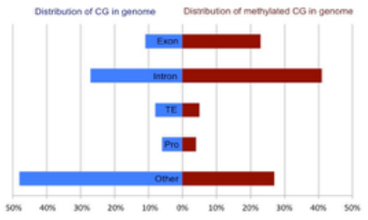
Timmins-Schiffman E, Coffey WD, Hua W, Nunn BL, Dickinson GH and Roberts SB. (**2014**). Shotgun proteomics reveals physiological response to ocean acidification in *Crassostrea gigas* BMC Genomics 2014, 15:951 doi:10.1186/1471-2164-15-951 Altmetric 6

Olson CE and Roberts SB. (**2014**). Genome-wide profiling of DNA methylation and gene expression in *Crassostrea gigas* male gametes Frontiers in Physiology. 5:224. doi: 10.3389/fphys.2014.0022 Altmetric 5

Gavery MR and Roberts SB. (**2014**) A context specific role for DNA methylation in bivalves Briefings in Functional Genomics. doi:10.1093/bfgp/elt054 (pdf) Altmetric 3

Gavery MR and Roberts SB. (**2013**) Predominant intragenic methylation is associated with gene expression characteristics in a bivalve mollusc PeerJ 1:e215. doi:10.7717/peerj.215 Altmetric 6



Garcia-Vedrenne AE, Groner M, Page-Karjian A, Siegmund G-F, Singhal S, Sziklay J and Roberts SB. (**2013**) Development of Genomic Resources for a thraustochytrid Pathogen and Investigation of Temperature Influences on Gene Expression PLoS ONE 8(9): e74196. doi:10.1371/journal.pone.0074196 Altmetric 2

Storer CS, Quinn TP and Roberts SB. (**2013**) Quantitative PCR analysis used to characterize physiological changes in brain tissue of senescent sockeye salmon Biogerontology. doi:10.1007/s10522-013-9448-1 (pdf)

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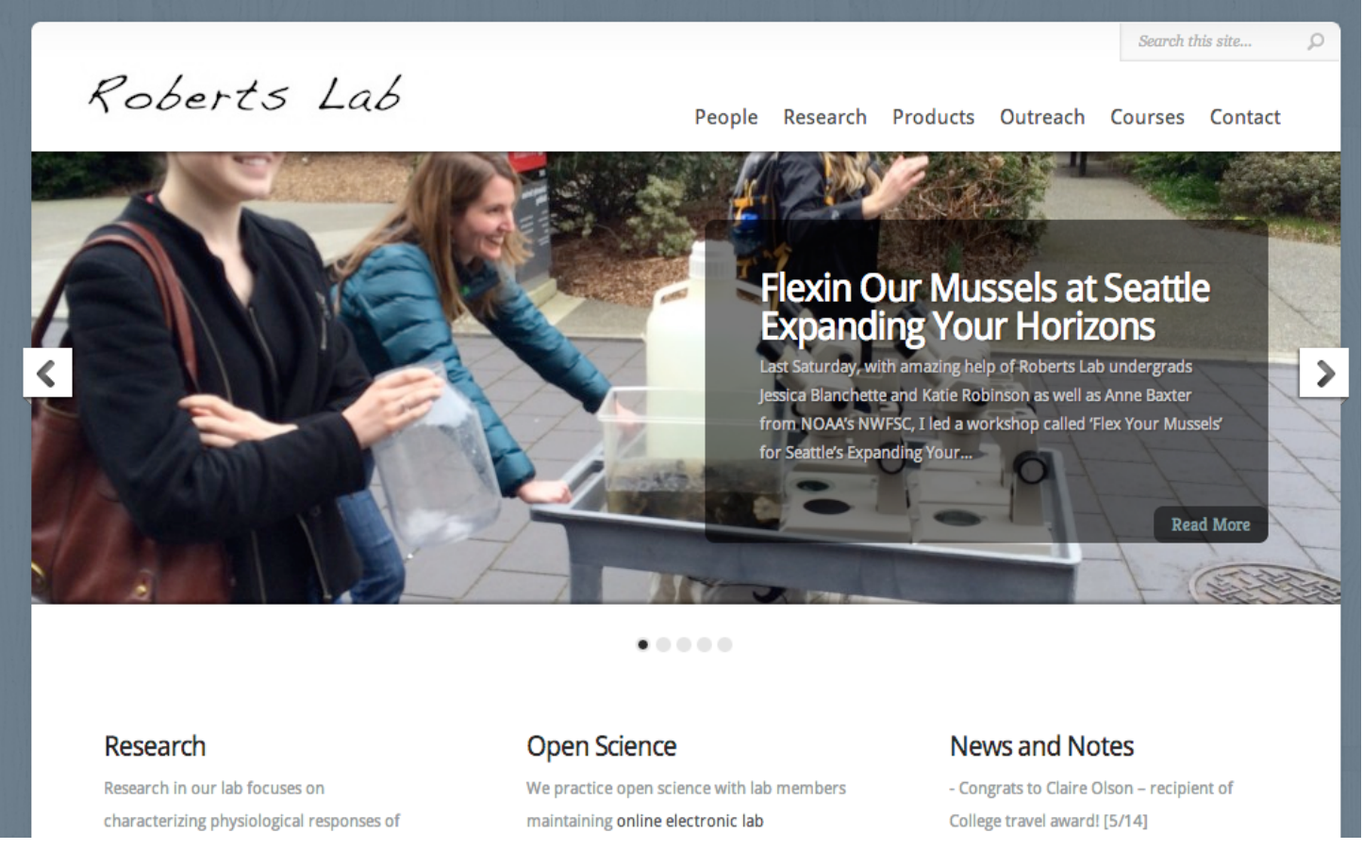

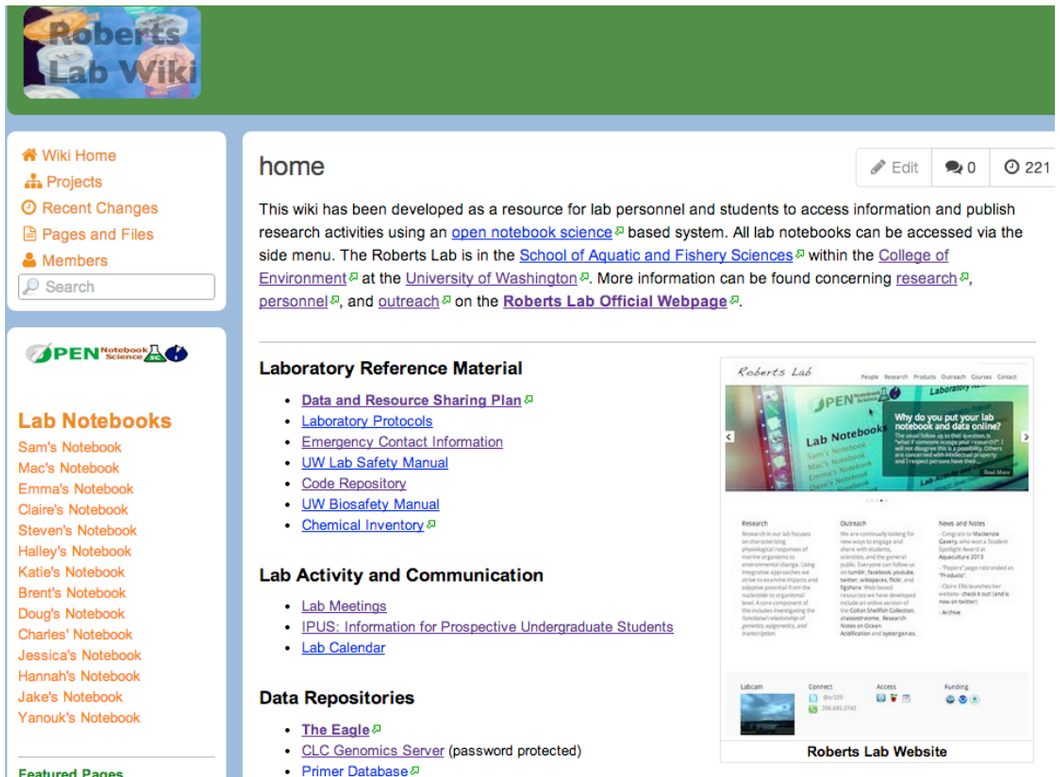

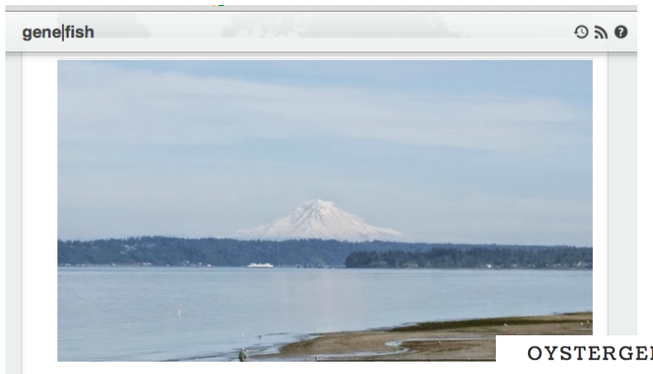

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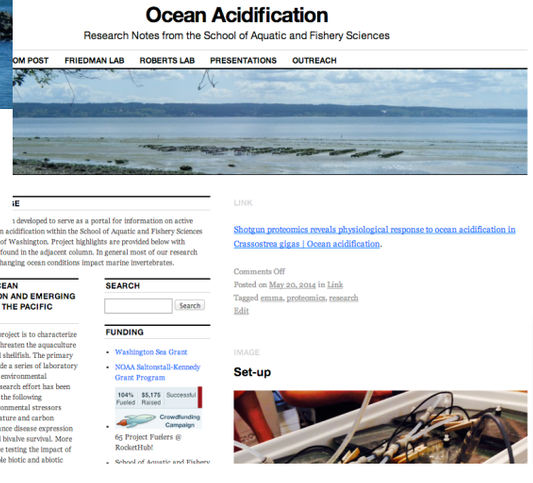
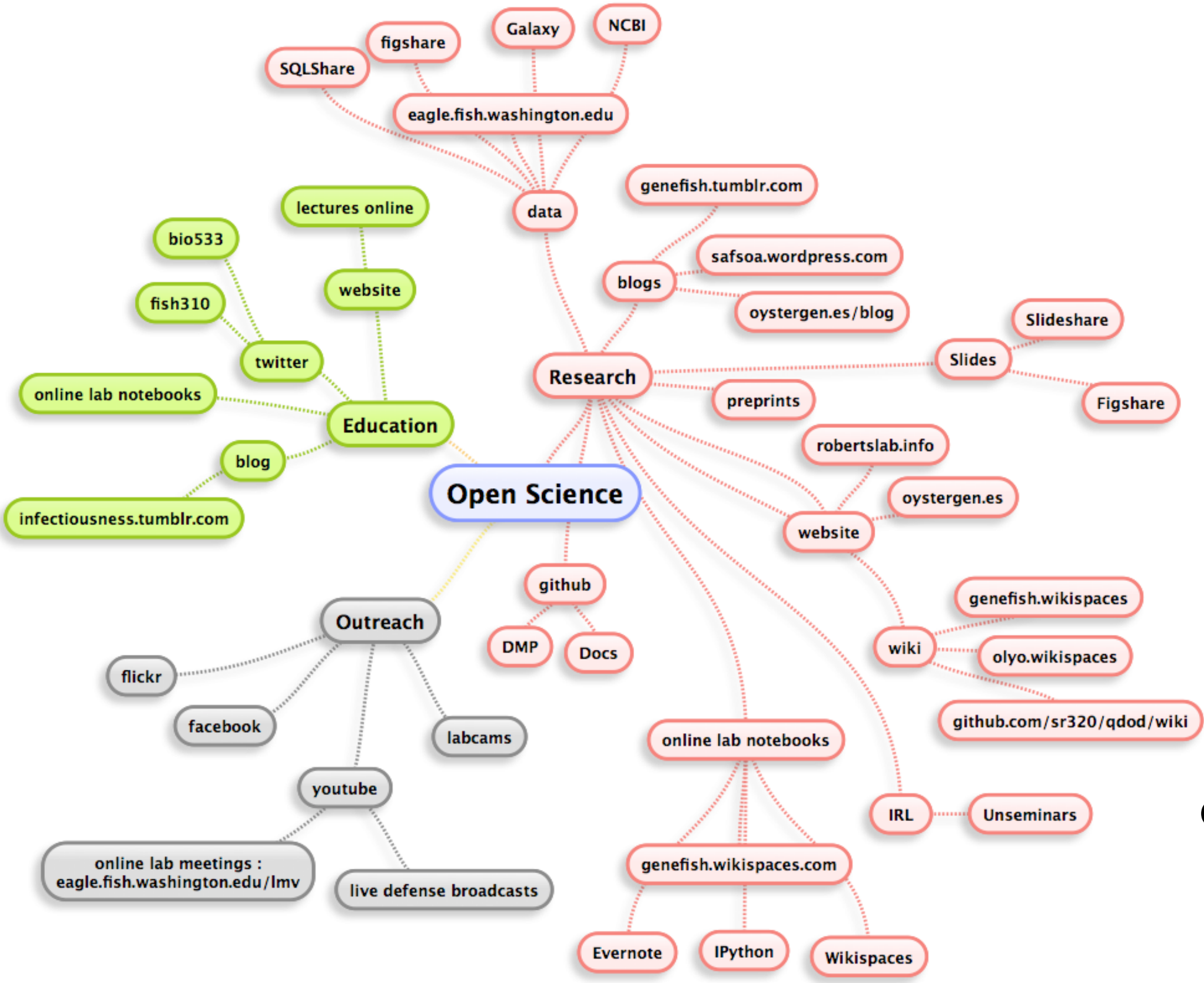


Open Science Philosophy

Transparency with limited effort

will try just about anything



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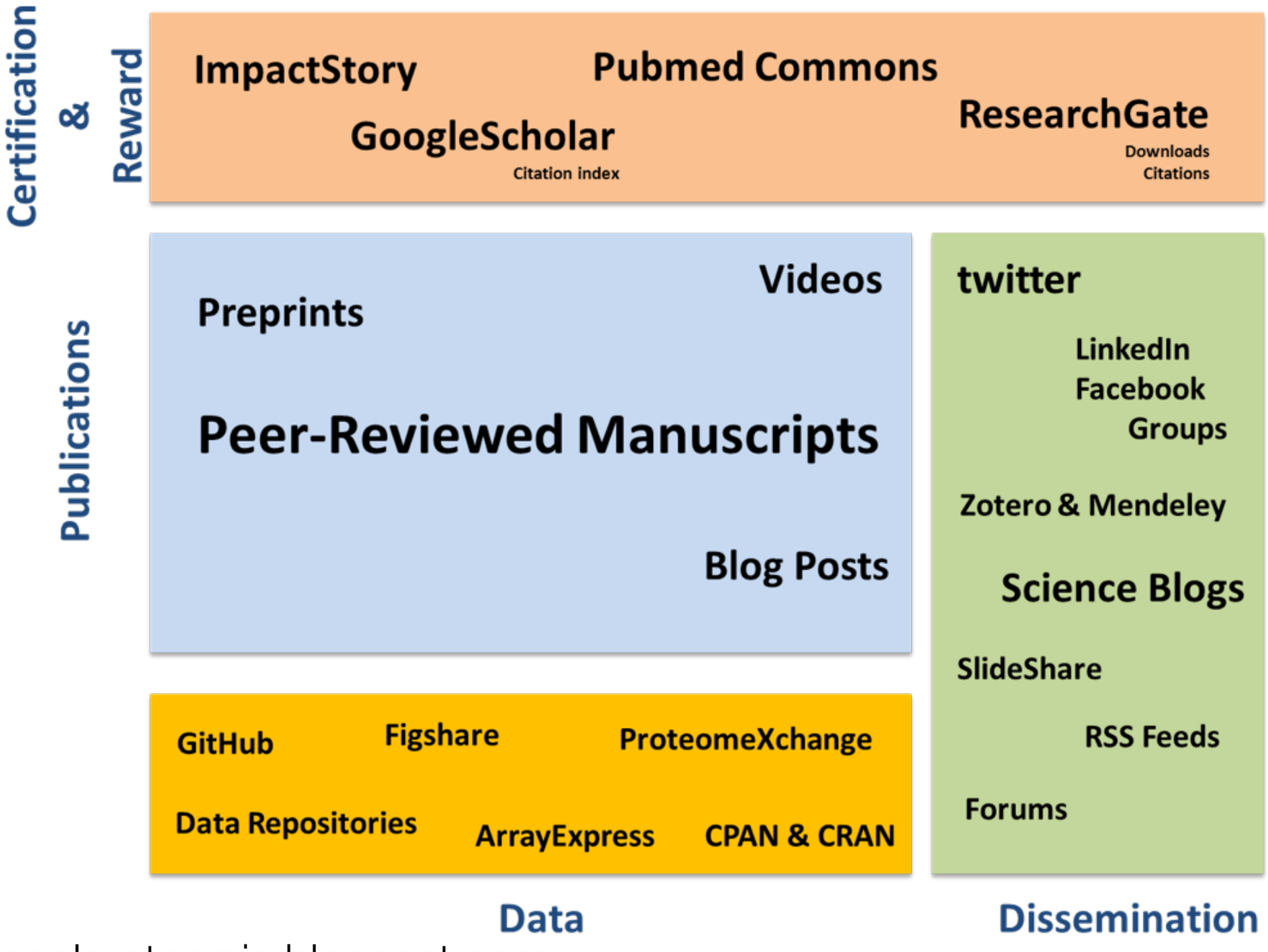

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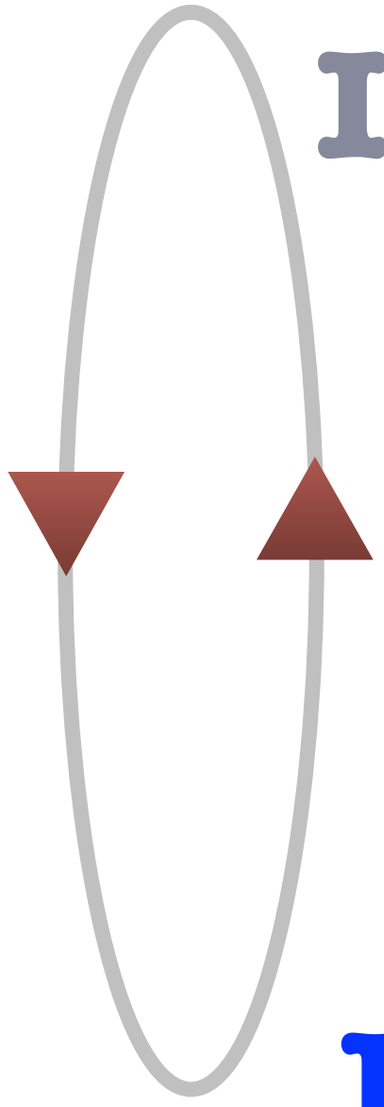

Getting Information

The stated mission of the University of Washington is "the advancement, ***dissemination*** and preservation of knowledge."

Sharing Information

Any metric to inform on efficiency is valuable

Lots of stuff

My recommendations

baby steps…?

thanks!

Steven Roberts

sr320@uw.edu

robertslab.info

@sr320