I need to publish more and read less

Cameron Neylon - Munin Conference

Tromsø - 22 November 2011

technologies...

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conceptual changes...

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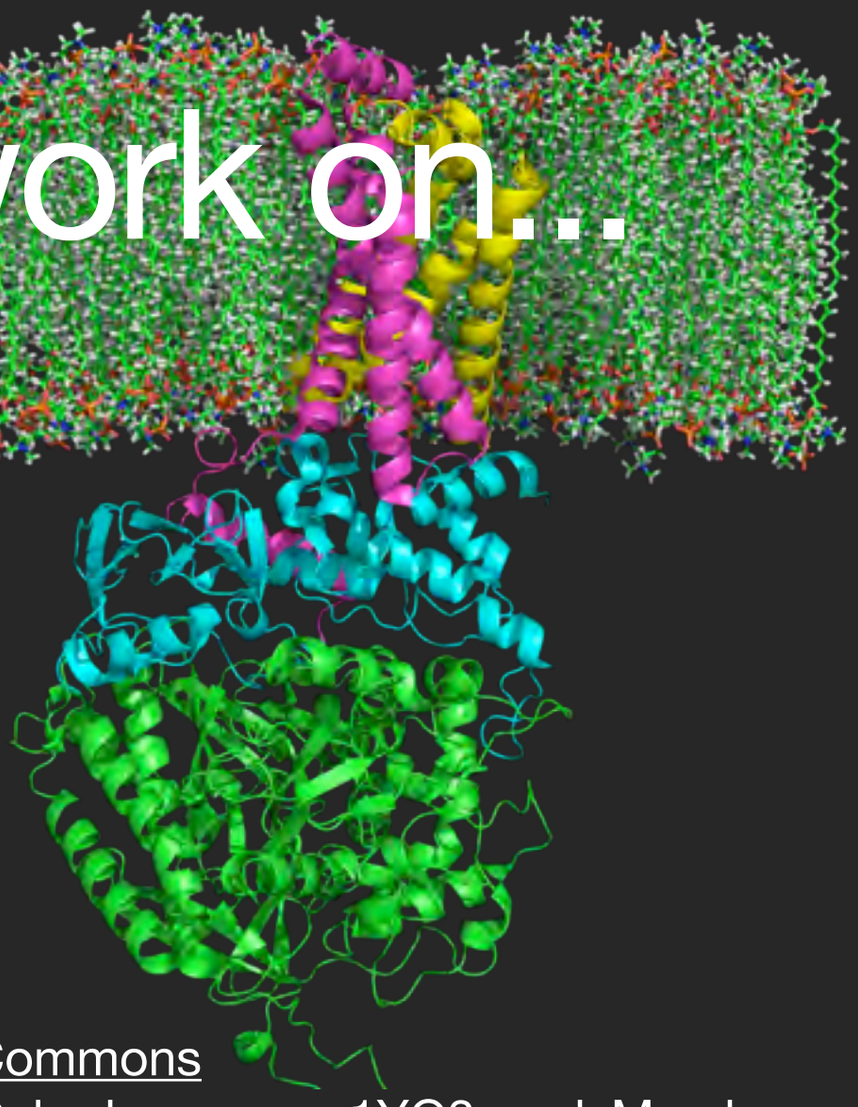

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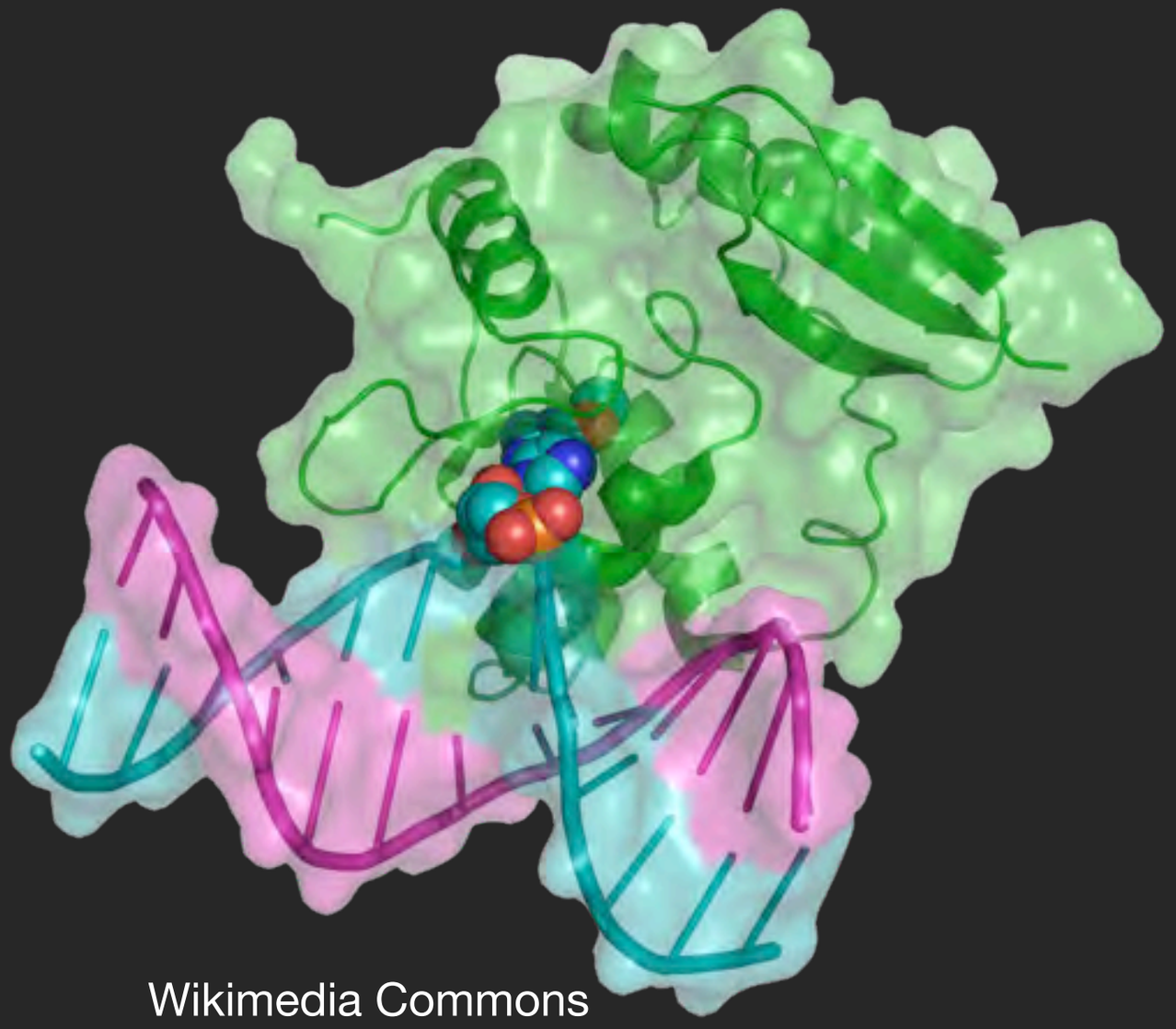

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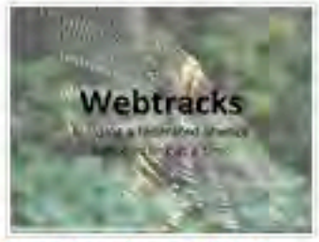

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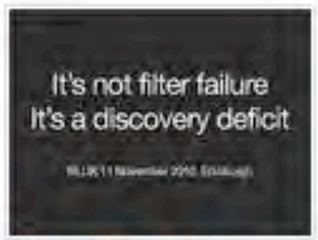

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Headline

Open Research Computation: An ordinary journal with extraordinary aims.

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I spend a lot of my time arguing that many of the problems in the research community are caused by journals. We have too many, they are an ineffective means of communicating the important bits of research, and as a filter they are inefficient and misleading. Today I am very happy to be publicly …

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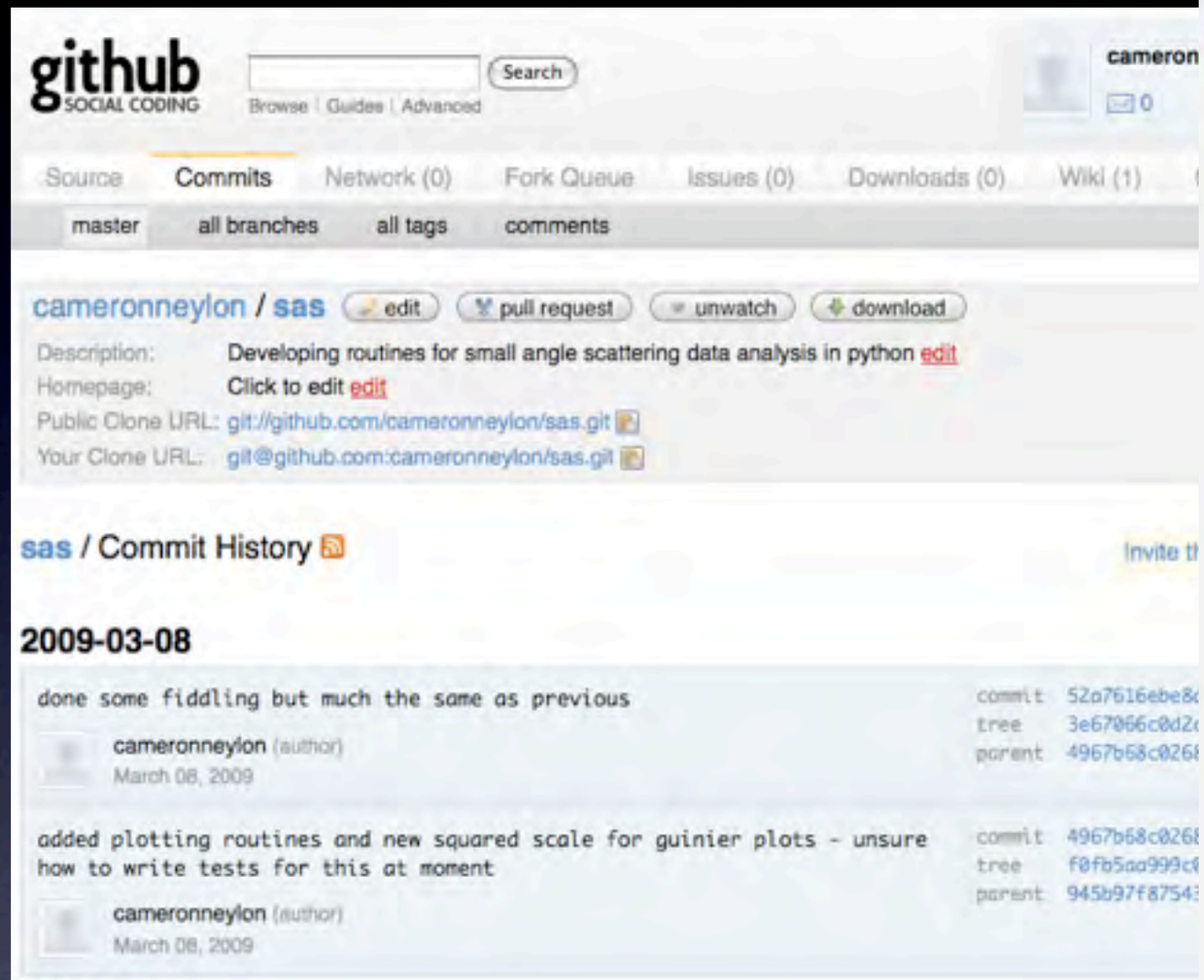
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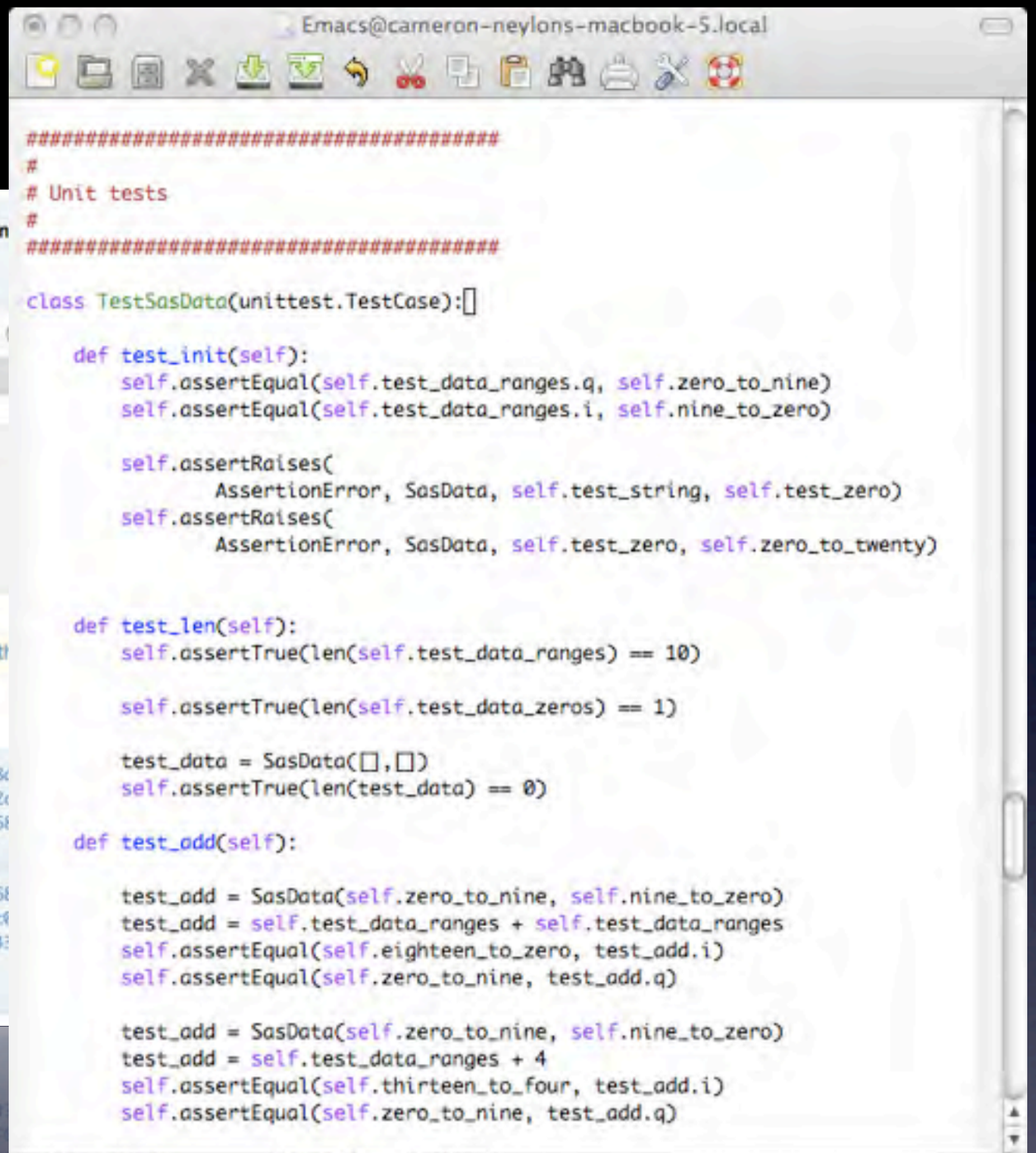
sas / Commit History
2009-03-08
done some fiddling but much the same as previous
commit 52a7616ebe8
tree 3e67066c0d2
parent 4967b68c026
cameronneylon (author)
March 08, 2009
added plotting routines and new squared scale for guinier plots - unsure how to write tests for this at moment
commit 4967b68c026
tree f0fb5aa999c
parent 945b97f87543
cameronneylon (author)
March 08, 2009


Emacs@cameron-neylons-macbook-5.local
##
#
Unit tests
#
##
class TestSasData(unittest.TestCase):
def test_init(self):
self.assertEqual(self.test_data_ranges.q, self.zero_to_nine)
self.assertEqual(self.test_data_ranges.i, self.nine_to_zero)
self.assertRaises(
AssertionError, SasData, self.test_string, self.test_zero)
self.assertRaises(
AssertionError, SasData, self.test_zero, self.zero_to_twenty)
def test_len(self):
self.assertTrue(len(self.test_data_ranges) == 10)
self.assertTrue(len(self.test_data_zeros) == 1)
test_data = SasData([],[])
self.assertTrue(len(test_data) == 0)
def test_add(self):
test_add = SasData(self.zero_to_nine, self.nine_to_zero)
test_add = self.test_data_ranges + self.test_data_ranges
self.assertEqual(self.eighteen_to_zero, test_add.i)
self.assertEqual(self.zero_to_nine, test_add.q)
test_add = SasData(self.zero_to_nine, self.nine_to_zero)
test_add = self.test_data_ranges + 4
self.assertEqual(self.thirteen_to_four, test_add.i)
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...software...

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...data...

Need to communicate...

Need to maximise “impact”...

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Many new ways and places to publish...

So...

group, and finally attachment to the solid support. In addition the use of intein based methods as well as the preparation of the solid support for Staudinger ligation often require reagents such as phosphines or thiophenols that are toxic and difficult to handle.

Therefore there remains a significant need for robust and simple methodologies for protein immobilization that can be applied to wide range of proteins and solid supports. The identification of the Sortase transpeptidase [19] provided an alternative approach to protein ligation. Sortases recognise a specific peptide sequence (LPETG for SrtA of *S. aureus* used in this work) in proteins targeted for covalent attachment to the cell wall peptidoglycan. The peptide tag sequence is cleaved and then ligated to the pentaglycine moiety on the peptidoglycan precursor Lipid II. Proteins expressed with the C-terminal recognition sequence can be covalently attached to a wide range of constructs with an N-terminal glycine amide motif including peptides [20], PNA [21], full length proteins [22] and small molecule substrates [23]. Another group has independently described an example of Sortase mediated ligation to a beaded solid support [22]. These reactions proceed under aqueous conditions without the addition of any further reagents beyond the protein, ligation substrate, and Sortase. Thus Sortase has the potential to provide a means of linking expressed proteins to a wide range of solid supports which is mild, selective, and can be carried out in a single step. Here we investigate the ability of *S. aureus* SrtA to ligate proteins to a range of solid supports.

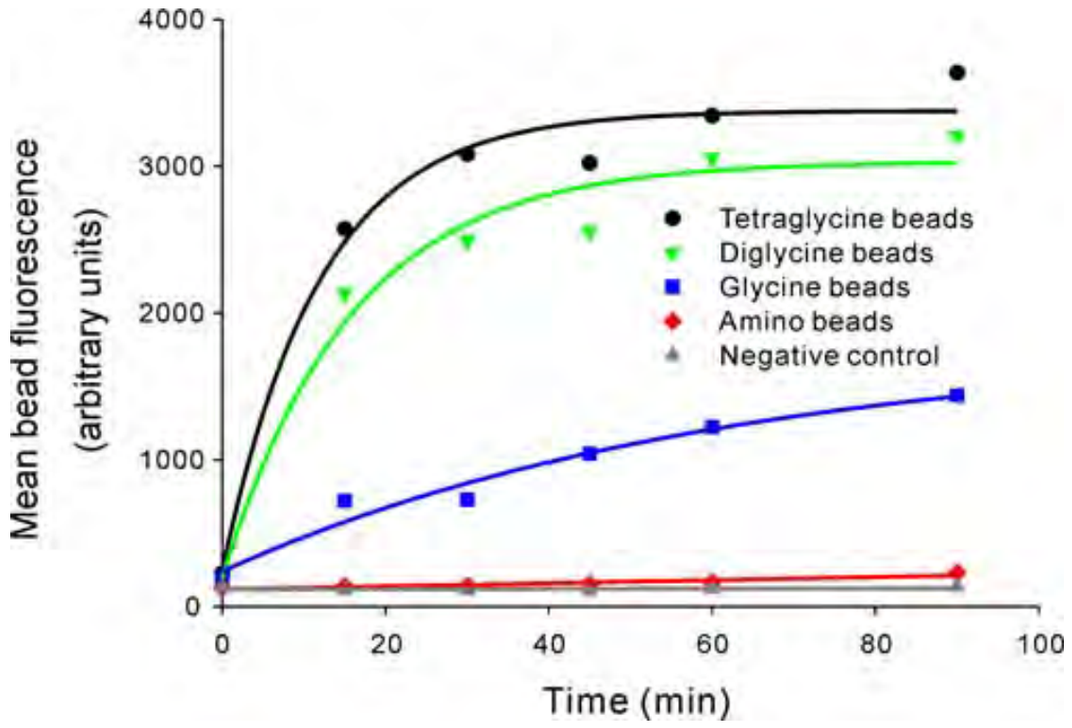

Figure 1. Ligation of fluorescent proteins to polymer beads. (a) GMA beads modified with one, two, or four glycine residues were incubated with EGFP-LPETGG-His_6 and Sortase. Samples were taken at specific time points and analyzed on a BD FACSAria. Controls contained beads with no glycine or diglycine beads without Sortase. Error bars showing the standard error in the mean fluorescence are omitted as they are generally smaller than the data symbols. Errors are given in Supplementary Data S2.
doi:10.1371/journal.pone.0001164.g001

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cameronneylon / sas — edit | pull request | unwatch | download

Description: Developing routines for small angle scattering data analysis in python edit

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sas / Commit History

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2009-03-08

done some fiddling but much the same as previous

commit 52a7616ebe8
tree 3e67066c0d2
parent 4967b68c026

cameronneylon (author)
March 08, 2009

added plotting routines and new squared scale for guinier plots - unsure how to write tests for this at moment

commit 4967b68c026
tree f0fb5aa999c
parent 945b97f8754

cameronneylon (author)
March 08, 2009

Emacs@cameron-neylons-macbook-5.local

```
##########################################
#
# Unit tests
#
##########################################

class TestSasData(unittest.TestCase):

    def test_init(self):
        self.assertEqual(self.test_data_ranges.q, self.zero_to_nine)
        self.assertEqual(self.test_data_ranges.i, self.nine_to_zero)

        self.assertRaises(
                AssertionError, SasData, self.test_string, self.test_zero)
        self.assertRaises(
                AssertionError, SasData, self.test_zero, self.zero_to_twenty)


    def test_len(self):
        self.assertTrue(len(self.test_data_ranges) == 10)

        self.assertTrue(len(self.test_data_zeros) == 1)

        test_data = SasData([],[])
        self.assertTrue(len(test_data) == 0)

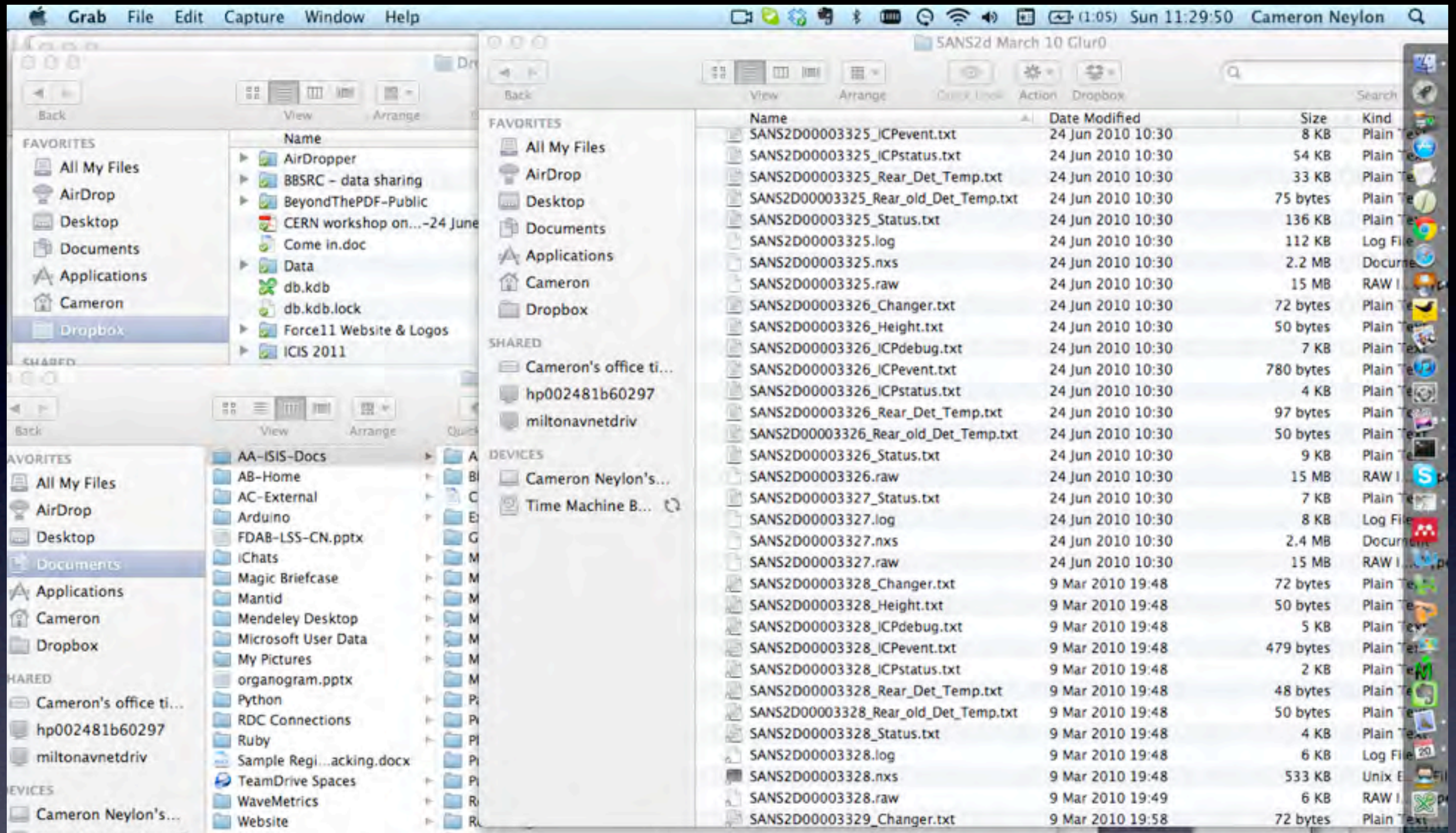
    def test_add(self):

        test_add = SasData(self.zero_to_nine, self.nine_to_zero)
        test_add = self.test_data_ranges + self.test_data_ranges
        self.assertEqual(self.eighteen_to_zero, test_add.i)
        self.assertEqual(self.zero_to_nine, test_add.q)

        test_add = SasData(self.zero_to_nine, self.nine_to_zero)
        test_add = self.test_data_ranges + 4
        self.assertEqual(self.thirteen_to_four, test_add.i)
        self.assertEqual(self.zero_to_nine, test_add.q)
```

--:** sas.py 72% L465 (Python)----------

...the software...



...and all the rest?

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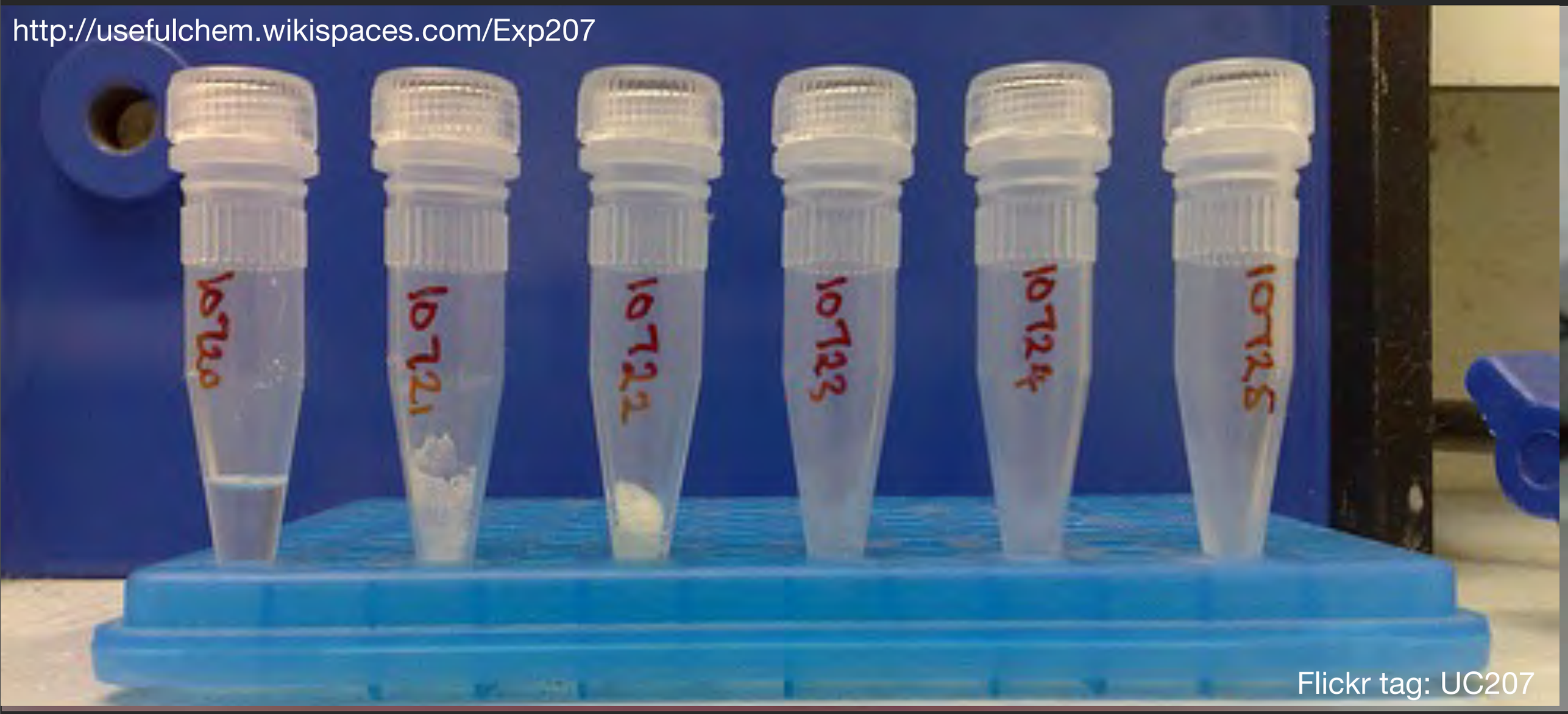

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CombiUgi Project

Objective

To establish a method of measuring the solubility of some compounds in organic solvents. For a justification of this project see here.

Procedure

Solid is added to 1.5 mL Eppendorf tubes containing 500 uL of solvent until saturated after 30 s of vortexing. The tubes are then centrifuged for 60 s then 200 uL of clear solution is transferred to pre-weighed 1.5 mL Eppendorf tubes. The tubes with the clear solution are then evaporated down in a SpeedVac for 2 h and re-weighed to obtain the amount of dissolved solid.

Results

The list of compounds, solvents and measurements is on workbook 207-WB1
The pics are tagged as EXP207 on Flickr.

Discussion

This technique was adequate to measure solubilities of the following compounds:
boc-glycine in methanol (4.40 M) and THF (3.45 M)
glycine methyl ester in methanol (1.32 M)
vanillin in methanol (4.19 M) ethanol (2.50 M) THF (3.89 M)

Reflections on research data management: RDM is on the up and up but data driven policy development seems a long way off.

11 NOVEMBER 2011 46 VIEWS NO COMMENT

Image by Idaho National Laboratory via Flickr

I wrote this post for the Digital Curation Centre blog following the Research Data Management Forum meeting run in Warwick a few weeks back. If you feel moved to comment I'd ask you to do it over there.

The Research Data Management movement is moving on apace. Tools are working and adoption is growing. Policy development is starting to back up the use of those tools and there are some big ambitious goals set out for the next few years. But has the RDM movement taken the vision of data intensive research to its heart? Does the collection, sharing, and analysis of data about research data management meet our own standards? And is policy development based on and assessed against that data? Can we be credible if it is not?

Watching the discussion on research data management over the past few years has been an exciting experience. The tools, that have been possible for some years, now show real promise as the somewhat raw and ready products of initial development are used and tested.

Practice is gradually changing, if unevenly across different disciplines, but there is a growing awareness of data and that it might be considered important. And all of this is being driven increasingly by the development of policies on data availability, data management, and data archiving that stress the importance of data as a core output of public research.

Recent Friendfeed activity

"Skitchrolling" - When an apparently interesting link leads you to Scholarly Kitchen...
Saturday 10:47

Yikes. Weather for Tromsø for next five days...might make it above zero...will be needing to pack warm...
Friday 17:51

Re-use as Impact: Linking the open and impact agendas
Re-use as Impact: Linking the open and impact agendas
Friday 16:59

BMJ Group blogs: BMJ » Blog Archive » Richard Smith: A woeful tale of the uselessness of peer review
Friday 21:01

Visual RDF
Friday 21:01

My FriendFeed profile ...

Lifestream

Yikes. Weather for Tromsø for next five days...might make it above zero...will be needing to pack warm... [cameronneylon]
— 2d ago via Twitter

Ok. A second attempt at

I am also found at...

Flickr
Friendfeed
Github
My lab notebook
Slideshare
Twitter

Document Figures

Peer Reviewed

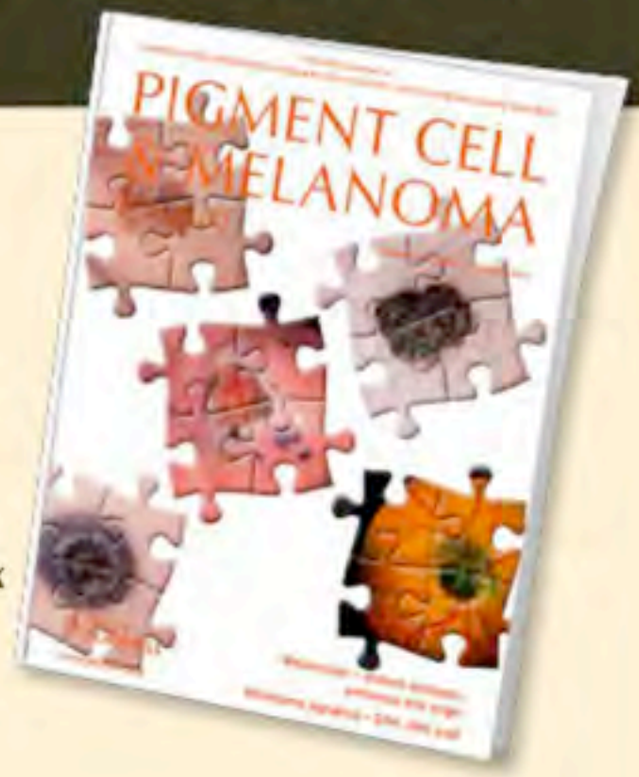
The official journal of
INTERNATIONAL FEDERATION O ETY FOR MELANOMA RESEARCH

PIGMENT CELL & MELANOMA Research

Embryonic stem-cell-preconditioned microenvironment induces loss of cancer cell properties in human melanoma cells

Myoung Ok Kim, Sung-Hyun Kim, Naomi Oi, Mee Hyun Lee, Dong Hoon Yu, Dong Joon Kim, Eun Jin Cho, Ann M. Bode, Yong-Yeon Cho, Tim G. Bowden and Zigang Dong

DOI: 10.1111/j.1755-148X.2011.00891.x
Volume 24, Issue 5, Pages 922-931



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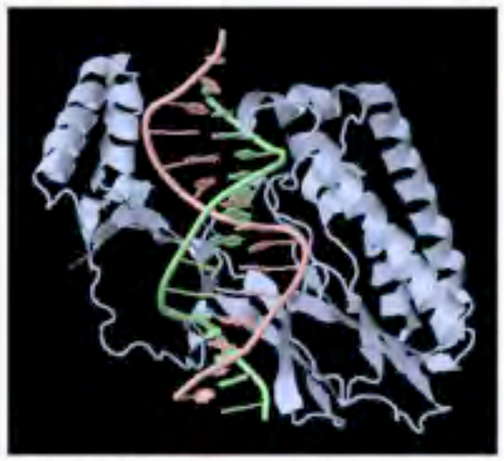
ment Ce noma Resear

Menu 0:05 / 4:20

Tus (biology)

From Wikipedia, the free encyclopedia
(Redirected from Tus protein)

Tus is a sequence-specific DNA-binding protein that promotes termination in the DNA replication process of prokaryotes. In *E Coli*, Tus binds to 10 closely related sites encoded in the chromosome. These sites bind 23 base-pairs. The 10 sites are called *Ter* sites, and are designated *TerA*, *TerB*, ..., *TerJ*. These binding sites are asymmetric, such that when a Tus-Ter complex (Tus protein bound to a Ter site) is encountered by a replication fork from one direction, the complex is dissociated and replication continues (permissive). But when encountered from the other direction, the Tus-Ter complex provides a much larger kinetic barrier and halts replication (non-permissive). The multiple *Ter* sites in the chromosome are oriented such that the two oppositely moving replication forks are both stalled in the desired termination region.[2]



Representation of the x-ray crystal structure of Tus-Ter protein-DNA complex. (Jmol rendering of coordinates from [1]. The DNA strands are shown in pink and green.)

Further reading [edit]

- "Interaction of the Escherichia coli replication terminator protein (Tus) with DNA: a model derived from DNA-binding studies of mutant proteins by surface plasmon resonance."[3]
- "Replication termination in Escherichia coli: structure and antihelicase activity of the Tus-Ter complex."[4]
- "A molecular mousetrap determines polarity of termination of DNA replication in E. coli."[2]
- "Isolation and characterization of mutants of Tus, the replication arrest protein of Escherichia coli." [5]
- "Biophysical characteristics of Tus, the replication arrest protein of Escherichia coli."[6]
- "Structure of a replication-terminator protein complexed with DNA."[1]
  - Structure at protein data bank

References [edit]

1. ^ a b Kamada, K.; Horiuchi, T.; Ohsumi, K.; Shimamoto, N.; Morikawa, K. (1996). "Structure of a replication-terminator protein complexed with DNA". *Nature* **383** (6601): 598–603. Bibcode 1996Natur.383..598K. doi:10.1038/383598a0. PMID 8857533. edit

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Toolbox

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Wednesday, 14 December 11

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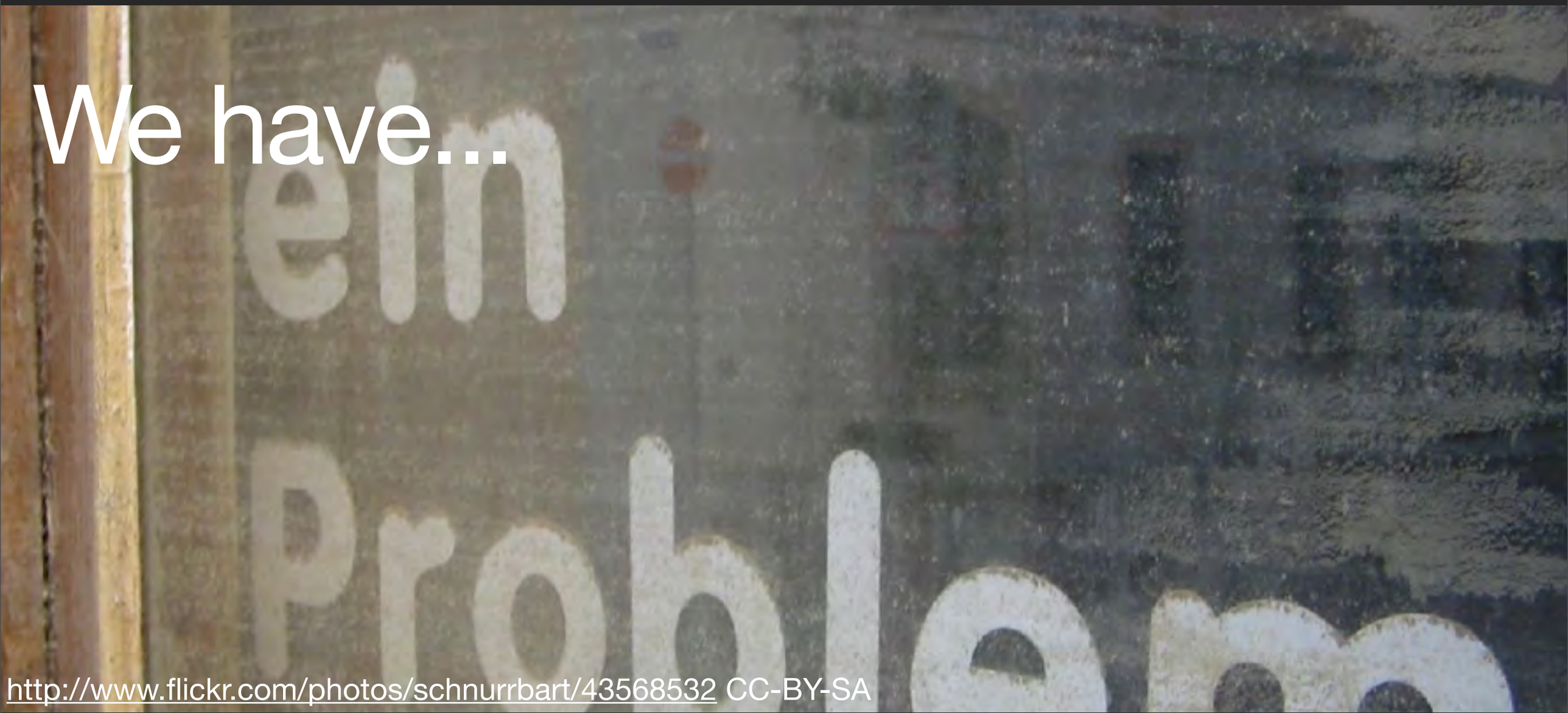
This is not sustainable...

“I need to publish more”

...not *work* more...

We have...



A resource problem...

Whether it’s money...

...or time...

Technical capacity is not enough

...either need to resource it

...or make it cheaper.

Paper

A. Author, A.N. Other

Introduction

Methods

Results

Discussion

Publication as a side effect of recording....

“Publish@Source”

Jeremy Frey,
Southampton

Wednesday, 14 December 11

Cameron's LaBLog

The online open laboratory notebook of Cameron Neylon

UV-Vis of 2mg/mL GFP

9th February 2009 @ 15:37

Data Type: UV-Vis

From UV-Vis of Lysozyme and GFP samples from I22 SAXS

This Post is Linked By: UV-Vis of Lysozyme and GFP samples from I22 SAXS;

Data

Cameron Neylon | View Source | Data | Comments (0)

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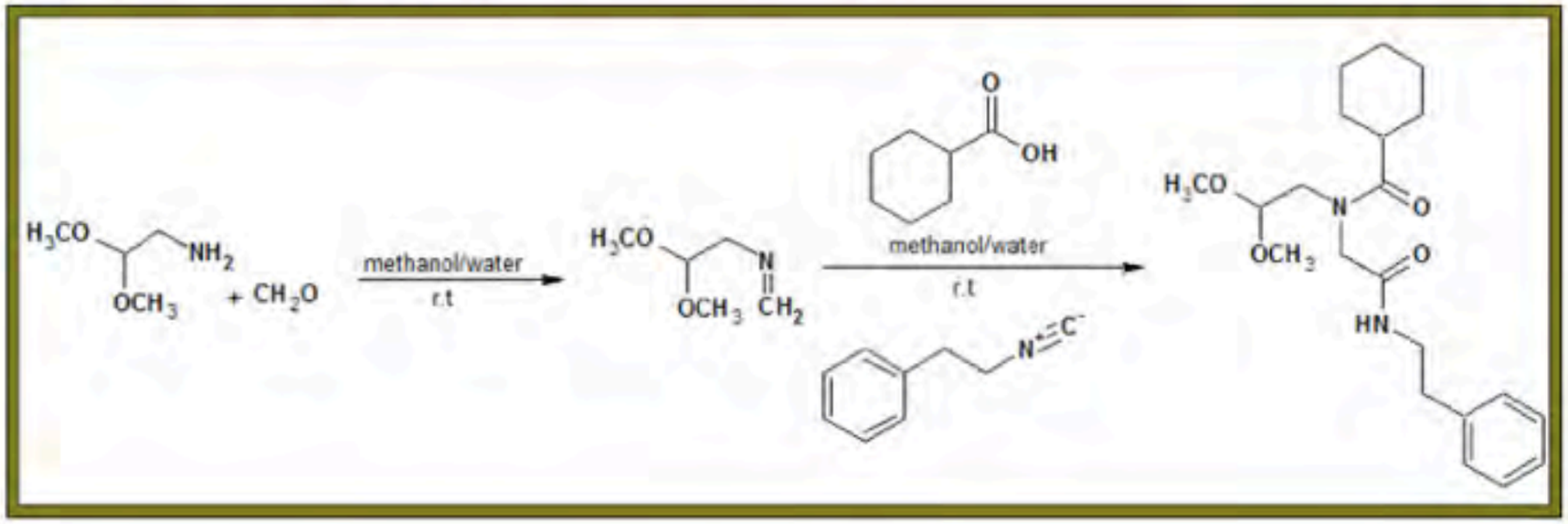
To Do List
Ugi Chemicals
Ugi NMR Analysis
Tim's Paper
SLchemPaper
ChemGamePaper
DoUgi
bots



Objective

To synthesize the precursor diamide to be used subsequently in the pictet spengler reaction affording praziquantel

Procedure

To a solution of formaldehyde/water in methanol, aminoacetaldehyde dimethylacetal was added. The reaction was monitored by HNMR to confirm a complete conversion to the corresponding imine. Subsequently cyclohexanecarboxylic acid and 2-phenylethyl isocyanide was added. The reaction was left undisturbed over night. The final Ugi product obtained as crystals was filtered out next day. The product was analyzed by NMR, MS and IR.

Results

1-cyclohexanoic acid

http://usefulchem.wikispaces.com/Exp258

CARL BOETTIGER

Theoretical Ecology and Evolution

Home Research Lab Notebook Publications Teaching Communities Calendar

WELCOME TO MY LAB NOTEBOOK

November 8, 2010 – 2:50 am

By *Carl*

Posted in *Open Notebook Thoughts*

Comments (1)

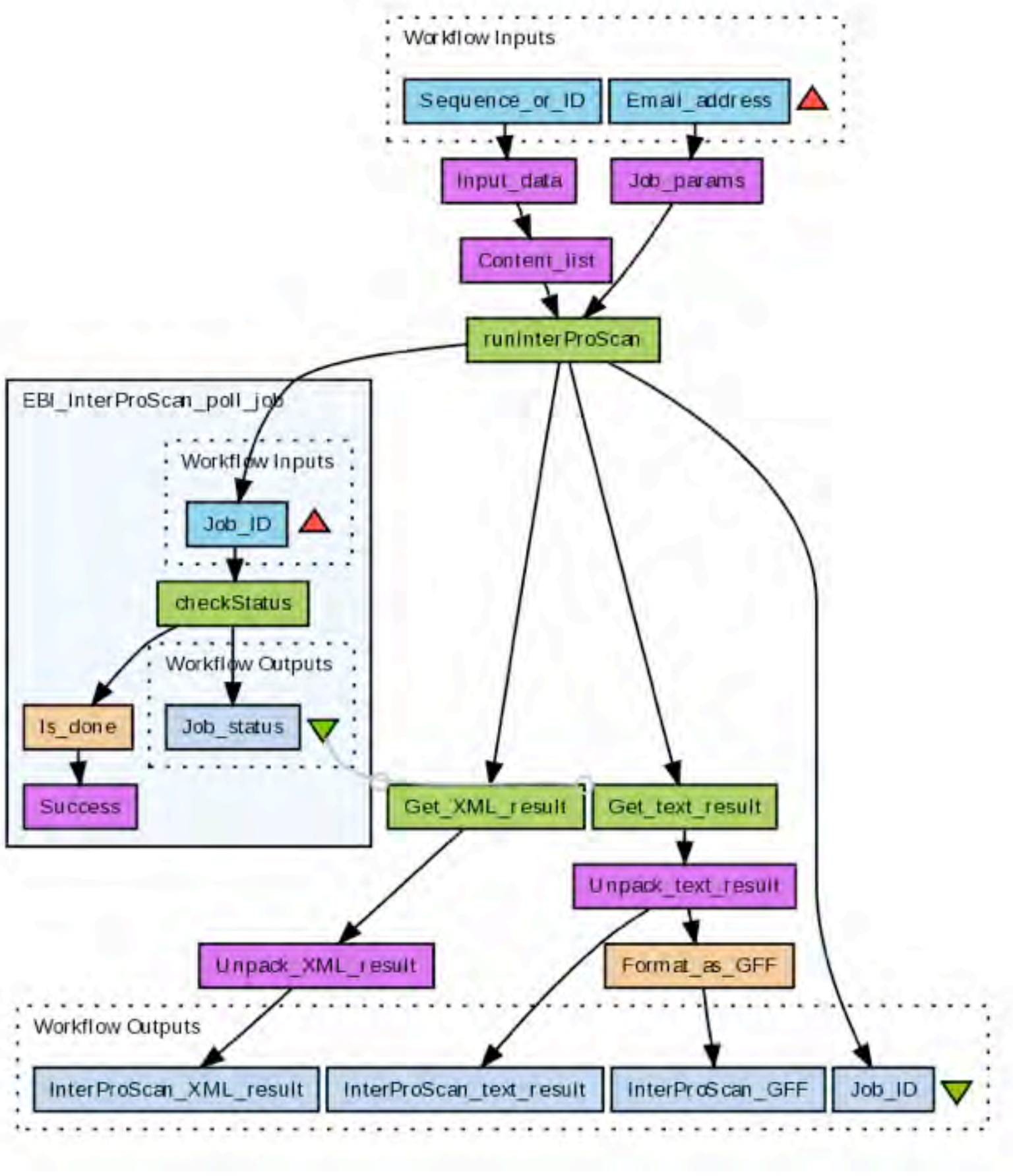
DISCLAIMER: NOT A BLOG

Welcome to my open lab notebook. This is the active, permanent record of all my scientific research, standing in place of the traditional bound lab notebook. It is a record of ideas, and intuitions; results and mistakes. Please bear in mind that the notebook is primarily a tool for me to do science, not communicate it. I write my entries with the hope that they are intelligible to my future self; and maybe intelligible to my collaborators and experts in my field. This is not a research blog, where each entry can be read alone and understood by a general audience in an edited and polished form.

PHILOSOPHY: WHY AN OPEN NOTEBOOK?

So you've probably noticed this lab notebook is openly accessible, you can read it online without passwords or permissions. And if you've read the

http://www.carlboettiger.info/



http://www.myexperiment.org/workflows/204.html

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cameronneylon / mantid

Watch Fork 1 1

Source Commits Network Pull Requests (0) Issues (0) Graphs Branch: master

Switch Branches (4) Switch Tags (2) Branch List

Cameron Neylon's Python scripts for use within mantid

Downloads

HTTP Git Read-Only https://github.com/cameronneylon/mantid.git This URL has **Read-Only** access

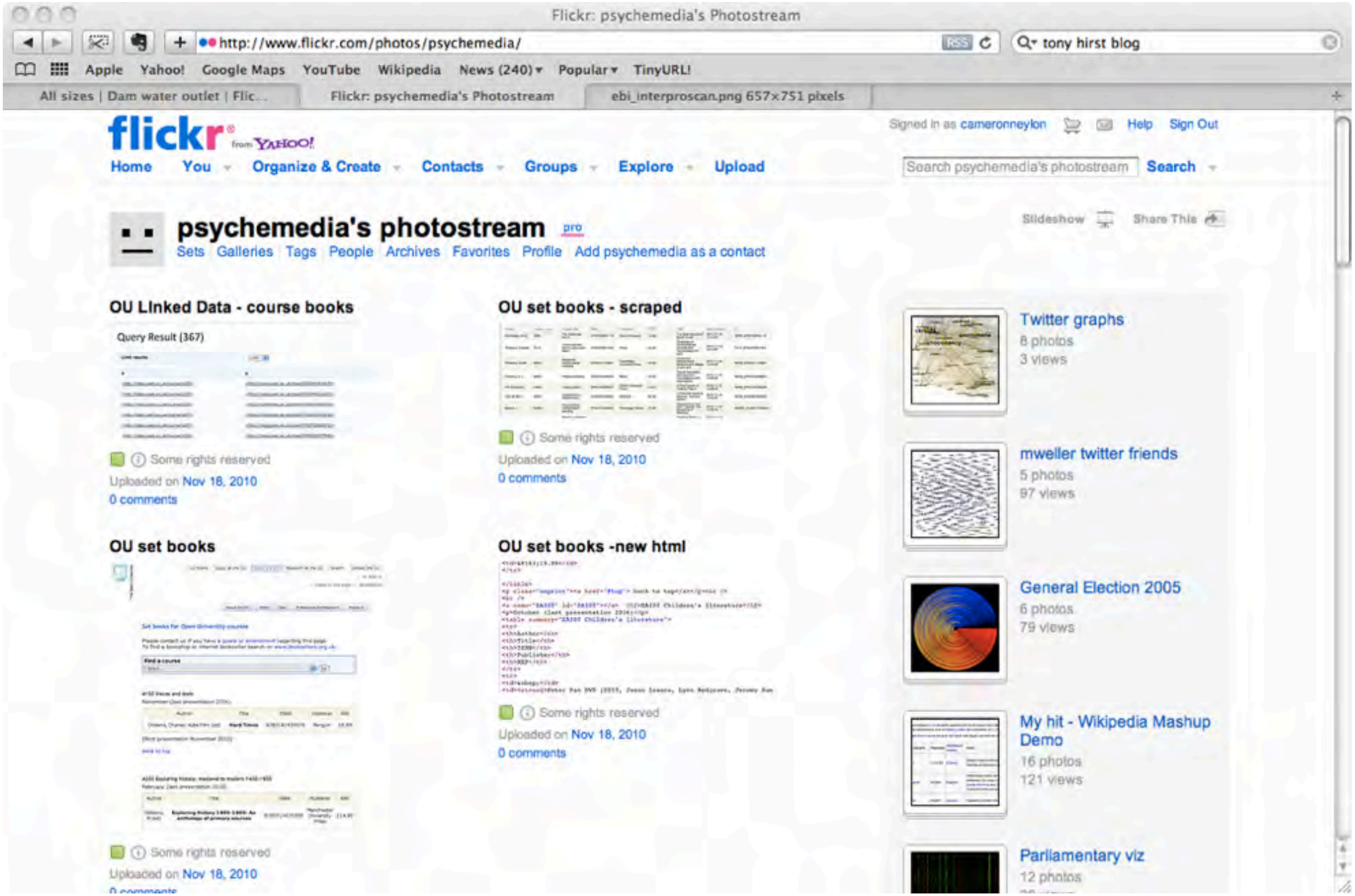
Corrected error in assignment of Can run - was setting with sample runno

cameronneylon (author)
September 14, 2010

commit 03365745cf7378240c90
tree 8390e7df90a4dba18124
parent 2372b8018a1da0bd0eee

mantid /

name	age	message	history
AddRawFilesGui.py	July 01, 2010	working towards displaying run titles for selec...	[cameronneylon]
SANSReduction_for_testing_only.py	June 30, 2010	Tested SansReduce as far as possible outside of...	[cameronneylon]
SansReduce.py	September 14, 2010	Corrected error in assignment of Can run - was ...	[cameronneylon]
SansReduceExamples.txt	September 08, 2010	Added some draft examples	[cameronneylon]
SansReduceGui.py	September 14, 2010	Working version, not yet tested for accurate mu...	[cameronneylon]
images/	June 23, 2010	Working version with some substandard documenta...	[cameronneylon]
lablogpost.py	July 07, 2010	Functional but not comprehensively tested blogg...	[cameronneylon]



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Easy to publish pieces...

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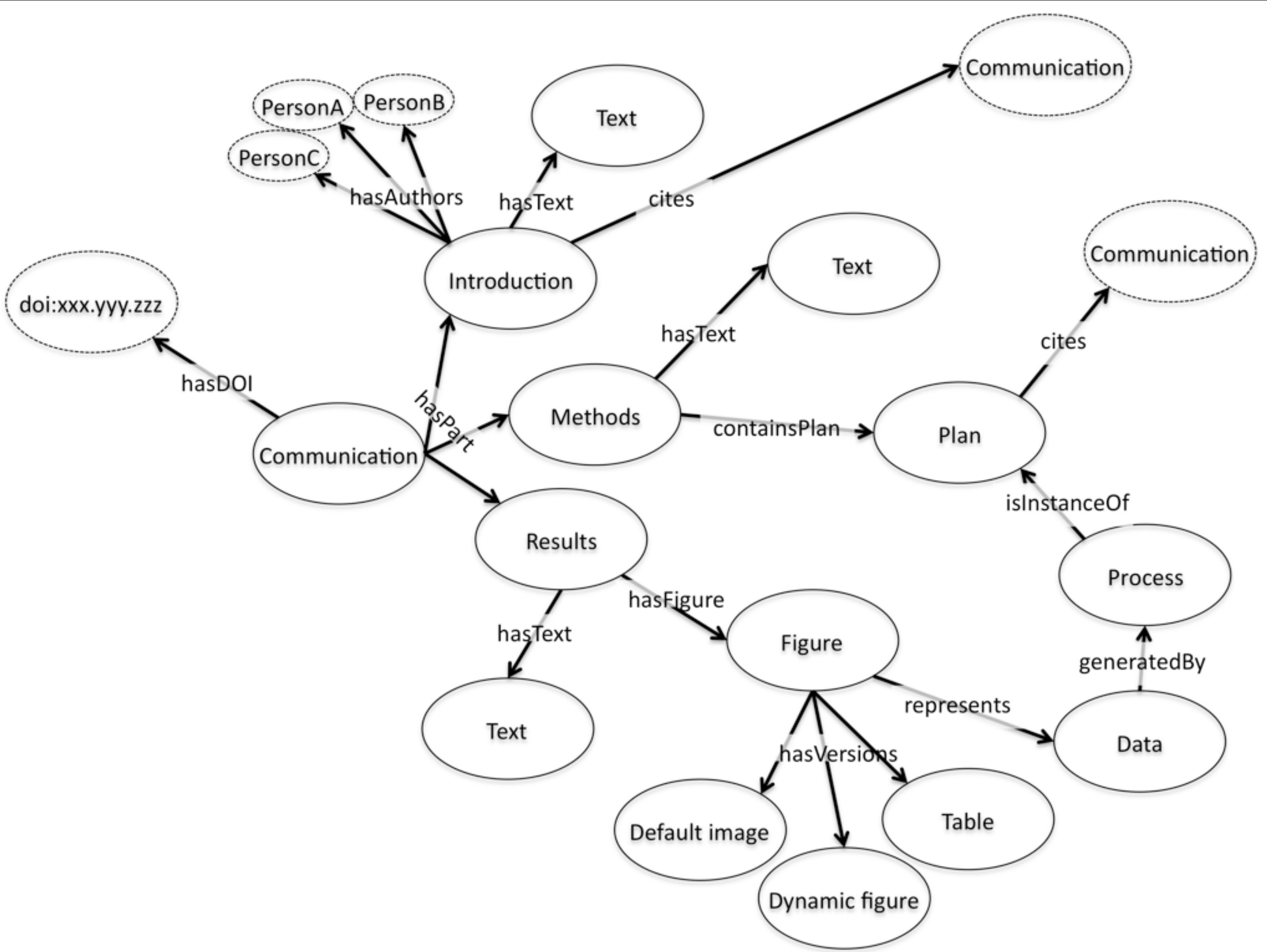
...and then collect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Storyful | Updated a day ago | Tweet 44 | Recommend 4

Silent protests at UC Davis after pepper-spray incident

From: @StopBeck

storyful.

Home | Now | Focus | Community | Search

Storyful | Updated a day ago | Tweet 44

Silent protests at UC Davis after pepper-

From: @StopBeck

From terrydatiger

Protesters changed tactics on Saturday with their protests, according to one blogger who filmed the silent treatment:

> A group of highly organized students formed large gap for the chancellor to leave. They chanted "we are peaceful" and "just walk home," but nothing changed for several hours. Eventually student representatives convinced the chancellor to leave after telling their fellow students to sit down and lock arms.
>
> One of the students pepper sprayed yesterday, a young man wearing a brown down coat over a tie-dye shirt, said he met with Kotehi and personally showed her a video of pepper spraying attack. Speaking to about a thousand students with the "human mic," the young man said he personally asked for her resignation.

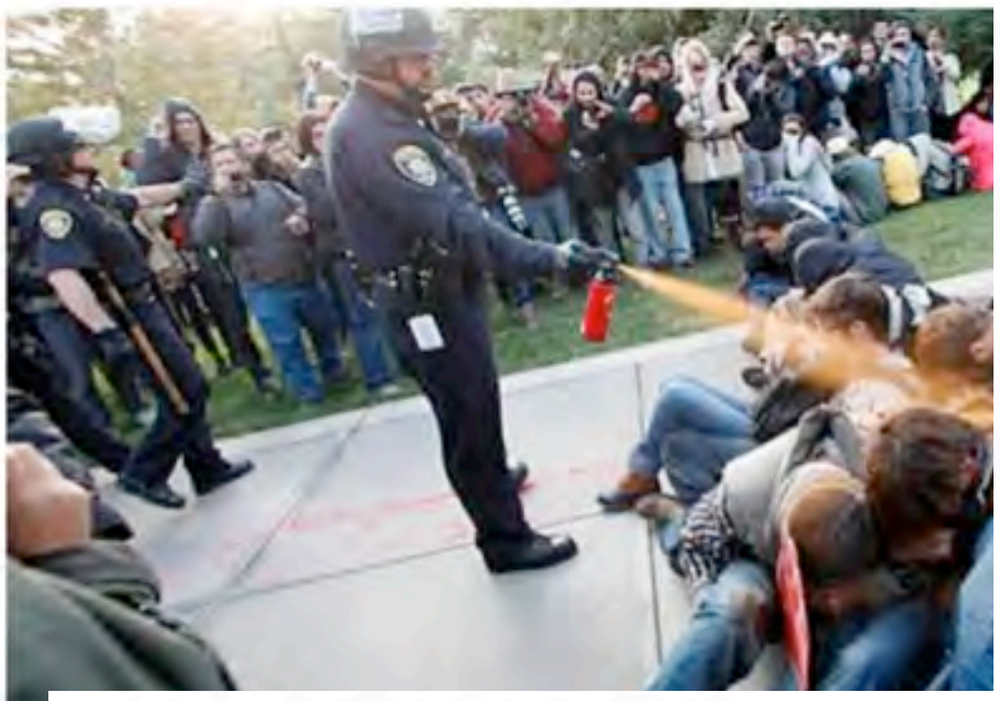
From The Second Alarm

storyful.

Home | Now | Focus | Community | Search

Storyful Updated a day ago Tweet 44

Silent protests at UC Davis after pepper-



Police pepper spraying and arresting students a...

0:00 / 8:34

From terrydatiger

Protesters changed tactics on Saturday with their protests, according to one blogger who filmed the silent treatment:

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ust walk home," but nothing changed for several hours.
es convinced the chancellor to leave after telling their fellow
ns.

yed yesterday, a young man wearing a brown down coat
with Kotehi and personally showed her a video of pepper
ut a thousand students with the "human mic," the young
r her resignation.

One professor went public with his concerns:

From @Powell_DA

Introduction

Add a link

This is a sample record pulled from a mocked up lab notebook.

An example of a sample record post that would be automatically created via the user GUI. The name of the sample given by the user would be the post title. Each sample should have its own post so that it receives a URI/URL. It might be possible to have the registered user be the author of the post?

Name	Role	Parameter Name	Parameter2 name
Sample Example	Sample	Value	Another value

Sample used in experiment:
http://fakedoiresolver.org/fake-doi-example

what I'd like to do here is add a rel="http://somenamespace.org/is-sample-in-experiment" to this link and for a Webtracks call to be initiated whenever there there a link with sufficient semantics to be represented as a triple

From C.Neylon@rl.ac.uk (Cameron Neylon)

Introduction

Add a link

This is a sample record pulled from a mocl

An example of a sample record post that v
user GUI. The name of the sample given b
Each sample should have its own post so
possible to have the registered user be the

Name	Role	Parameter Name
Sample Example	Sample	Value

Sample used in experiment:
http://fakedoiresolver.org/fake-doi-example

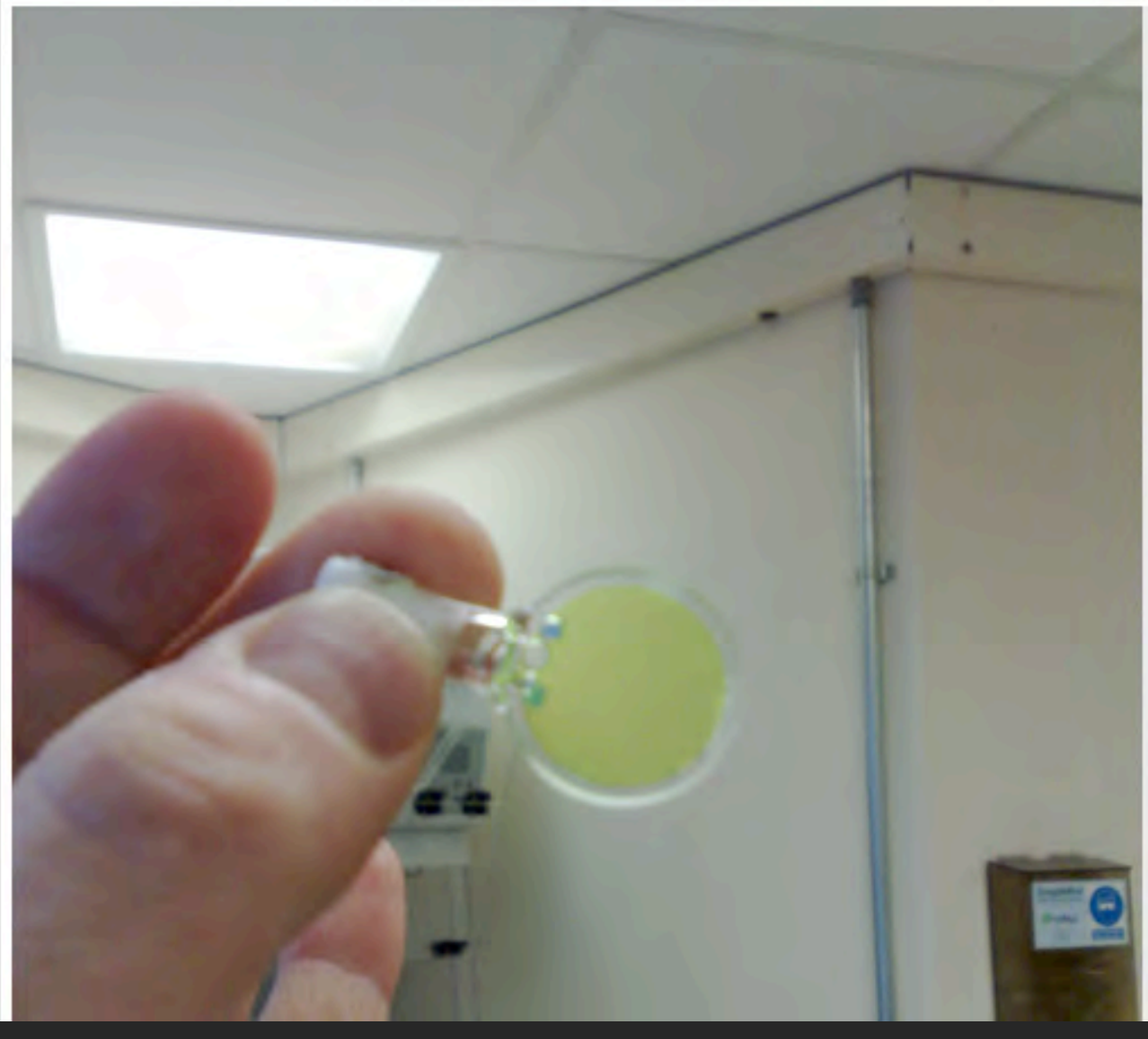
**what I'd like to do here is add a rel="http
experiment" to this link and for a Webtra
there a link with sufficient semantics to**

From C.Neylon@rl.ac.uk (Cameron Neylon)

I got a good picture of the sample and posted it to flickr. Got so excited I even tweeted about it...

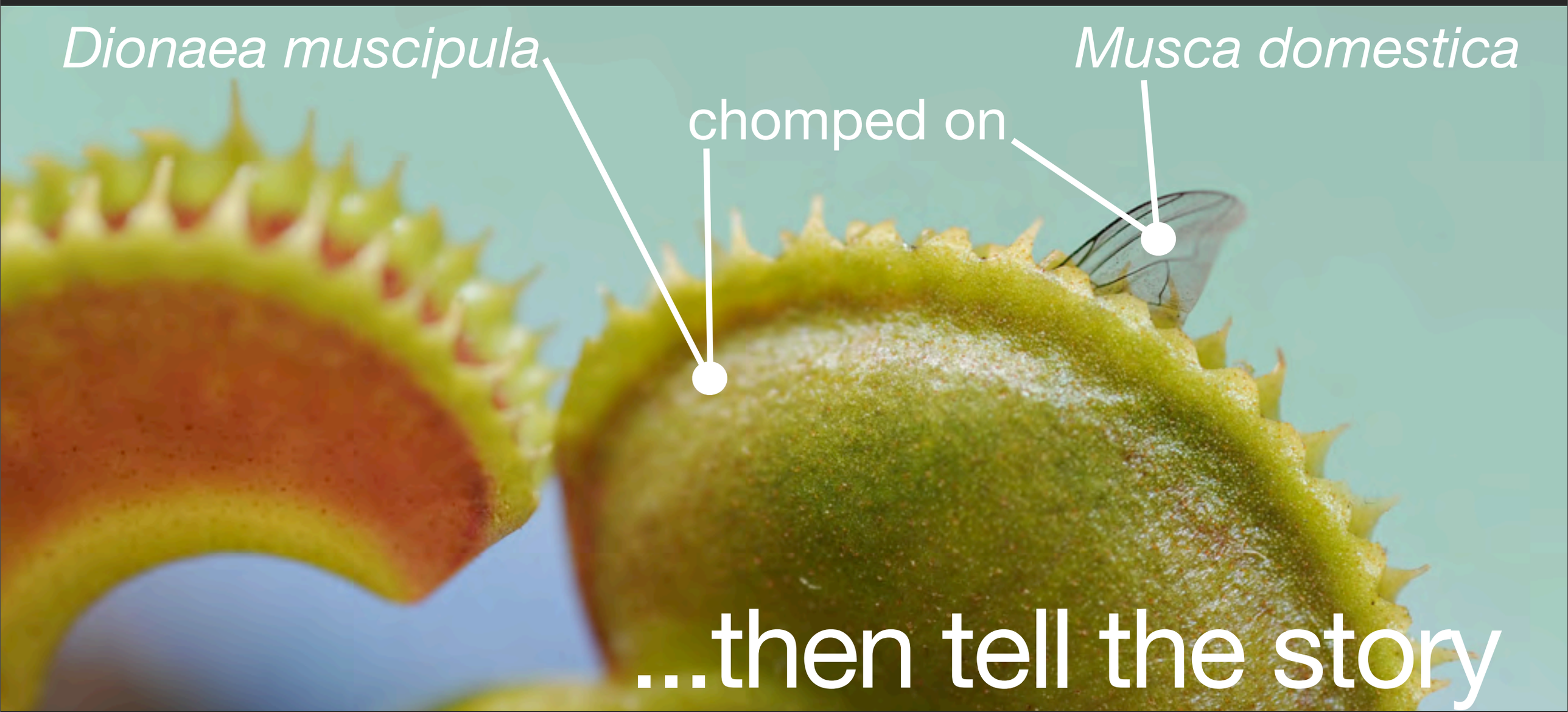
What a beautiful green sample we have for the experiment! Looking good for the measurement!

Tweeted by @tweetthelab

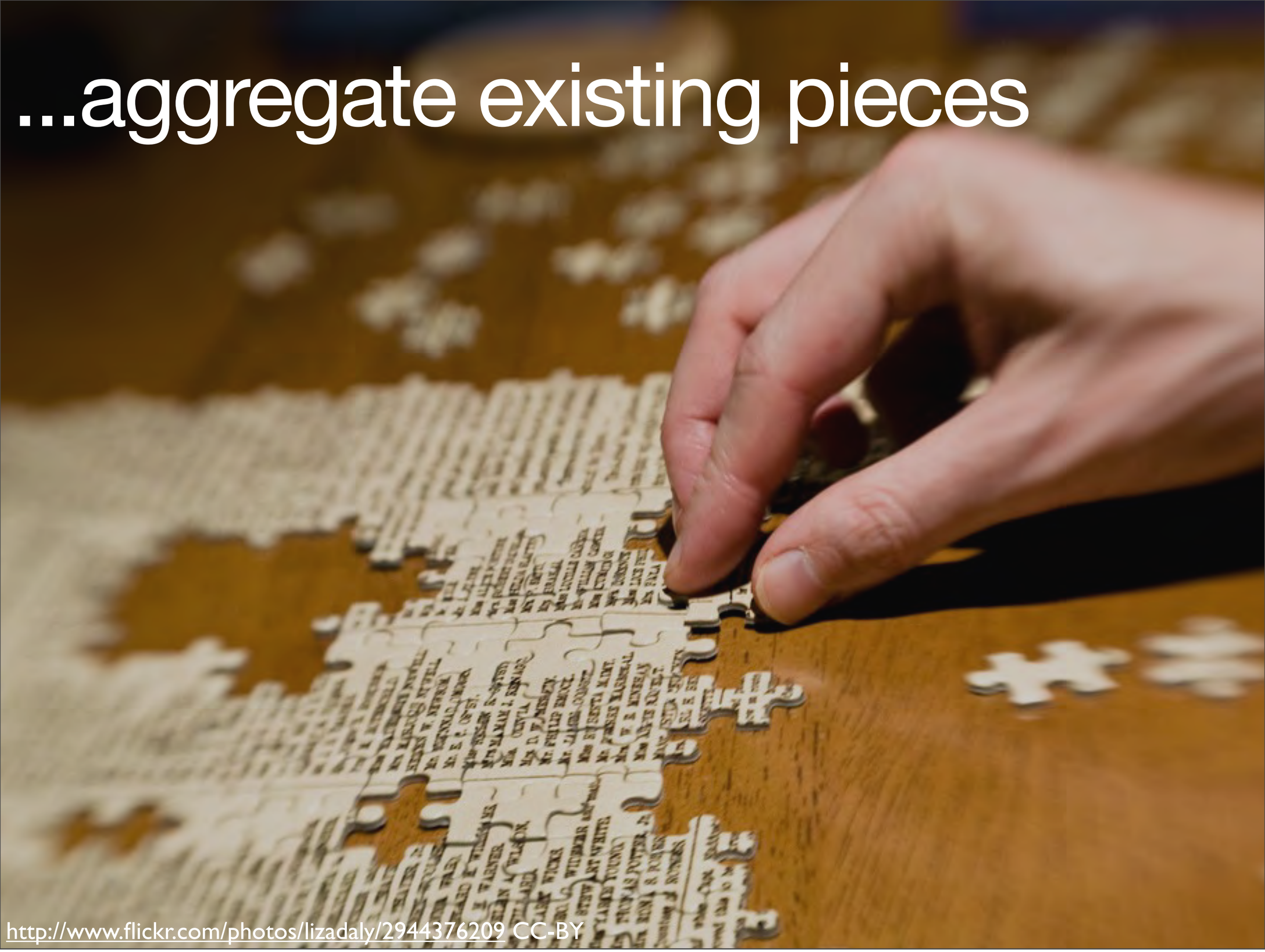


So we capture and collect...

http://www.flickr.com/photos/furtwangl/3851841424


Dionaea muscipula
chomped on
Musca domestica
...then tell the story

...aggregate existing pieces



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...we can open the floodgates...

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It’ll be great...right?

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group, and finally attachment to the solid support. In addition the use of intein based methods as well as the preparation of the solid support for Staudinger ligation often require reagents such as phosphines or thiophenols that are toxic and difficult to handle.

Therefore there remains a significant need for robust and simple methodologies for protein immobilization that can be applied to wide range of proteins and solid supports. The identification of the Sortase transpeptidase [19] provided an alternative approach to protein ligation. Sortases recognise a specific peptide sequence (LPETG for SrtA of *S. aureus* used in this work) in proteins targeted for covalent attachment to the cell wall peptidoglycan. The peptide tag sequence is cleaved and then ligated to the pentaglycine moiety on the peptidoglycan precursor Lipid II. Proteins expressed with the C-terminal recognition sequence can be covalently attached to a wide range of constructs with an N-terminal glycine amide motif including peptides [20], PNA [21], full length proteins [22] and small molecule substrates [23]. Another group has independently described an example of Sortase mediated ligation to a beaded solid support [22]. These reactions proceed under aqueous conditions without the addition of any other reagents beyond the protein ligation substrate and Sortase. Thus Sortase has the potential to provide a means of linking expressed proteins to a wide range of solid supports which is mild, selective, and can be carried out in a single step. Here we investigate the ability of *S. aureus* SrtA to ligate proteins to a range of solid supports.

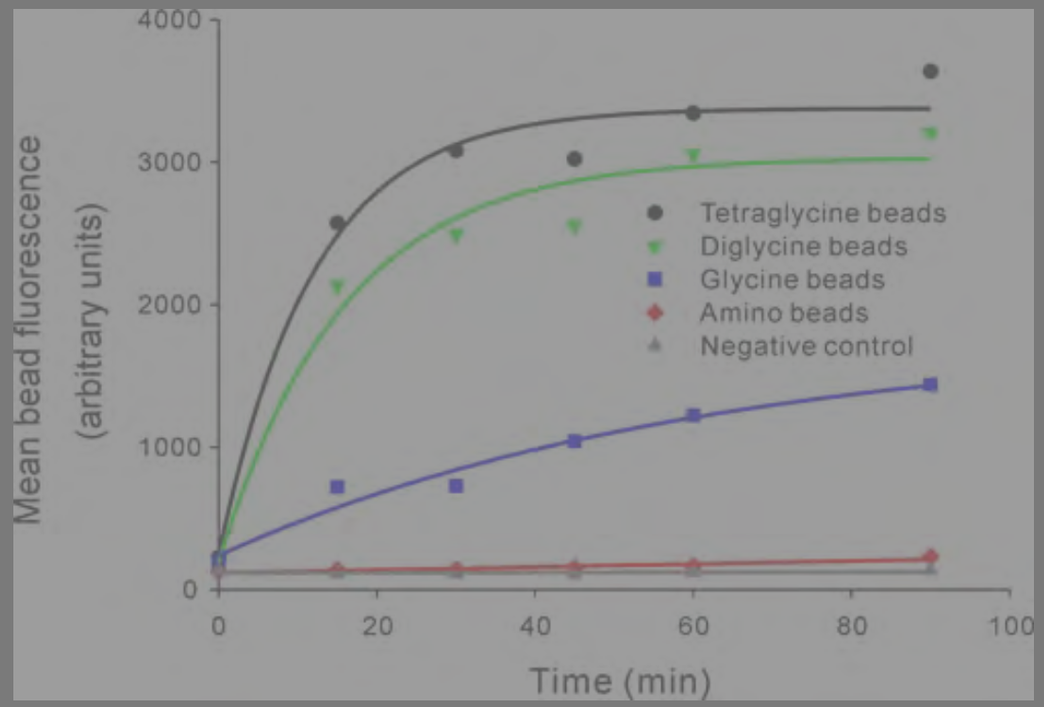

Figure 1. Ligation of fluorescent proteins to polymer beads. (a) GMA beads modified with one, two, or four glycine residues were incubated with EGFP-LPETGG-His_6 and Sortase. Samples were taken at specific time points, analyzed on a BD FACSAria, and the mean fluorescence of labeled beads with no, one, two or four glycine residues without Sortase are shown. The standard error in the mean fluorescence of labeled beads are generally smaller than the data symbols. Errors are given in Supplementary Data S2.
doi:10.1371/journal.pone.0001164.g001

All of this information...data....

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Genotypes Kit-1 (Genalex format) Locus 4:csolfagus_31; Locus 6:sfc_1143; Locus 8:csolfagus_05; Locus 9: FS1_15; Locus 10:sfc_0036; Locus 11: csolfagus_06; Locus 12:csolfagus_19; Locus 13:csolfagus_29

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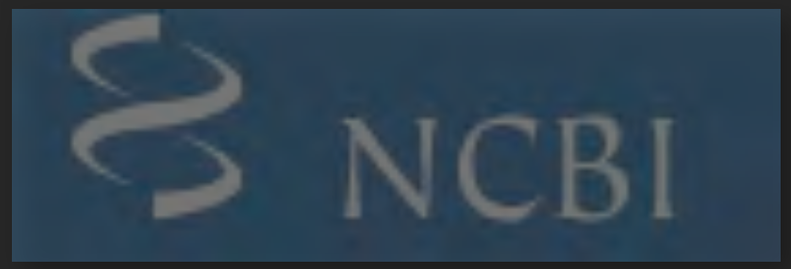

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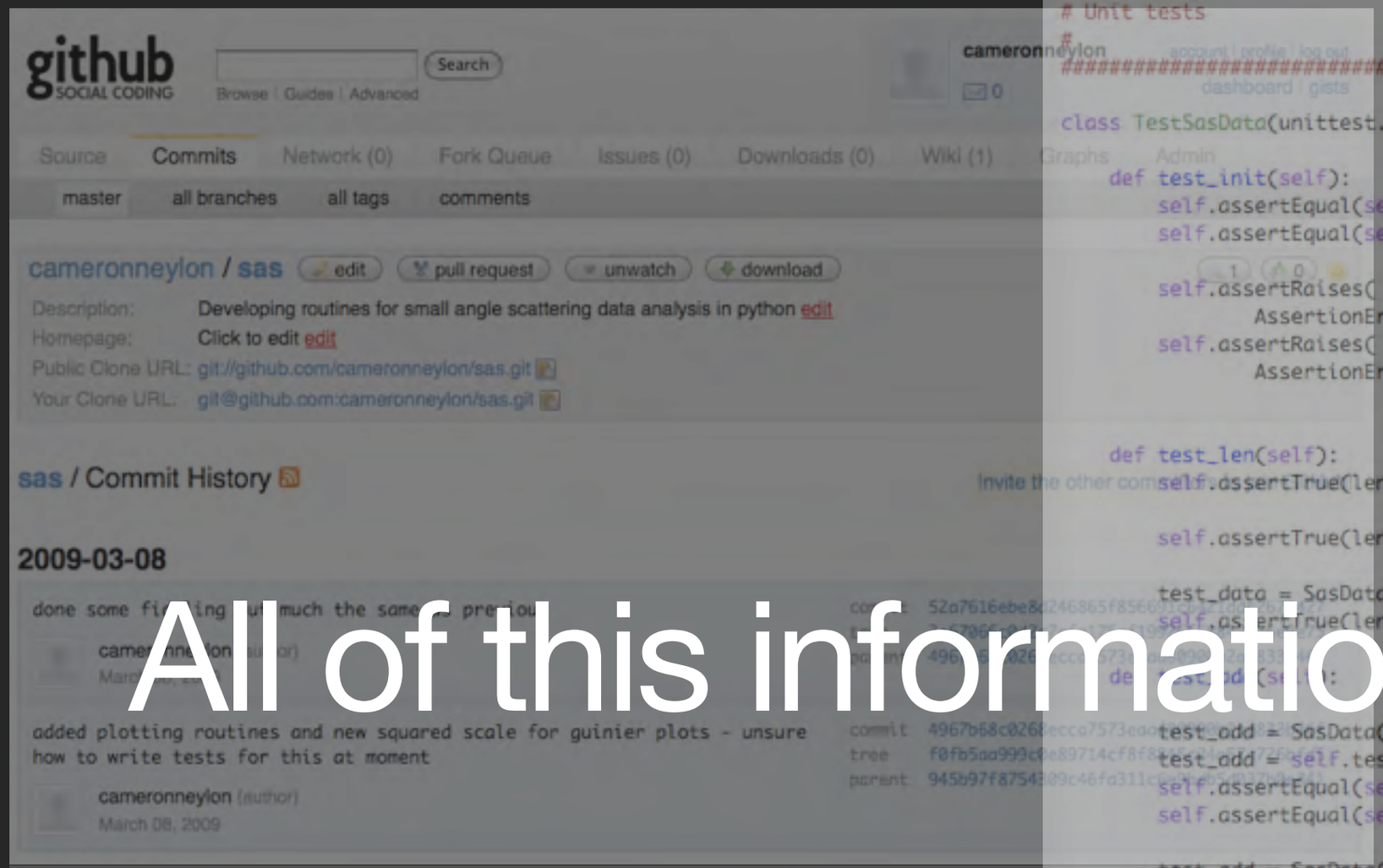

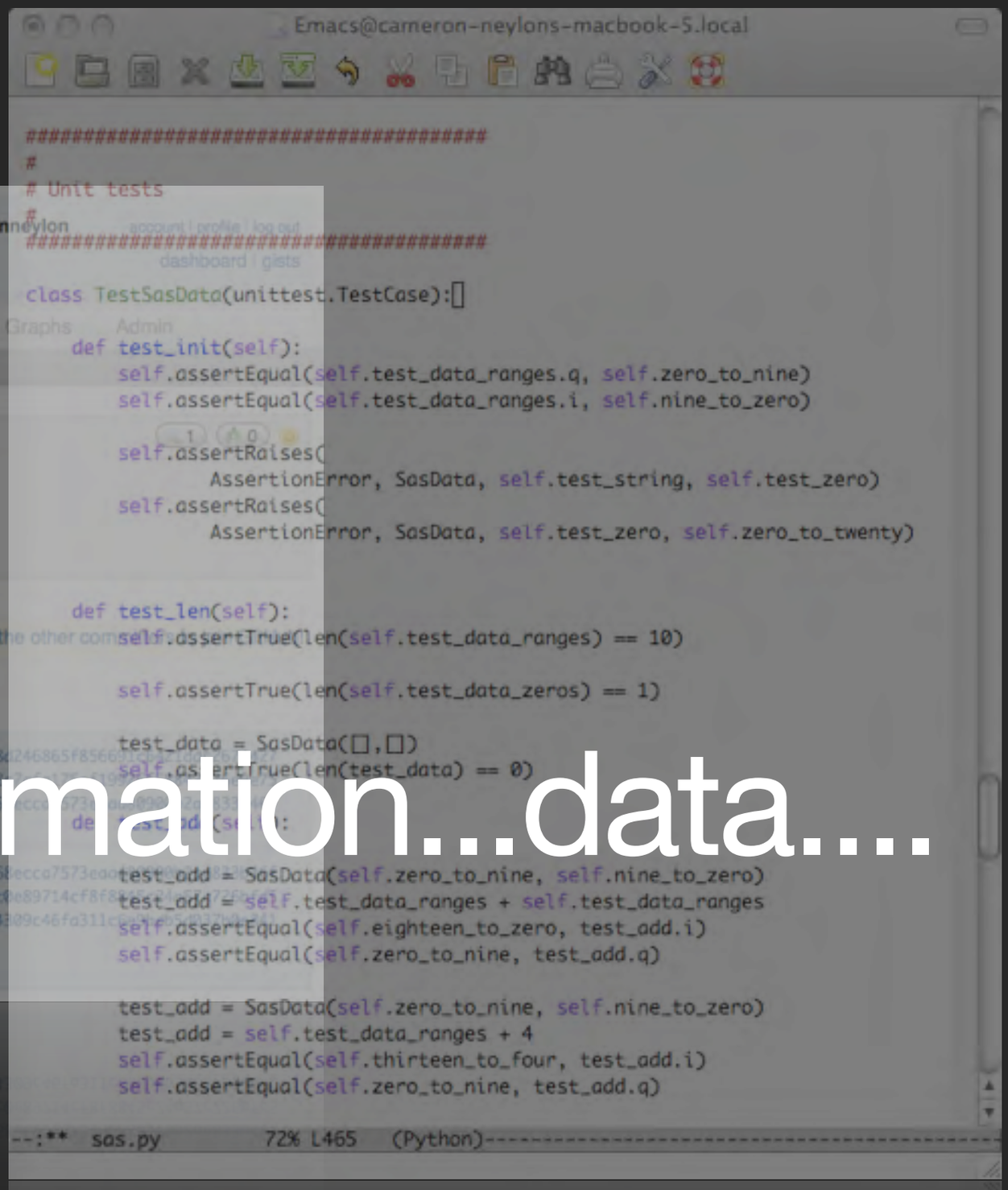

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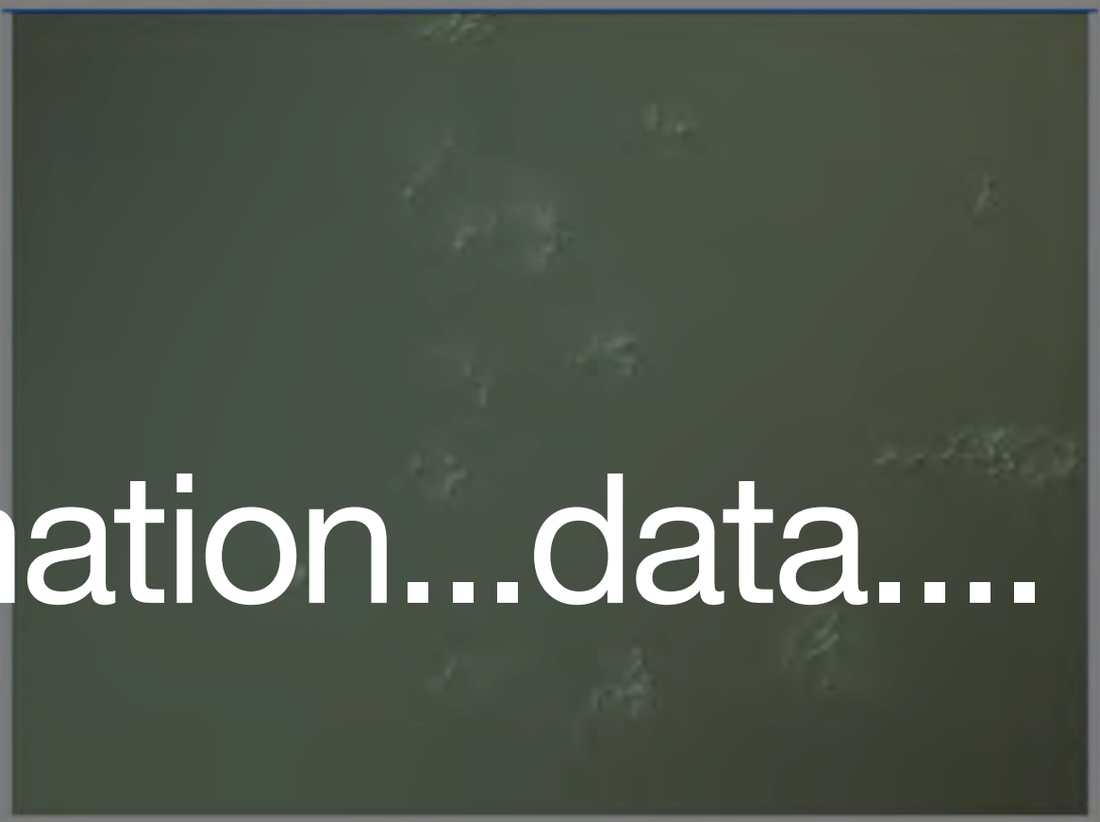

Comments (0)

All of this information...data....

http://usefulchem.wikispaces.com/Exp207

All of this information...data....

Flickr tag: UC207

UsefulChem

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Paper03 Draft
Isolated Compounds
Alicia's Masters Thesis
CombiUgi Project

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glycine methyl ester in methanol (1.32 M)
vanillin in methanol (4.19 M) ethanol (2.50 M) THF (3.89 M)

All of this information...data....

Reflections on research data management: RDM is on the up and up but data driven policy development seems a long way off.

11 NOVEMBER 2011 46 VIEWS NO COMMENT

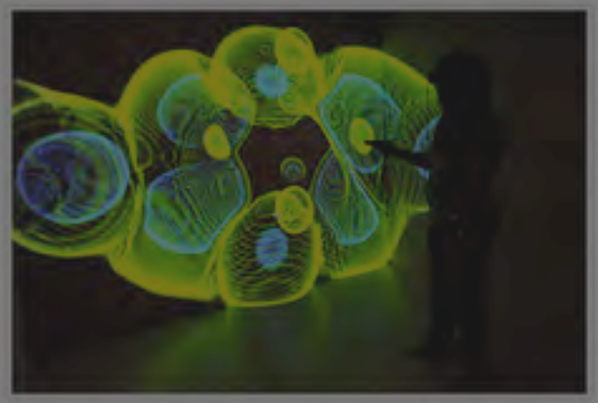

Image by Idaho National Laboratory via Flickr

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The Research Data Management movement is moving on apace. Tools are working and adoption is growing. Policy development is starting to back up the use of those tools and there are some big ambitious goals set out for the next few years. But has the RDM movement taken the vision of data intensive research to its heart? Does the collection, sharing, analysis of data [illegible] based on [illegible] assessed against that data? Can we [illegible]

Watching the discussion on research data management over the past few years has been an exciting experience. The tools, that have been possible for some years, now show real promise as the somewhat raw and ready products of initial development are used and tested.

Practice is gradually changing, if unevenly across different disciplines, but there is a growing awareness of data and that it might be considered important. And all of this is being driven increasingly by the development of policies on data availability, data management, and data archiving that stress the importance of data as a core output of public research.

Recent Friendfeed activity

"Skitchrolling" - When an apparently interesting link leads you to Scholarly Kitchen...
Saturday 10:47

Yikes. Weather for Tromsø for next five days...might make it above zero...will be needing to pack warm...
Friday 17:51

Re-use as Impact: Linking the open and impact agendas
Re-use as Impact: Linking the open and impact agendas
Friday 16:59

BMJ Group blogs: BMJ » Blog Archive » Richard Smith: A woeful tale of the uselessness of peer review
Friday 21:01

Visual RDF
Friday 21:01

My FriendFeed profile

Lifestream

Yikes. Weather for Tromsø for next five days...might make it above zero...will be needing to pack warm... [cameronneylon]
— 2d ago via Twitter

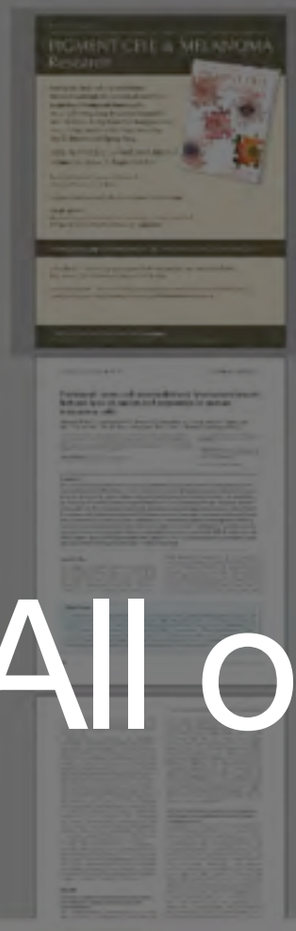
Ok. A second attempt at [illegible]

I am also found at...

Flickr
Friendfeed
Github
My lab notebook
Slideshare
Twitter

All of this information....data....

Document Figures



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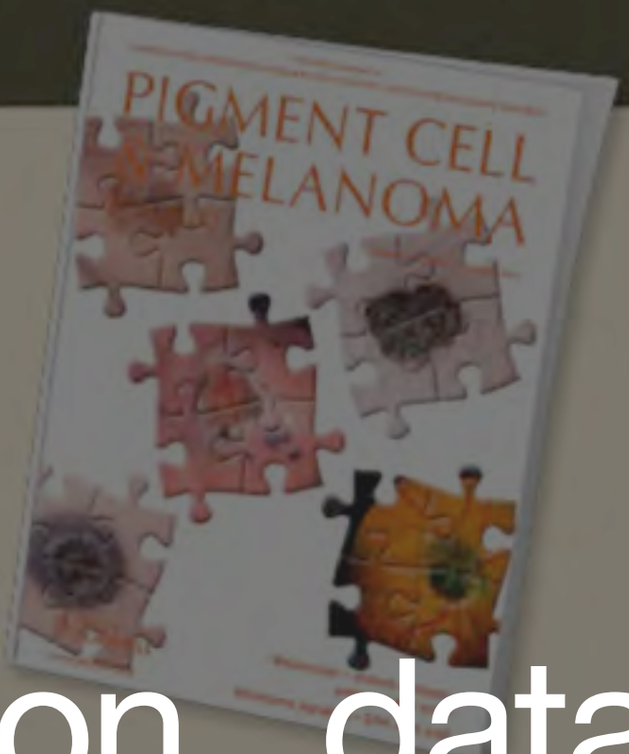
PIGMENT CELL & MELANOMA Research

Embryonic stem-cell-preconditioned microenvironment induces loss of cancer cell properties in human melanoma cells

Myoung Ok Kim, Sung-Hyun Kim, Naomi Oi, Mee Hyun Lee, Dong Hoon Yu, Dong Joon Kim, Eun Jin Cho, Ann M. Bode, Yong-Yeon Cho, Tim G. Bowden and Zigang Dong



DOI: 10.1111/j.1755-148X.2011.00891.x
Volume 24, Issue 5, Pages 922-931

Supporting Information for this article is freely available here

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All of this information....data.....

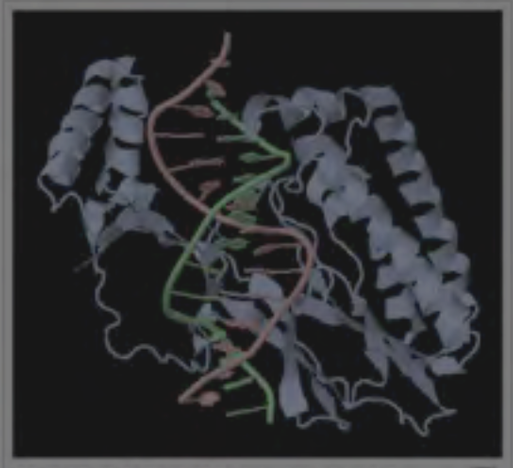
Menu 0:05 / 4:20

Wednesday, 14 December 11

Tus (biology)

From Wikipedia, the free encyclopedia
(Redirected from Tus protein)

Tus is a sequence-specific DNA-binding protein that promotes termination in the DNA replication process of prokaryotes. In *E Coli*, Tus binds to 10 closely related sites encoded in the chromosome. These sites bind 23 base-pairs. The 10 sites are called *Ter* sites, and are designated *TerA*, *TerB*, ..., *TerJ*. These binding sites are asymmetric, such that when a Tus-Ter complex (Tus protein bound to a Ter site) is encountered by a replication fork from one direction, the complex is dissociated and replication continues (permissive). But when encountered from the other direction, the Tus-Ter complex provides a much larger kinetic barrier and halts replication (non-permissive). The multiple *Ter* sites in the chromosome are oriented such that the two oppositely moving replication forks are both stalled in the desired termination region.[2]



Representation of the x-ray crystal structure of Tus-Ter protein-DNA complex. (Jmol rendering of coordinates from [1]. The DNA strands are shown in pink and green.)

Further reading [edit]

- "Interaction of the Escherichia coli replication terminator protein (Tus) with DNA: a model derived from DNA-binding studies of mutant proteins by surface plasmon resonance."[3]
- "Replication termination in Escherichia coli: structure and antihelicase activity of the Tus-Ter complex."[4]
- "A molecular mousetrap determines polarity of termination of DNA replication in E. coli."[5]
- "Isolation and characterization of human cDNA for the replication arrest protein of Escherichia coli."[6]
- "Biophysical characteristics of Tus, the replication arrest protein of Escherichia coli."[6]
- "Structure of a replication-terminator protein complexed with DNA."[1]
  - Structure at protein data bank

References [edit]

1. ^ a b Kamada, K.; Horiuchi, T.; Ohsumi, K.; Shimamoto, N.; Morikawa, K. (1996). "Structure of a replication-terminator protein complexed with DNA". *Nature* **383** (6601): 598–603. Bibcode 1996Natur.383..598K. doi:10.1038/383598a0. PMID 8857533. edit

All of this information...data....

Wednesday, 14 December 11

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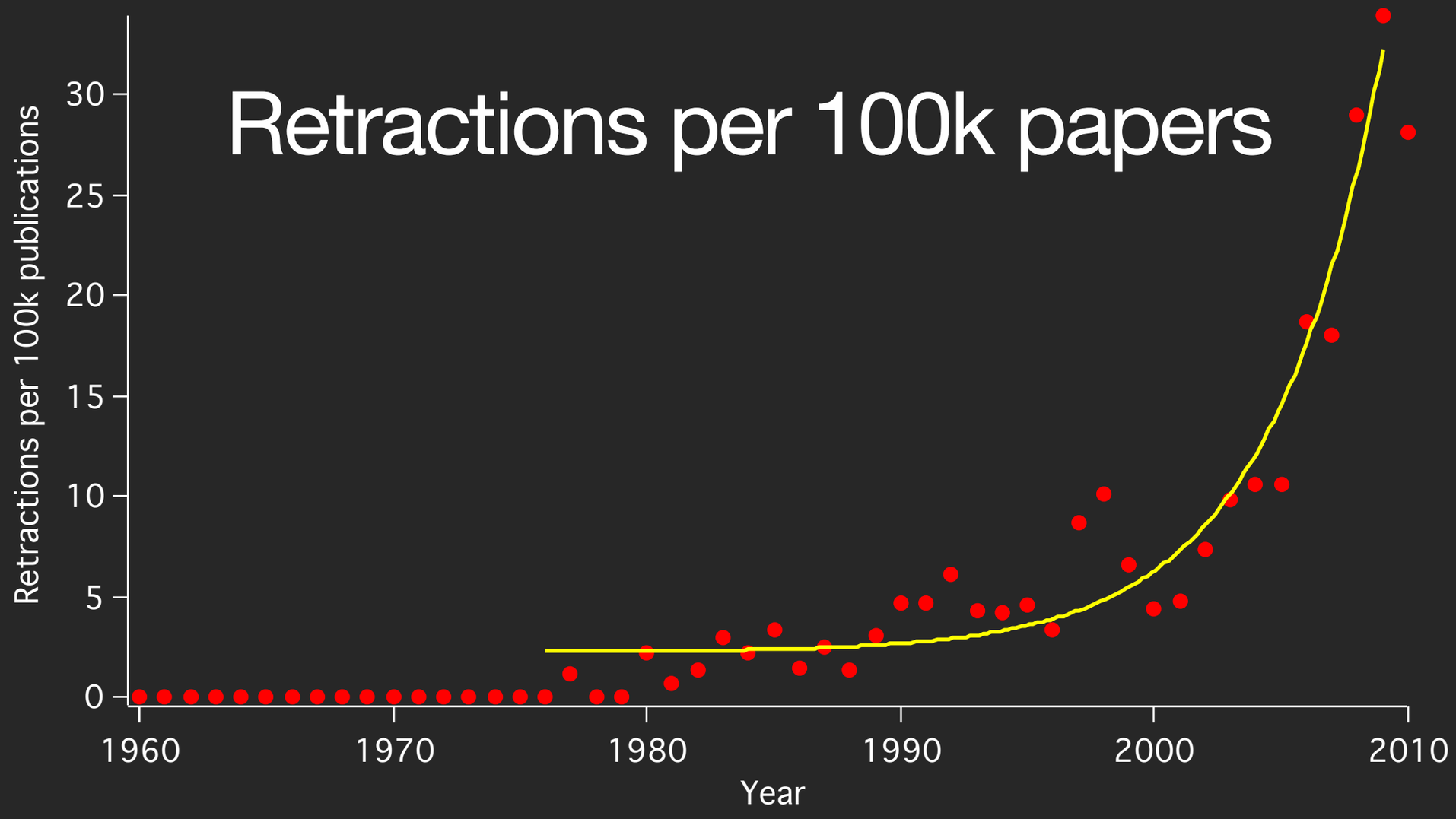
Retractions per 100k papers



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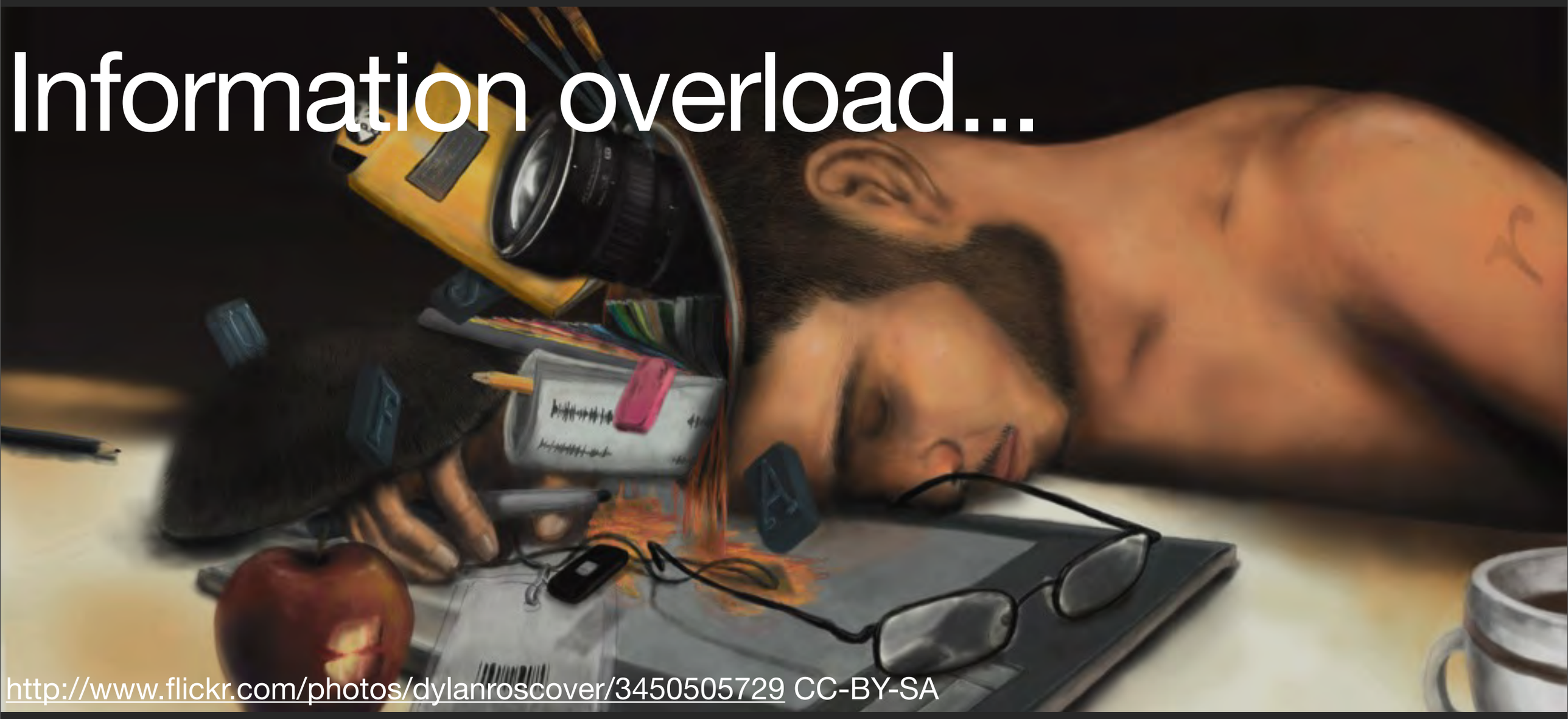
http://www.flickr.com/photos/7827294@N04/4621721577 CC-BY

Information overload...



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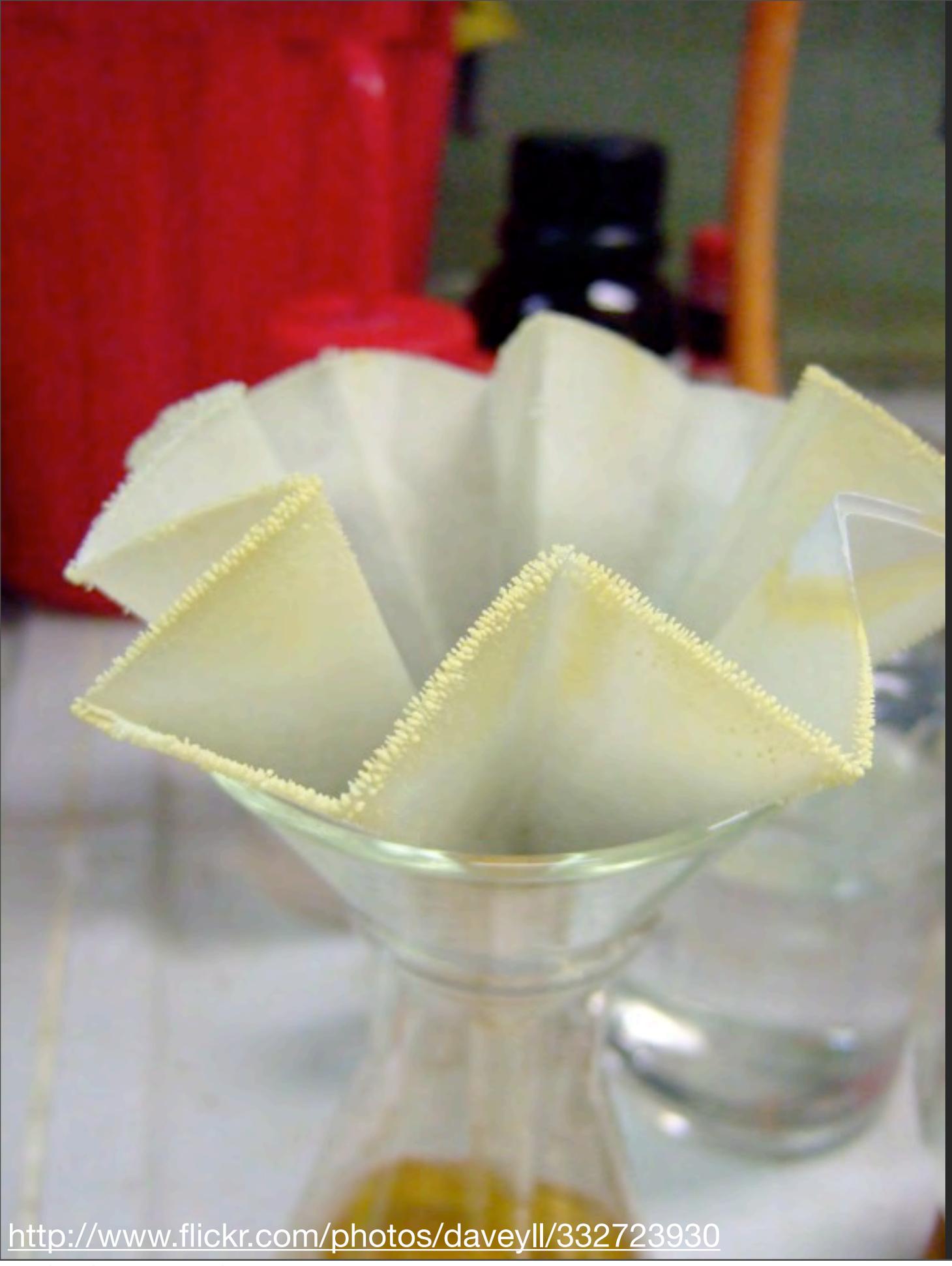
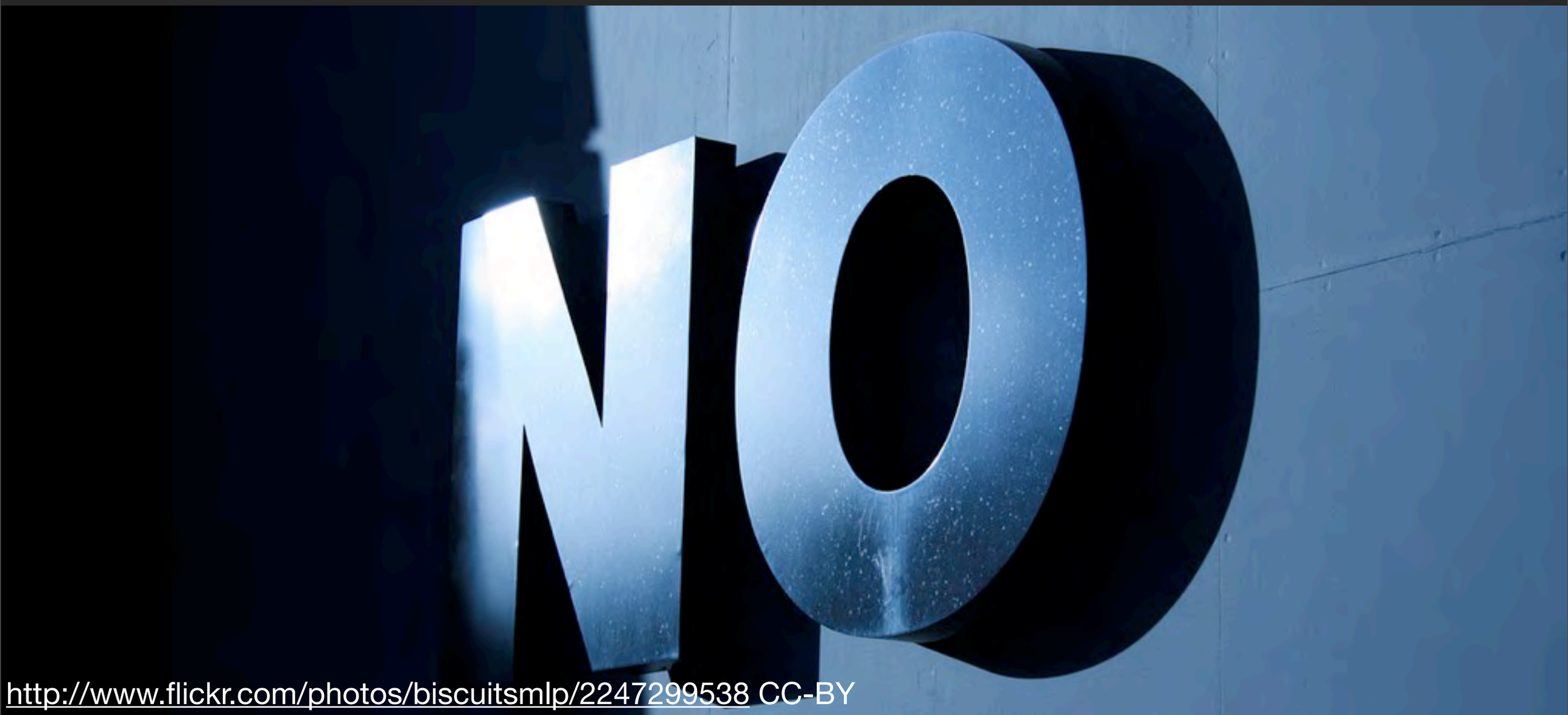
“I need to read less”



http://www.flickr.com/photos/daveyll/332723930

Filter failure?



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Filters block.

You think this is a good thing...

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...staying on the straight and narrow...

Or are we just limiting
our ability to explore...?

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...and discover...?

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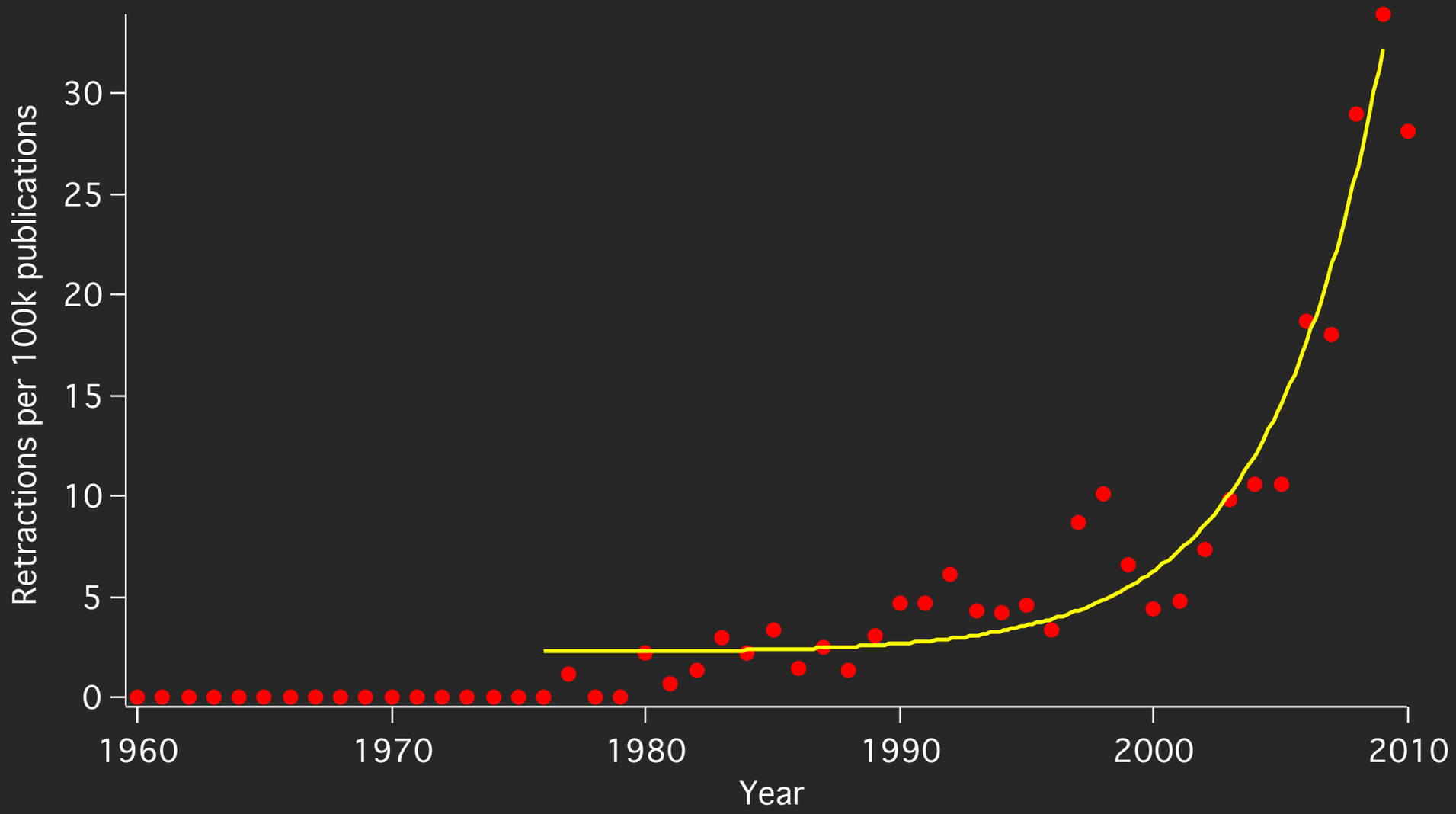
Filters block.

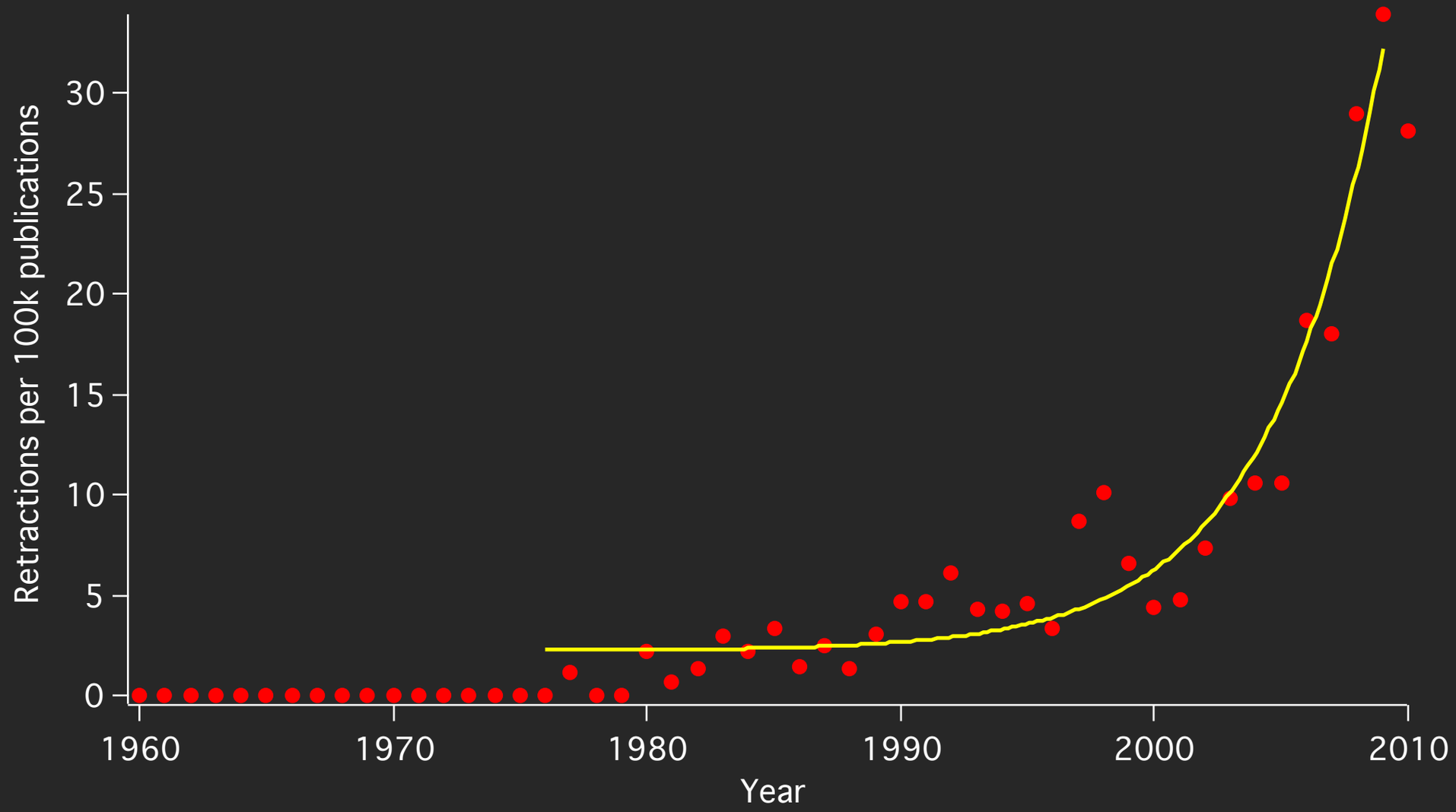
The right filter for me?
Right filter for now?

Wednesday, 14 December 11

Remember this graph?

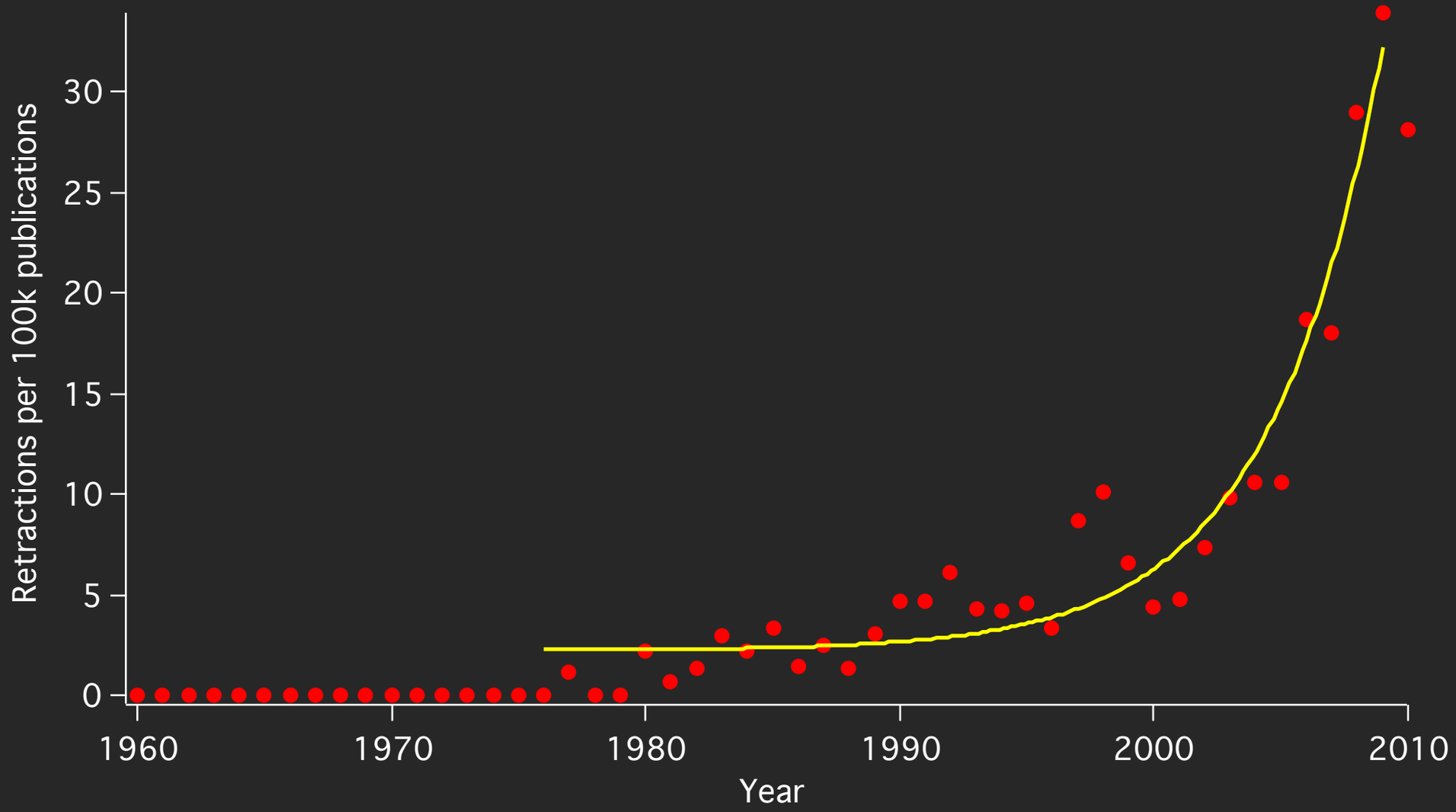


Remember this graph?



Where is the data from?

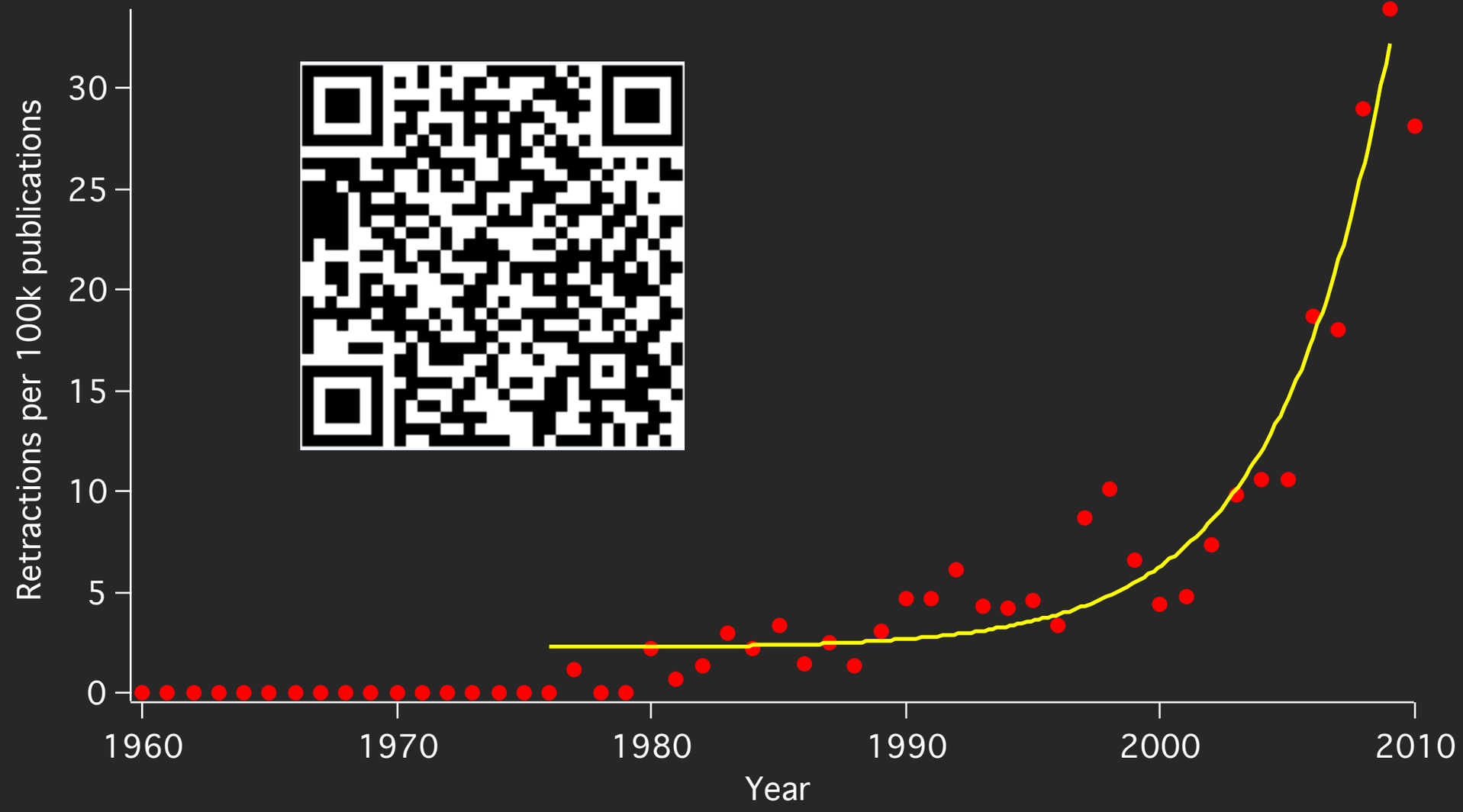
Remember this graph?



https://github.com/neilfws/PubMed/blob/master/data/retractions.txt

Where is the data from?

Remember this graph?



https://github.com/neilfws/PubMed/blob/master/data/retractions.txt

Where is the data from?

But how did I discover it?

FriendFeed

Geoffrey Bilder

So how many retractions are there every year, anyway?
« Retraction Watch -
http://retractionwatch.wordpress.com/2010...

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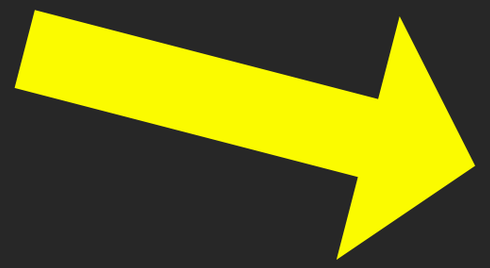
You, Bill Hooker, Greg Tyrelle and 8 other people liked this (Un-like)

For PubMed, use the query "Retraction of Publication[Publication Type]". This returns 1621 results. Last year (2009), there were 289, from 852 183 total publications. And here's a quick graph - http://twitpic.com/3bazq4 - based on this code - http://nsaunders.wordpress.com/2010.... - Neil Saunders

Here's a graph of the same, but normalized by # of published papers. http://i.imgur.com/NVkEF.png See this thread:http://friendfeed.com/neilfws... - Chris Miller

http://friendfeed.com/gbilder/711e6278/so-how-many-retractions-are-there-every-year



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http://friendfeed.com/gbilder/711e6278/so-how-many-retractions-are-there-every-year

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1621 results. Last year (2009), there were 289, from 852 183 total
here's a quick graph - http://twitpic.com/3bazq4 - based on this
http://nsaunders.wordpress.com/2010.... - Neil Saunders

Remember these people?


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Plausible Accuracy
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Mummi Thorisson
Fabiana Kubke
Richard Grant
Pedro Beltrao
John
Neil Saunders
Steve Wilson
@gnat
Branwen Hide
Dupuis
Simon Philips
Pawel Szczesny
SIMON COLES
Paul Miller
Gabriel Cavalli
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Nico Adams
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Noel Gorelick
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AJCann
Allyson Lister
Andrew Lang
Andrew Su
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Anna Croft
Anne Marie Cunningh
Ant Beck
Antony Williams
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Ariel Waldman
Arikia
Attila Csordas
Bill Hooker
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BioGang Classics
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Bosco Ho
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ISMB 2008
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Michael Nielsen
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Nav
Neil Saunders
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Open Notebook Science Solubility Project
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OpenWet
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Pedro Beltrao
Peter Ballantyn
peter murray-rust
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Polly Potter
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sciencea
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Shirley Wu
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Soton Open Science
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TAC_NISO Todd Carp
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eronel Lenore Ramm
younglandis Ben You
alex77 Neil Ernst
Scrazzl David Kavanag
TheRepoRat Dorothe

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telescoper Peter Coles
edsu Ed Summers
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LouWoodley Lou Woo
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doctorblogs annabel
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hughesbethan Betha
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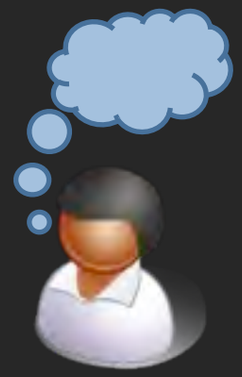

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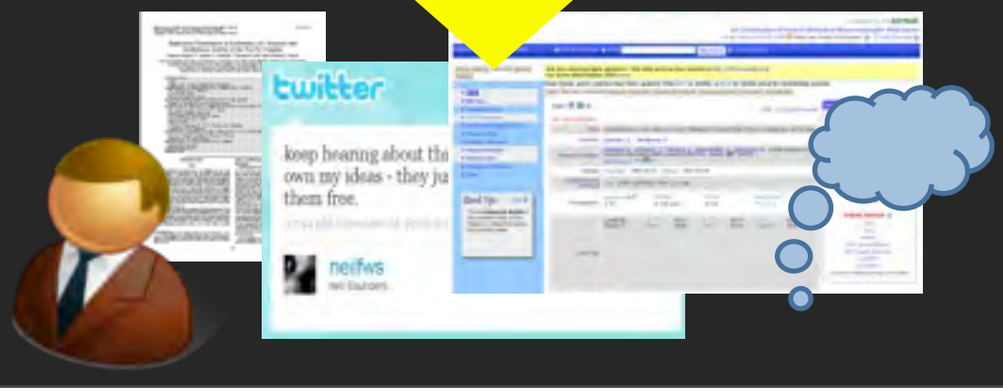
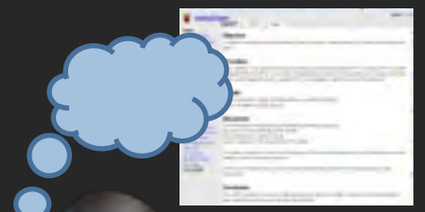
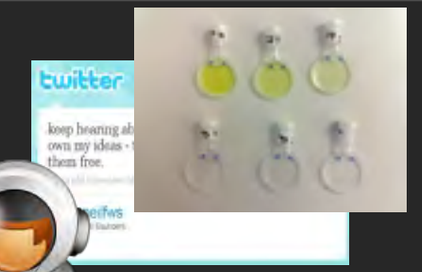


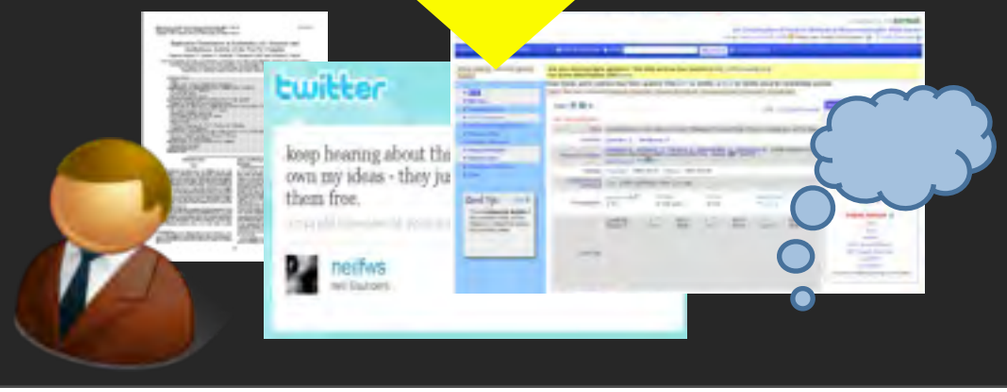




friendfeed

twitter

Google+



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Feed Reader

Social *aggregation*...

...but also...

FriendFeed

Geoffrey Bilder

So how many retractions are there every year, anyway?
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Here's a graph of the same, but normalized by # of published papers. http://i.imgur.com/NVkEF.png See this thread:http://friendfeed.com/neilfws... - Chris Miller

Social *annotation*

...and quality assessment

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...but also...

What You're Doing Is Rather Desperate

Notes from the life of a bioinformatics researcher

Analysis of retractions in PubMed

As so often happens these days, a brief post at FriendFeed got me thinking about data analysis. Entitled "So how many retractions are there every year, anyway?", the post links to this article at Retraction Watch. It discusses ways to estimate the number of retractions and in particular, a recent article in the *Journal of Medical Ethics* (subscription only, sorry) which addresses the issue.

As Christina pointed out in a comment at Retraction Watch, there are thousands of scientific journals of which PubMed indexes only a fraction. However, PubMed is relatively easy to analyse using a little Ruby and R. So, here we go...

Code and raw data used for this post are available at Github.

1. Searching for retractions

In the *Journal of Medical Ethics* article, the authors state: "Every research paper noted as retracted in the PubMed database from 2000 to 2010 was evaluated. PubMed was searched on 22 January 2010 with the limits of 'items with abstracts, retracted publication, English.' A total of 788 retracted papers were identified..."

Not a bad approach. There's another way: at the PubMed website, find a retraction and examine the record in XML format. You'll see this:

```
<PublicationTypeList>
  <PublicationType>Retraction of Publication</PublicationType>
</PublicationTypeList>
```

http://nsaunders.wordpress.com/2010/11/30/analysis-of-retractions-in-pubmed/

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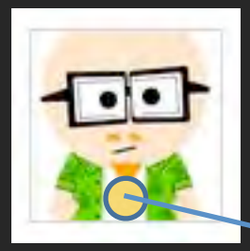
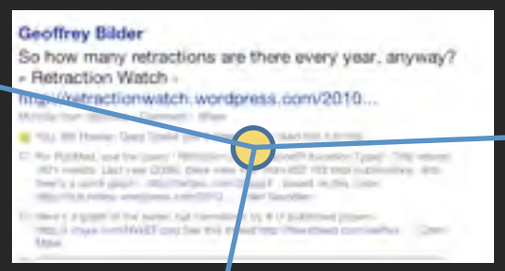
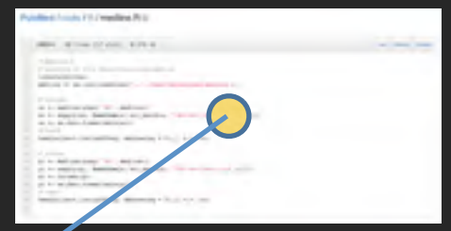
```

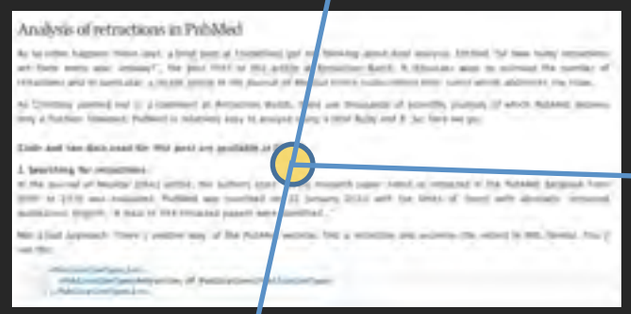
http://nsaunders.wordpress.com/2010/11/30/analysis-of-retractions-in-pubmed/

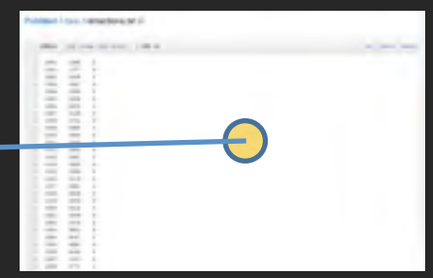


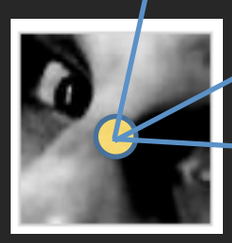


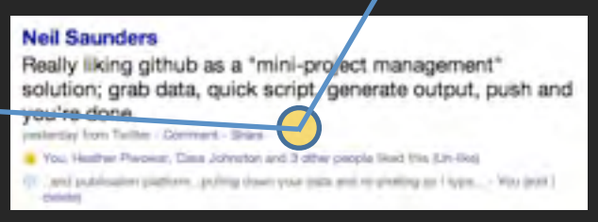


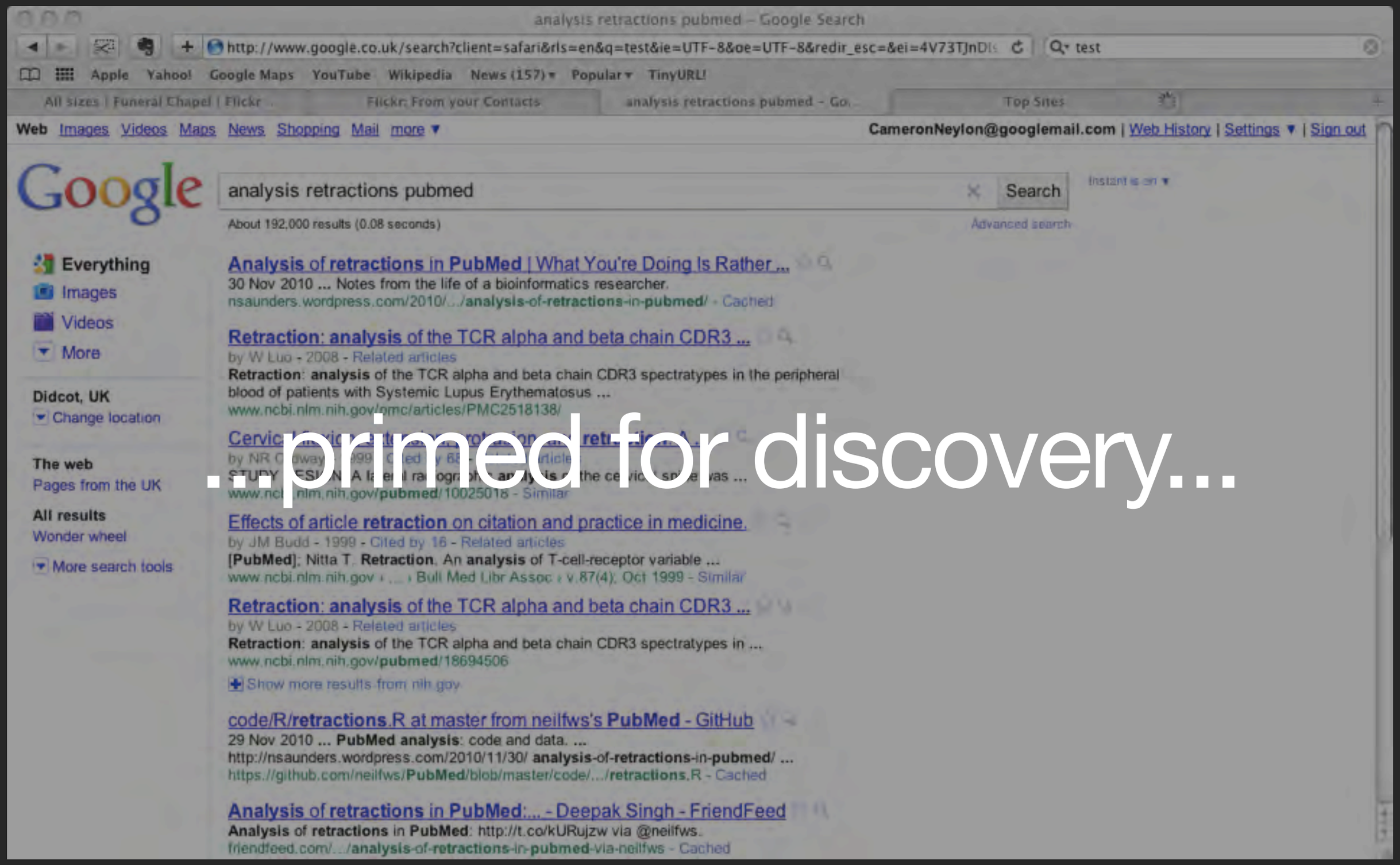
A network of linked objects...









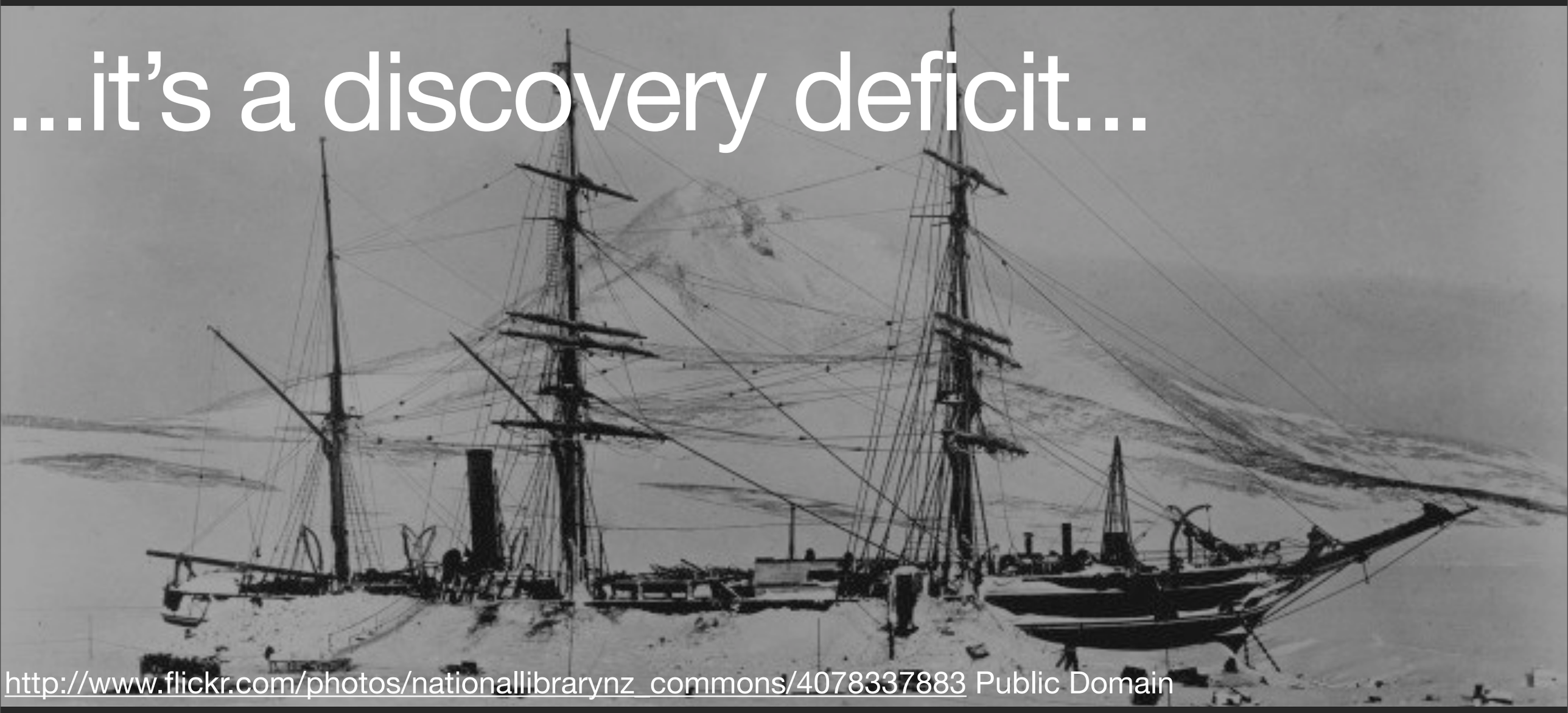


...primed for discovery...

Wednesday, 14 December 11

It’s not filter failure

...it's a discovery deficit...



http://www.flickr.com/photos/nationallibrarynz_commons/4078337883 Public Domain


In the last year...?
http://flickr.com/photos/stewart/461099066/

...in the past 24 hours?

Is search the answer?

http://www.flickr.com/photos/ezioman/2096469724 CC-BY

...or something more...?

http://www.flickr.com/photos/mangostrawberry/5490992826 CC-BY

Need the right instrument...

...not every problem is a nail

Upload digital objects

PubMed

myexperiment

flickr

ChemSpider

PDB

Online file stores

Google docs

slideshare

Scribd

LIMS

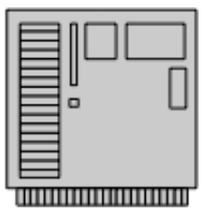
Blog/Wiki

Local file stores

Data repository

RSS/Atom Feeds

Feed Reader



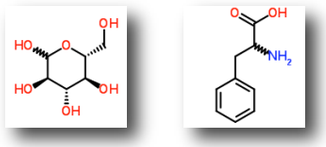
Upload digital objects

PubMed www.pubmed.gov

my experiment

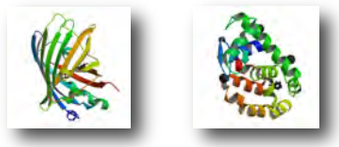
flickr

ChemSpider



RSS/Atom Feeds

PDB PROTEIN DATA BANK



Online file stores

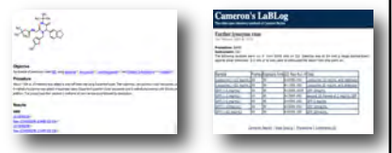
Google docs

slideshare Present Yourself

Scribd

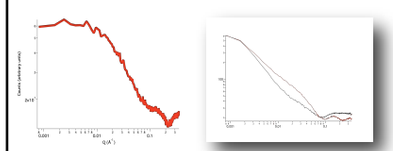
LIMS

Blog/Wiki



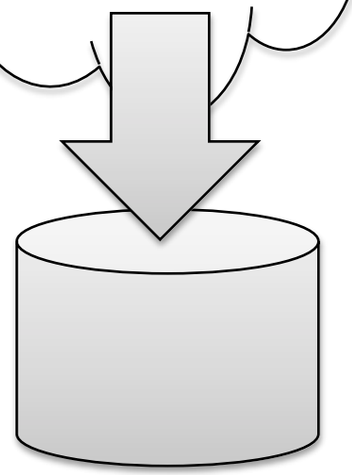
Local file stores

Data repository

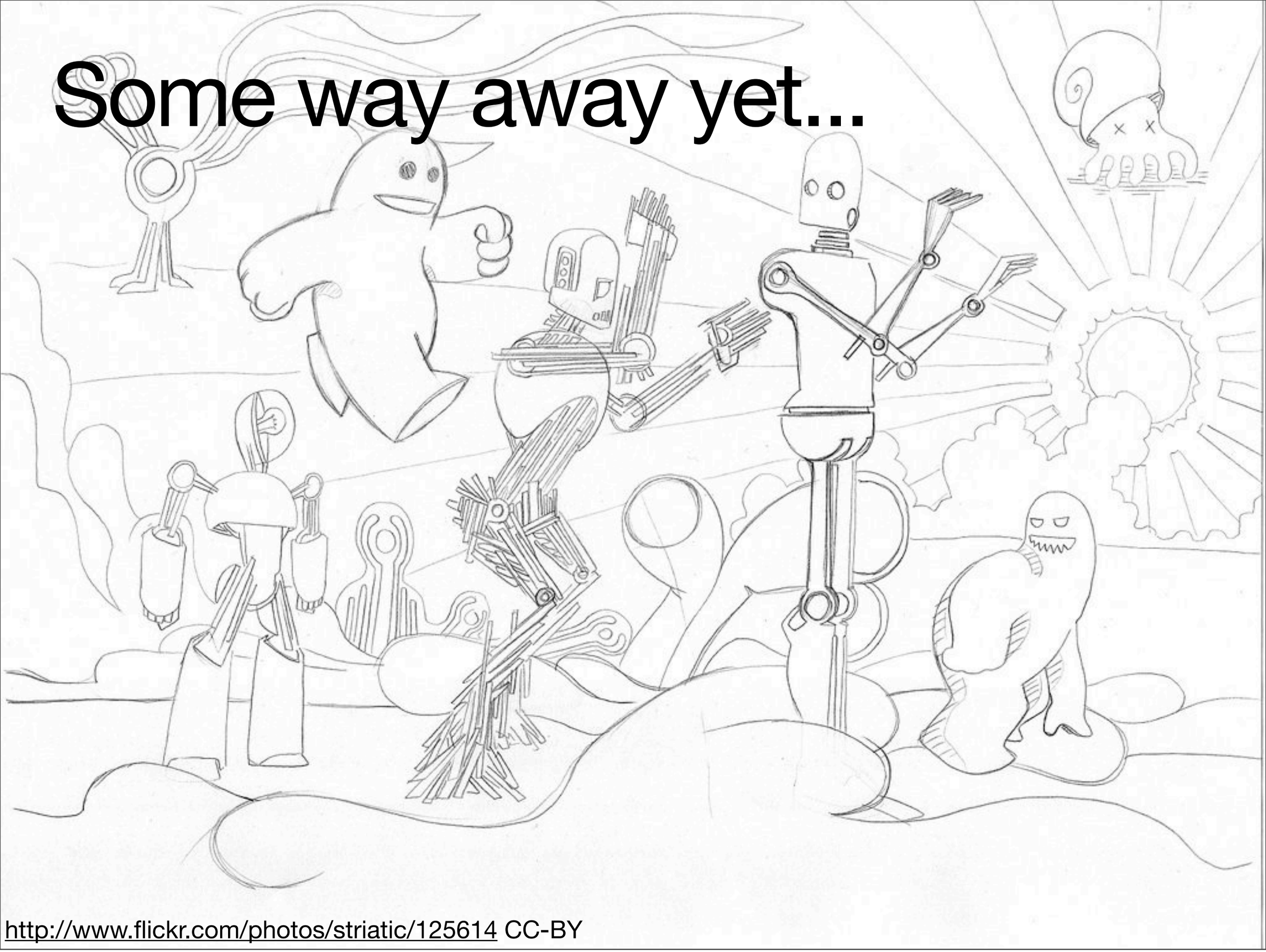


Workflows

Map Reduce/ Hadoop



Some way away yet...



http://www.flickr.com/photos/striatic/125614 CC-BY

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technologies...

p://www.flickr.com/photos/cappellmeister/39508741 CC-BY

Publication
Aggregation
Discovery

~~Publication~~

Aggregation

Discovery

~~Publication~~

~~Aggregation~~

Discovery

~~Publication~~

~~Aggregation~~

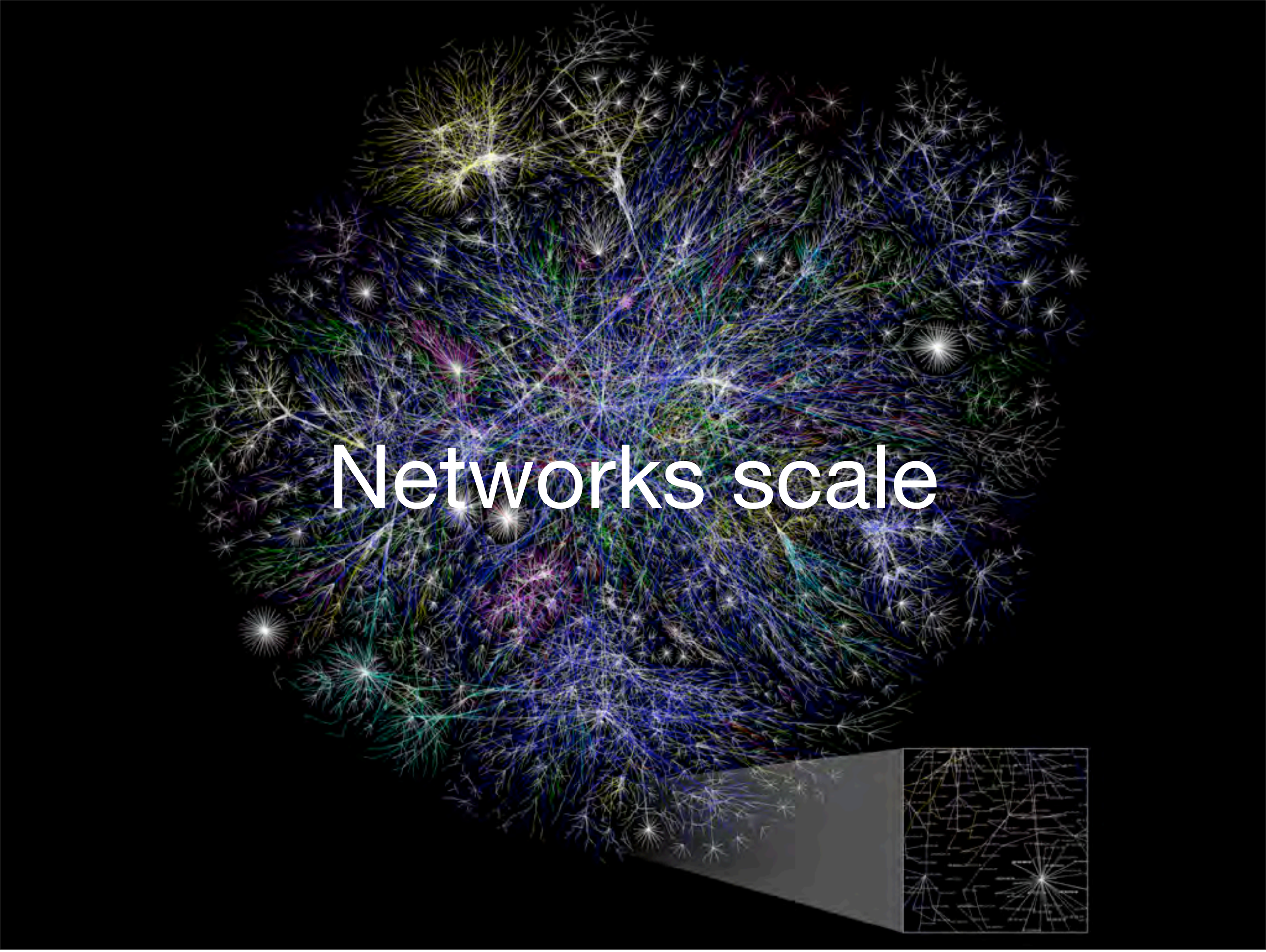
Discovery

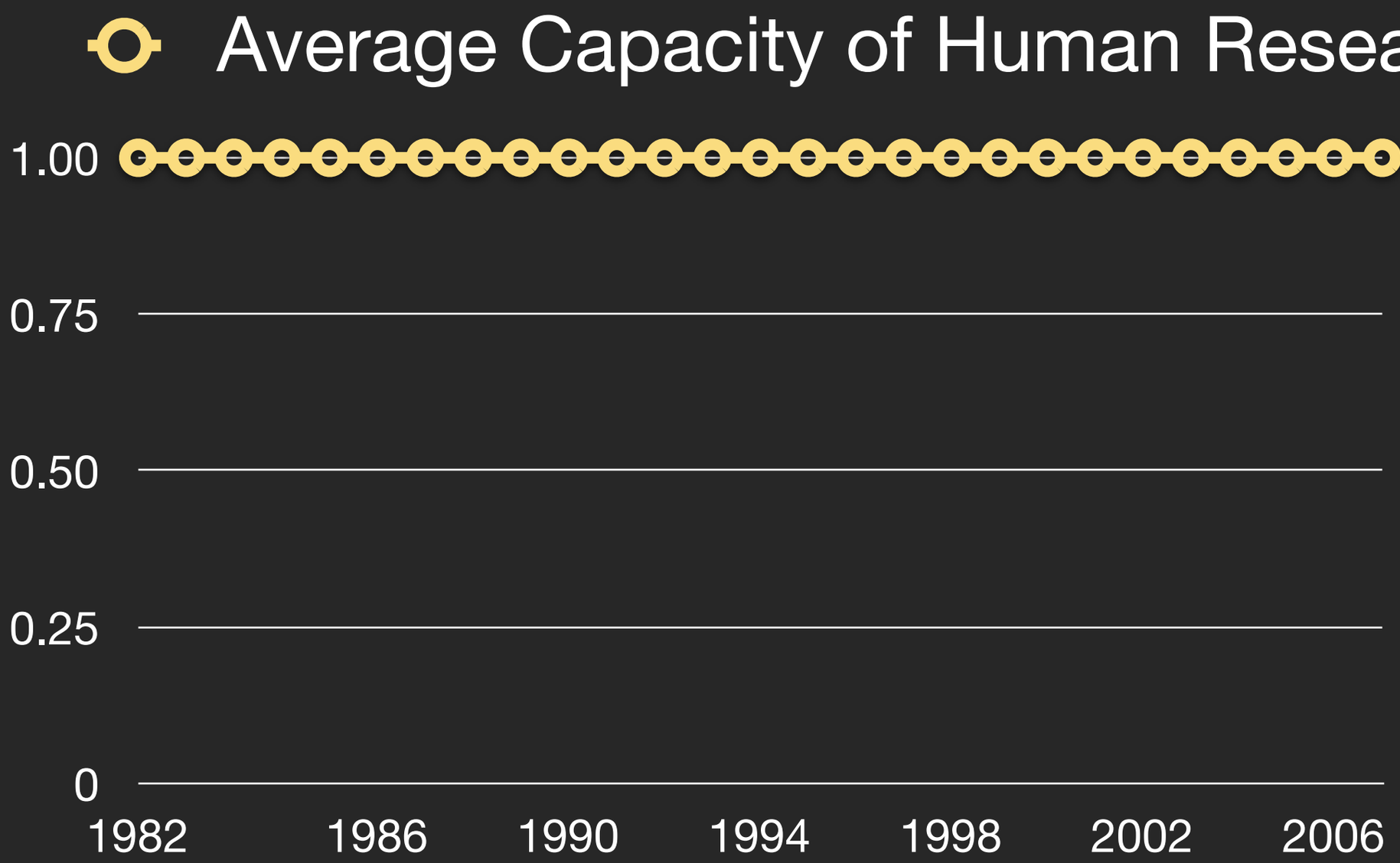
conceptual changes...

Publish pieces...then aggregate

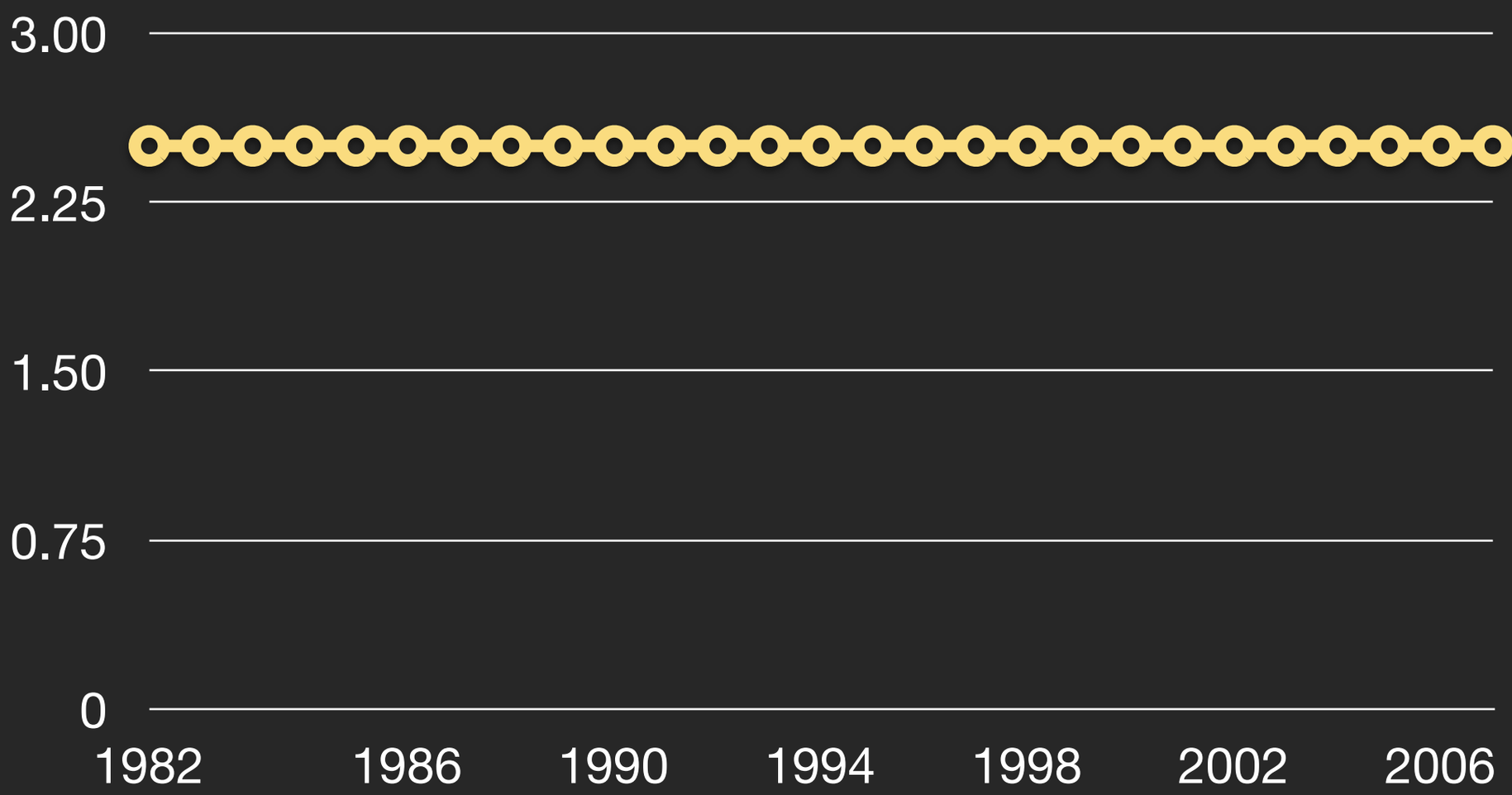
Don’t filter...enable discovery

Networks scale




Average Capacity of Human Researcher
1.00
0.75
0.50
0.25
0
1982
1986
1990
1994
1998
2002
2006

Average Capacity of Norwegian Researcher

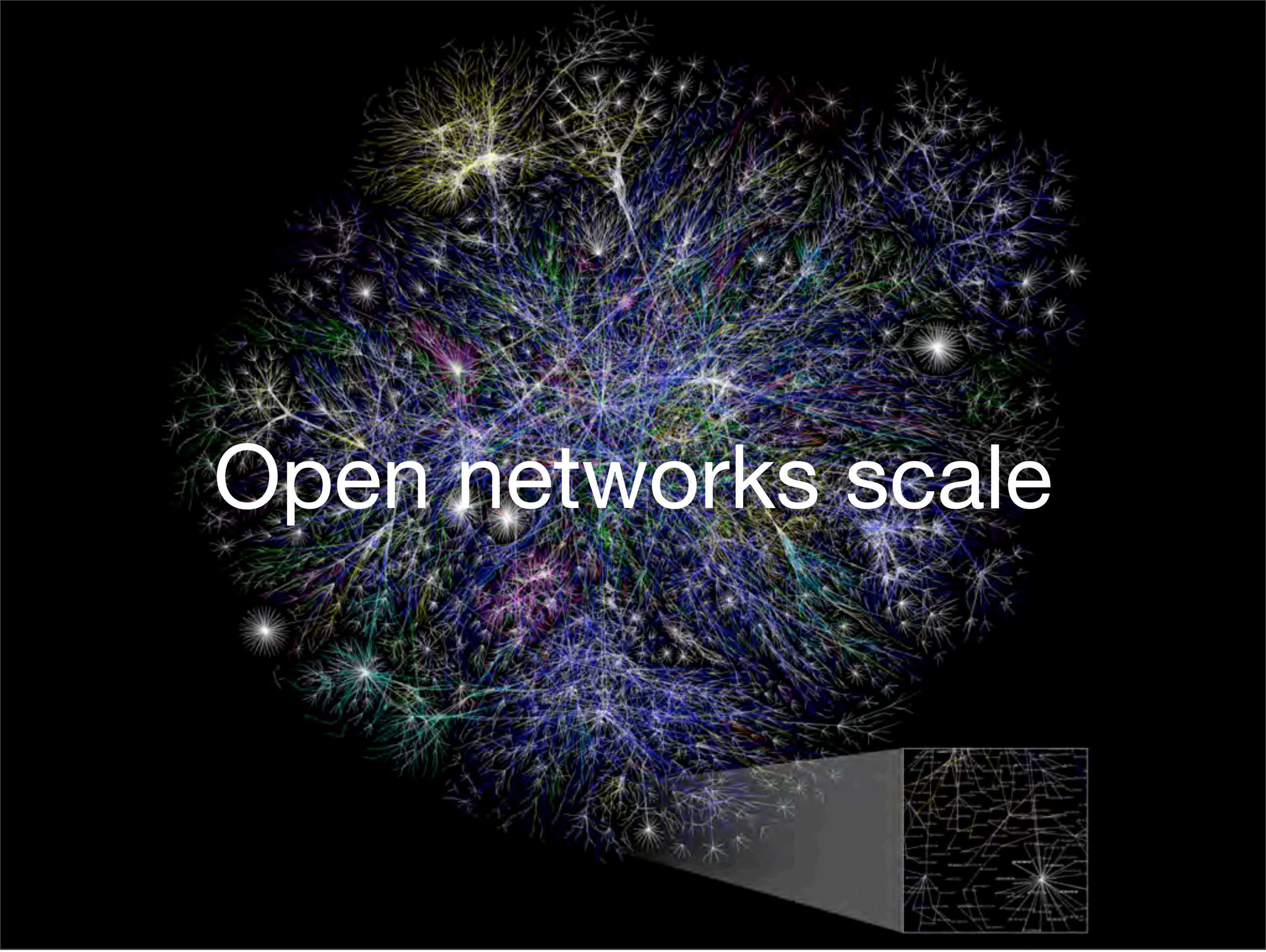


People don’t scale...

Neither do computers...

...at least not on their own

Open networks scale



http://www.flickr.com/photos/andypowe11/3759152528

We need...

http://flickr.com/photos/virtualsugar/316200555/ CC-BY


OPEN ACCESS

Open data...

http://www.flickr.com/photos/jwyg/4528443760/ CC-BY-SA

...but also...

...open platforms for innovation

Optimise for....

http://www.flickr.com/photos/tomarthur/3593729997

.....not this

http://www.flickr.com/photos/vrogy/514733529

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http://www.flickr.com/photos/biscuitsmlp/2247299538 CC-BY-SA


http://www.flickr.com/photos/tammra/2836906694/

Because every time a permanent job is advertised...

http://www.flickr.com/photos/t3rmin4t0r/3947963283 CC-BY

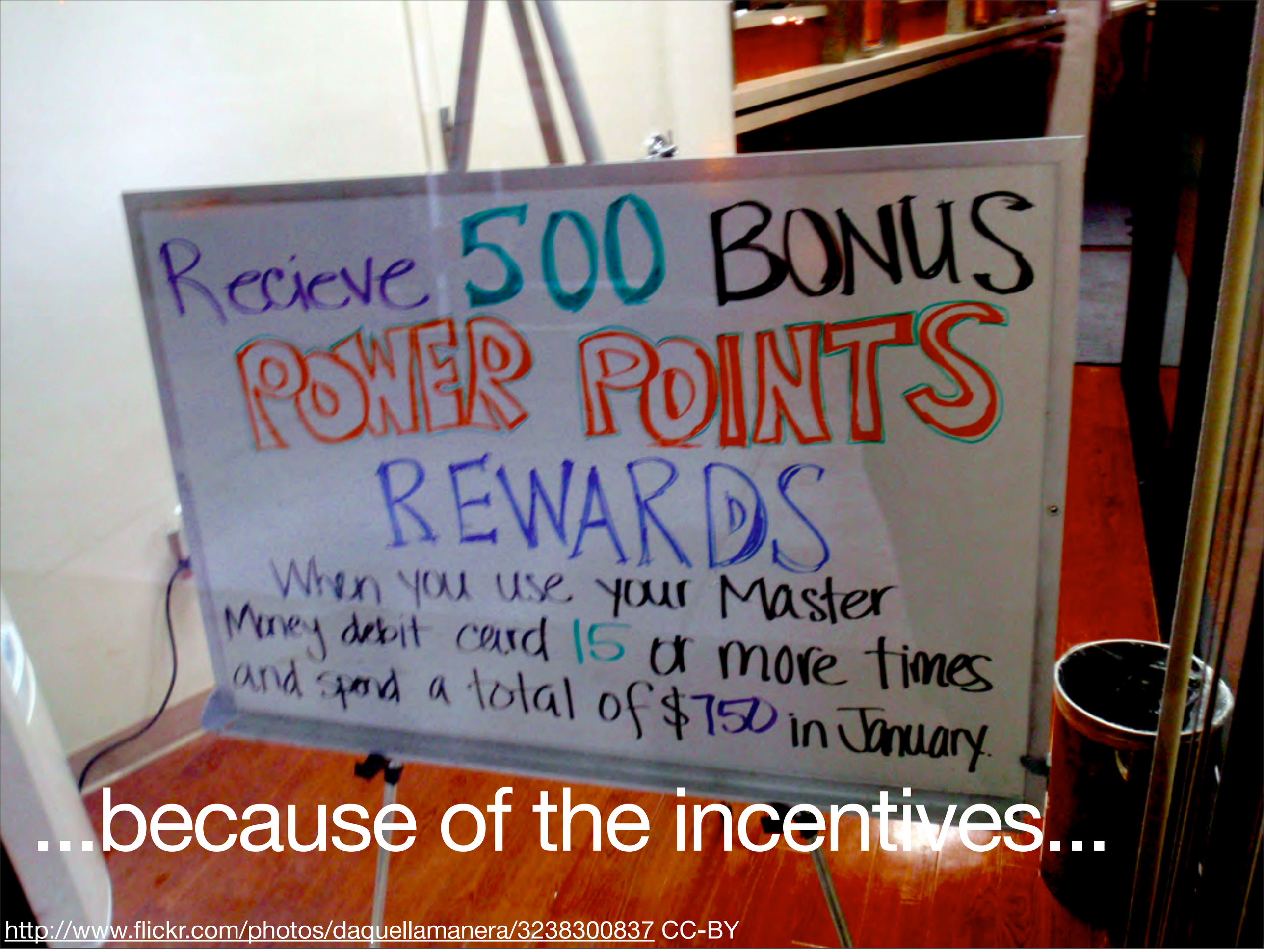
http://www.flickr.com/photos/t3rmin4t0r/3947963283 CC-BY

We optimise for...

http://www.flickr.com/photos/klausnahr/4437823757 CC-BY-SA

Rather than for use and re-use...

http://www.flickr.com/photos/frozenchipmunk/197591546 CC-BY



...because of the incentives...

http://www.flickr.com/photos/lifeontheedge/24[illegible]73398 CC-BY-SA

http://www.flickr.com/photos/turtlemom_nancy CC-BY-SA

We are stuck with “impact”...

...but we can mould it.

http://www.flickr.com/photos/waltstoneburner/5745387762 CC-BY

An assertion.

We want to see
research *used*.

In the right places...

http://www.flickr.com/photos/ol1/6048544977 CC-BY-SA

In the right places...

http://www.flickr.com/photos/velkr0/3472576304 CC-BY

http://www.flickr.com/photos/argonne/3465398655 CC-BY

...at the right time.

http://www.flickr.com/photos/robbie73/3387189144 CC-BY-SA

We want research to be re-used and *re-usable*

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Impact = Re-use

Application = Re-use

Commercialised = Re-use

Education = Re-use

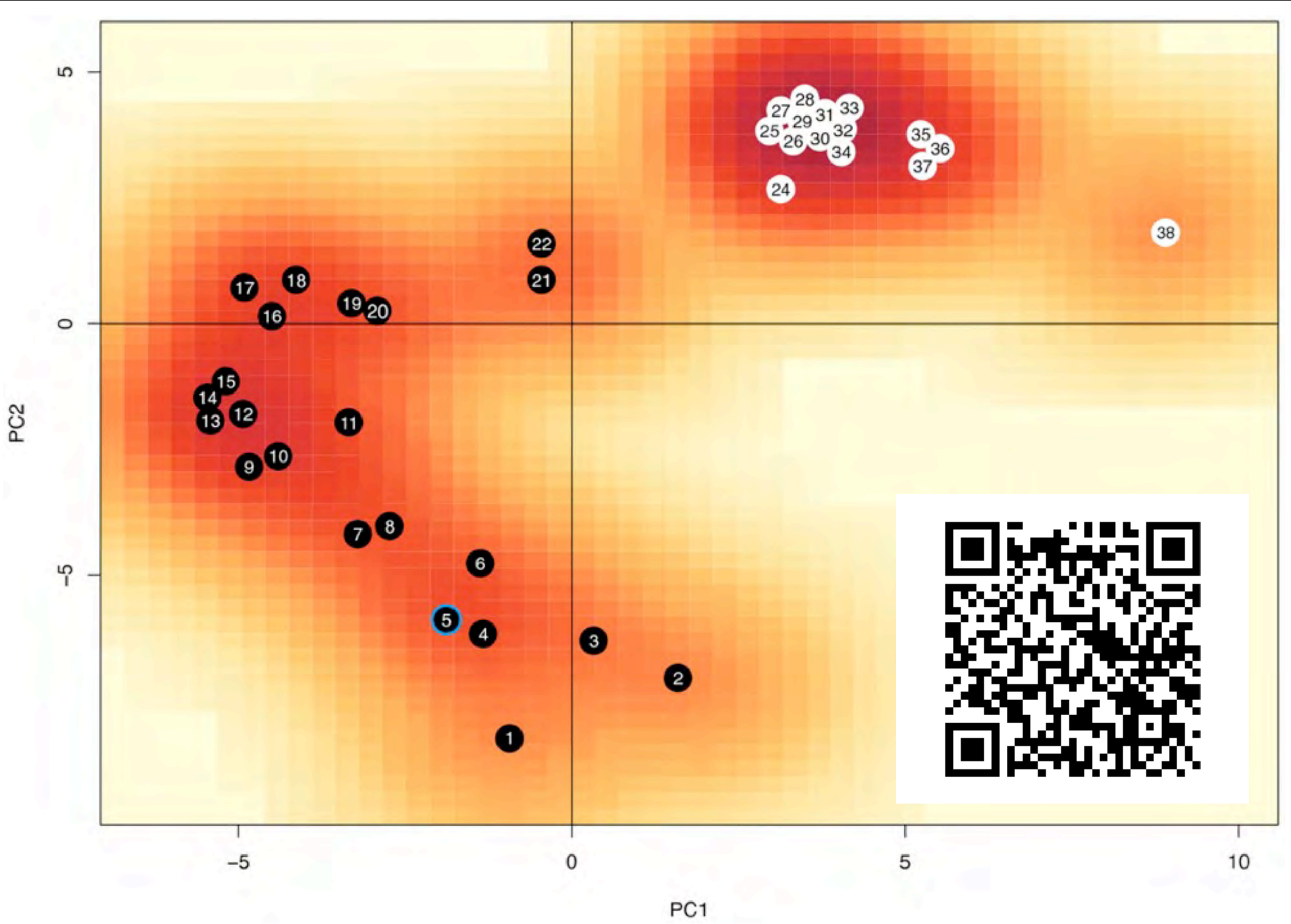
Engagement = Re-use

...but also...

Citation = Re-use

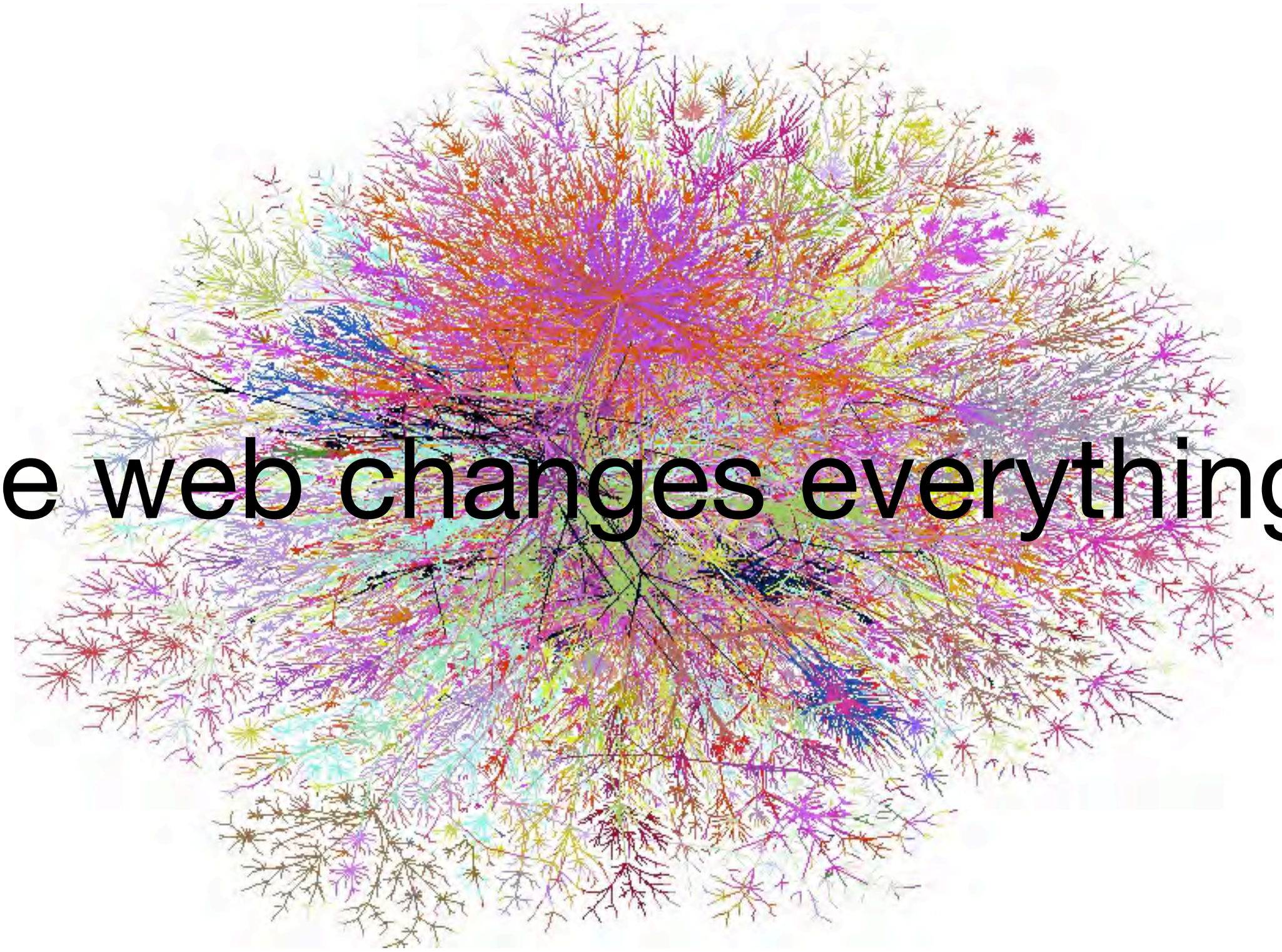
Can we measure re-use?

http://www.flickr.com/photos/sterlic/4299631538 CC-BY-SA

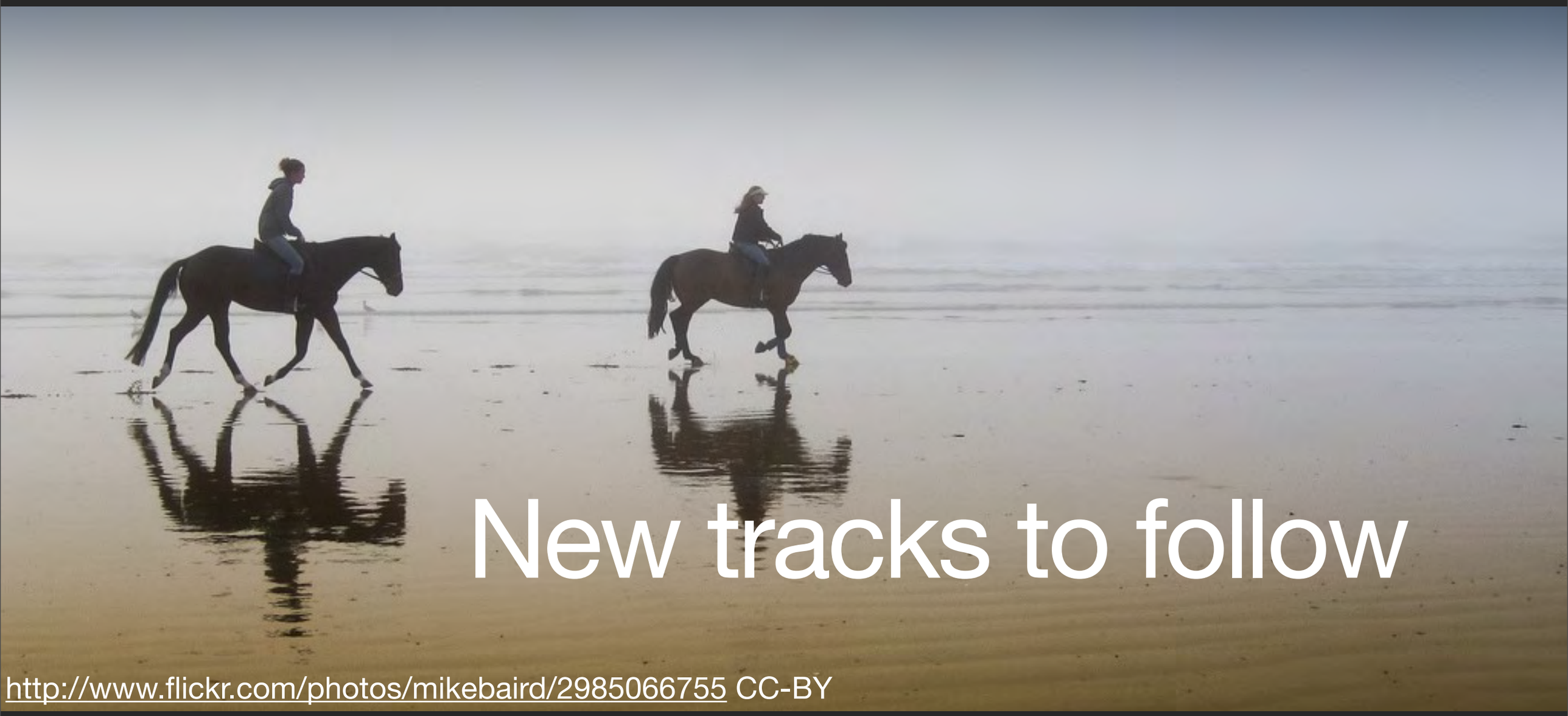


Bollen et al., PLoS ONE 4(6): e6022 doi:10.1371/journal.pone.0006022.g002

The web changes everything...



http://www.flickr.com/photos/jurvetson/916142 CC-BY



New tracks to follow

ScienceCard

Authors Groups Articles Journals About Sign out **Signed in as Cameron Neylon**

Cameron Neylon

N 55°56' 0" / W 3°11' 0"

Open Science, Open Access, and bringing more experimental techniques to the biosciences. I work for the UK STFC but tweets are my personal opinion.
http://cameronneylon.net

@CameronNeylon

cameronneylon

5646847

not set

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Small angle neutron and X-ray scattering in structural biology: recent examples from the literature European Biophysics Journal. 2008:37 (5);531-541 http://doi.org/d26 Cameron Neylon	4	24			4	16
Diffractive Micro Bar Codes for Encoding of Biomolecules in Multiplexed Assays Analytical Chemistry. 2008:80 (6);1902-1909 http://doi.org/d3v Cameron Neylon	1	5			6	15
Multistep Synthesis on SU-8: Combining Microfabrication and Solid-Phase Chemistry on a Single Material Journal of Combinatorial Chemistry. 2007:9 (3);462-472 http://doi.org/d6g	1	10			2	15

ScienceCard by Martin Fenner - http://sciencecard.org/CameronNeylon

Times of Flight between a Source and a Detector observed from a GPS satelite

relativity explains missing 64ns ; superluminal neutrinos now luminal. back to work. (h/t matt knepley)

Relax, neutrinos don't travel faster than light - flaw identified in the OPERA experimenters' analysis

Recommended reading for the thousands who believed the 'faster-than-light' neutrinos signalled the end of relativity

Faster-Than-Light Neutrino Puzzle Claimed Solved by Special Relativity arXiv

Vitamin E and the Risk of Prostate Cancer: The Selenium and Vitamin E Cancer Prevention Trial (SELECT)

JAMA: The Journal of the American Medical Association

JAMA Study: #VitaminE and the Risk of #ProstateCancer

Latest JAMA study shows vit E may ↑prostate cancer risk – sure, b/c they used 400 IU/d of all rac-α-tocopheryl acetate!

De acuerdo a nuevos estudio, consumo de #VitaminaE incrementa riesgo d

Yo se que dijeron que la vitamina E no incrementaba el riesgo de cancer, per opinion

Altmetric.com by Euan Adie - http://altmetric.com/interface/explorer.html

Bookmarks = Re-use

Discussion = Re-use

...and we can track them all

http://www.flickr.com/photos/paul_white/5831407787 CC-BY

...on an open network.

But what about...?

Maximise potential...

http://www.flickr.com/photos/pinksherbet/3370498053 CC-BY

...for discovery and re-use...

http://www.flickr.com/photos/pagedooley/3797236989 CC-BY

Measure re-use and re-usability...

Optimise for impact

http://www.flickr.com/photos/gsfc/6147894106 CC-BY

...and the easiest way...

http://www.flickr.com/photos/virtualsugar/316200555 CC-BY

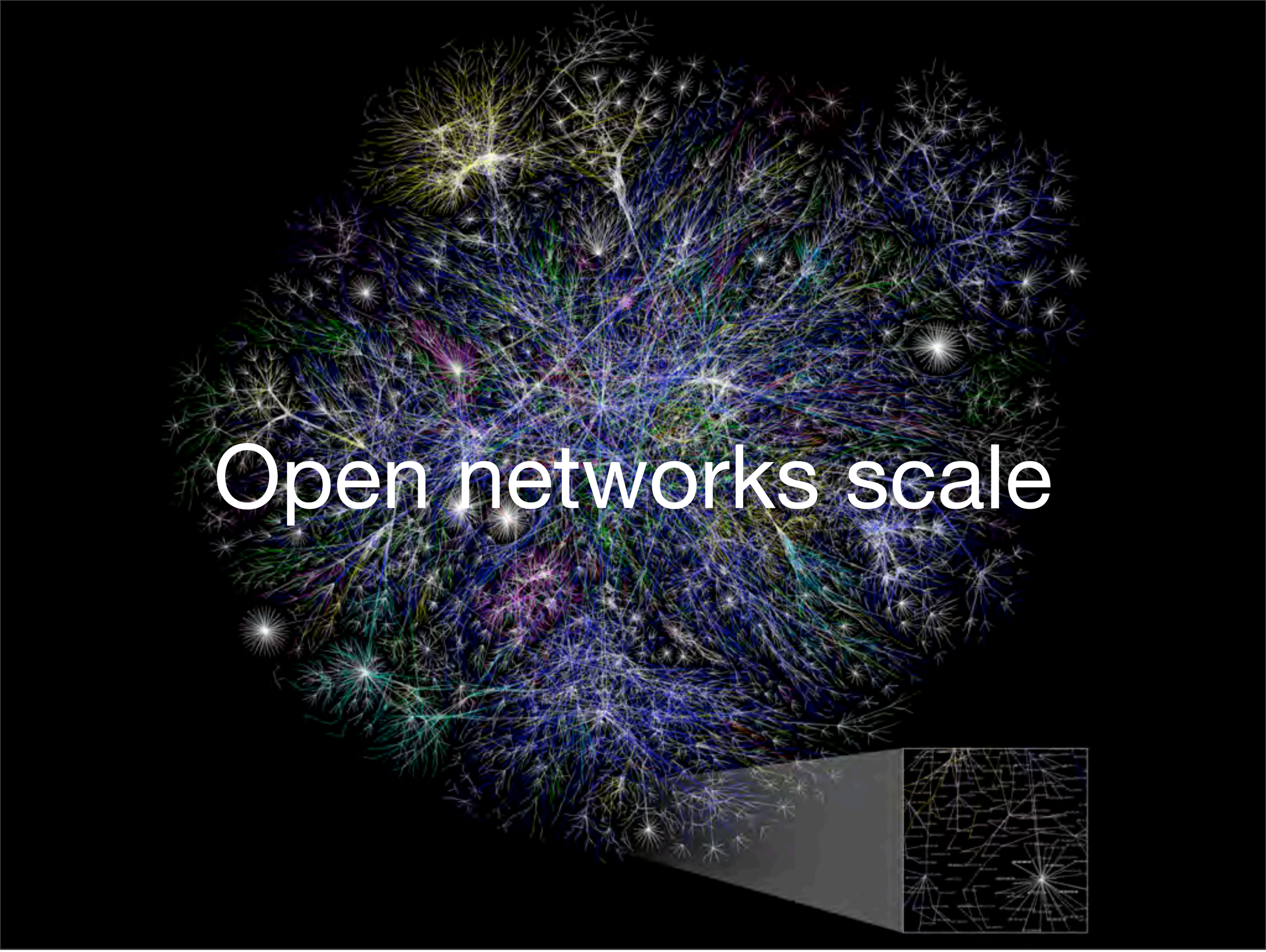
Not the only way.

...but the easiest and most common

http://www.flickr.com/photos/ehamiter/4607728796 CC-BY-SA

The solutions won’t come from where we expect...

Open networks scale



...enable solutions to discover problems...

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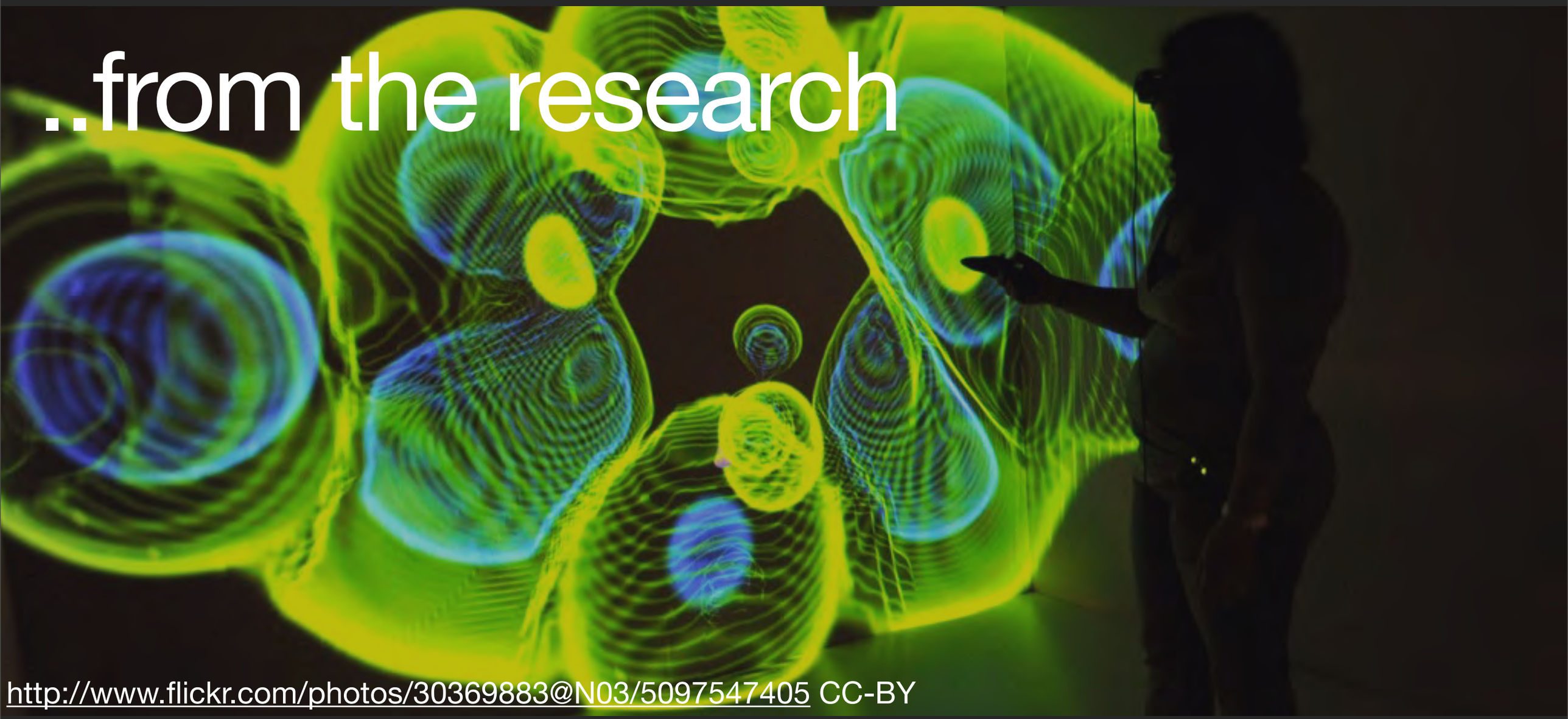
..from the research



http://www.flickr.com/photos/30369883@N03/5097547405 CC-BY

...to the technology...

...to the architecture

http://www.flickr.com/photos/yakobusan/2436481628 CC-BY

Build open networks...

http://www.flickr.com/photos/22746515@N02/4468871811 CC-BY

Enable discovery...

http://www.flickr.com/photos/pagedooley/2836337974 CC-BY

The rest will follow...

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