

knowledge sharing in the sciences

kaitlin thaney

program manager, science commons
costa rica - aCCCeso - 11 nov 2009



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xi.

open science,
knowledge sharing,
and the commons



make sharing easy, legal and scalable

integrated approach

**building part of the infrastructure for
knowledge sharing**

knowledge sharing is at the root of
scholarship and science

the system of print publishing is a
system of sharing knowledge

then came the ***move to digital ...***

knowledge sharing

journal articles

data

ontologies

annotations

plasmids and cell lines

knowledge sharing

journal articles

data

ontologies

annotations

plasmids and cell lines

access is step one

content needs to be ***legally*** and
technically accessible

indexing, translation, redistribution: disallowed

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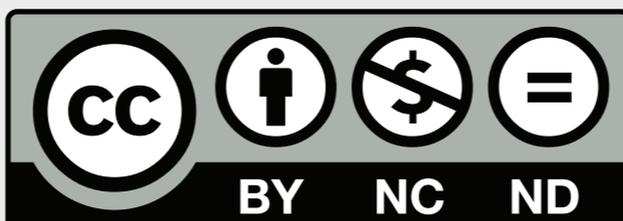
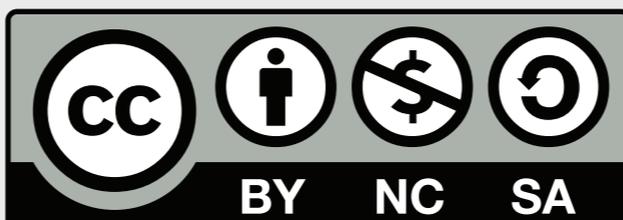
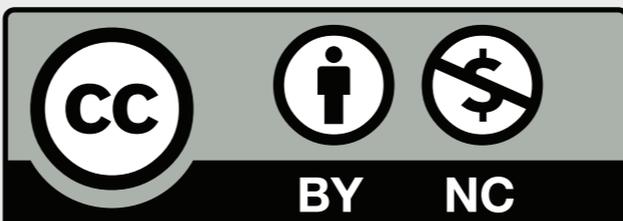
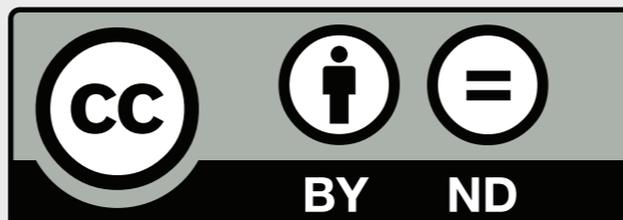
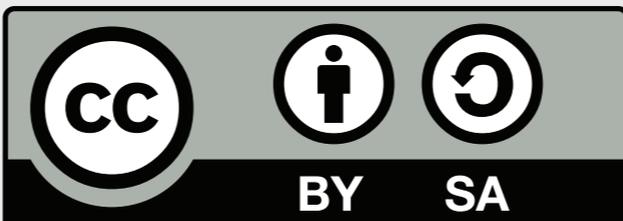
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knowledge sharing

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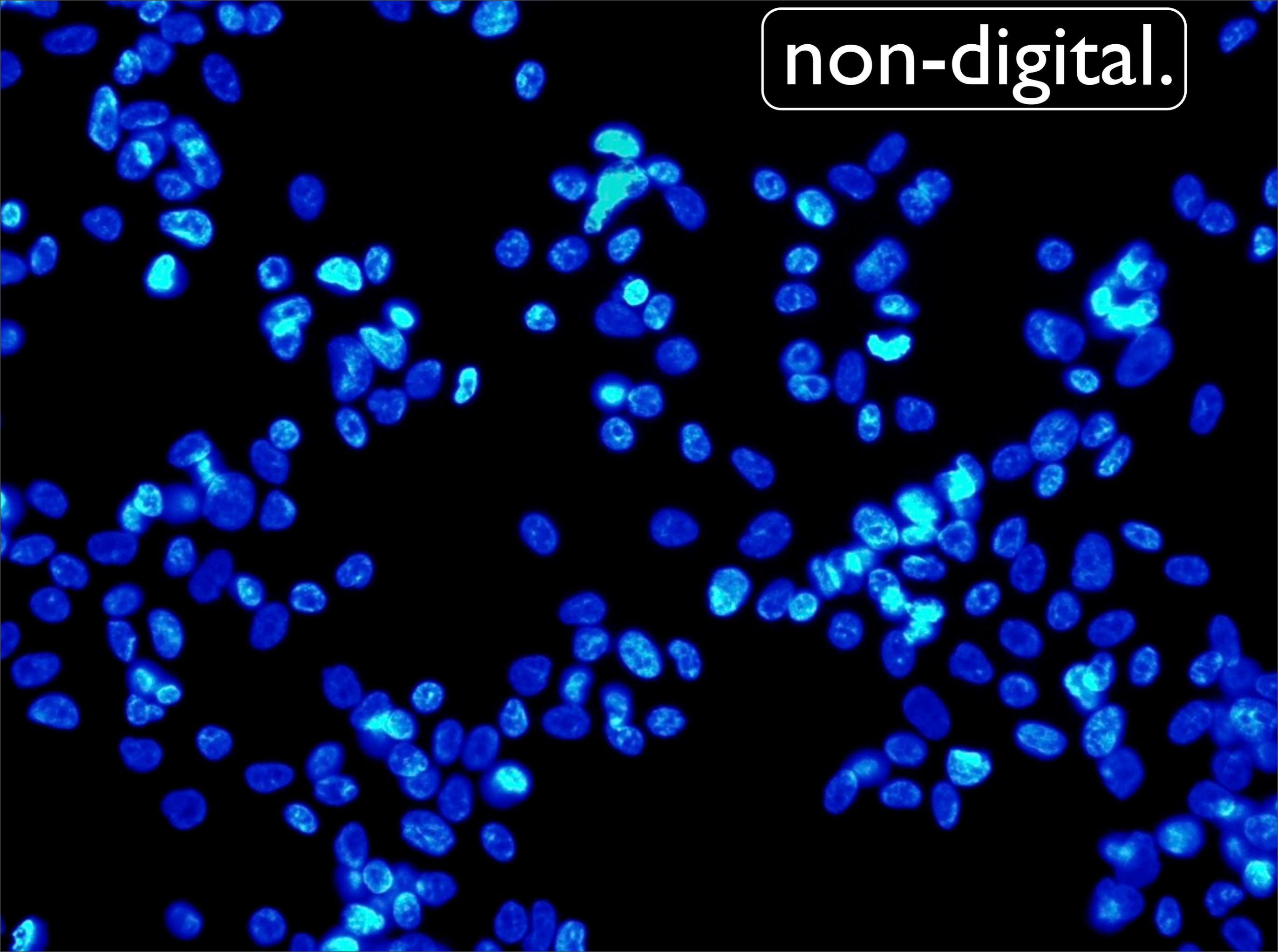
annotations

plasmids and cell lines



... what about the
physical
materials?

non-digital.



non-digital.



non-digital.



ideally ...

contact author, obtain material,
recreate experiment

build on the existing work, publish

and ***repeat ...***

the reality ...

**materials difficult to find, fulfill, lack
resources**

**reagents and assays often re-invented
or reverse engineered**

**locked in contracts, bureaucracy,
deliberate withholding, “club mentality”**



solves the access problem via
contract

(standardized material
transfer agreements, or
MTAs)



standard icons, CC
methodology, metadata



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scientist

 **science commons**

Uniform Biological Material Transfer Agreement
ubmta 1.0

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lawyer

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(dated March 8, 1995)

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- UNMODIFIED DERIVATIVES:** Substances created by the RECIPIENT which constitute an unmodified functional subunit or product expressed by the ORIGINAL MATERIAL. Some examples include: subclones of unmodified cell lines, purified or fractionated subsets of the ORIGINAL MATERIAL, proteins expressed by DNA/RNA supplied by the PROVIDER, or monoclonal antibodies secreted by a hybridoma cell line.
- MODIFICATIONS:** Substances created by the RECIPIENT which contain/incorporate the MATERIAL.
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machine

```
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xmlns:rdfs="http://www.w3.org/2000/01/rdf-schema#"
xmlns:dc="http://purl.org/dc/elements/1.1/"
xmlns:dcq="http://purl.org/dc/terms/">
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disease
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<permits rdf:resource="http://web.resource.org/cc/Retention" />
</TransferAgreement>
```

knowledge sharing

journal articles

data

ontologies

annotations

plasmids and cell lines

... how to treat? like content? software?

the data web



as a means to achieve Open Access
but what about ***data***?

I.

**three layers of resistance:
technical, semantic, legal**

[IngentaConnect Gene expression in developing rat hippocampal ...](#)

In the absence of mossy fiber input, the CA3 **pyramidal neurons** exhibit ... of a number of **genes** involved in activity-dependent **signal transduction**, ...

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DARPP-32 is specifically localized to **neurons** containing dopamine Citation: H. K. Manji, I. I. Gottesman, T. D. Gould, **Signal Transduction** and ...

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[Biological Research - Signal transduction and gene expression ...](#)

Signal transduction and **gene** expression regulated by calcium release from presynaptic long-term potentiation in hippocampal CA1 **pyramidal neurons**. ...

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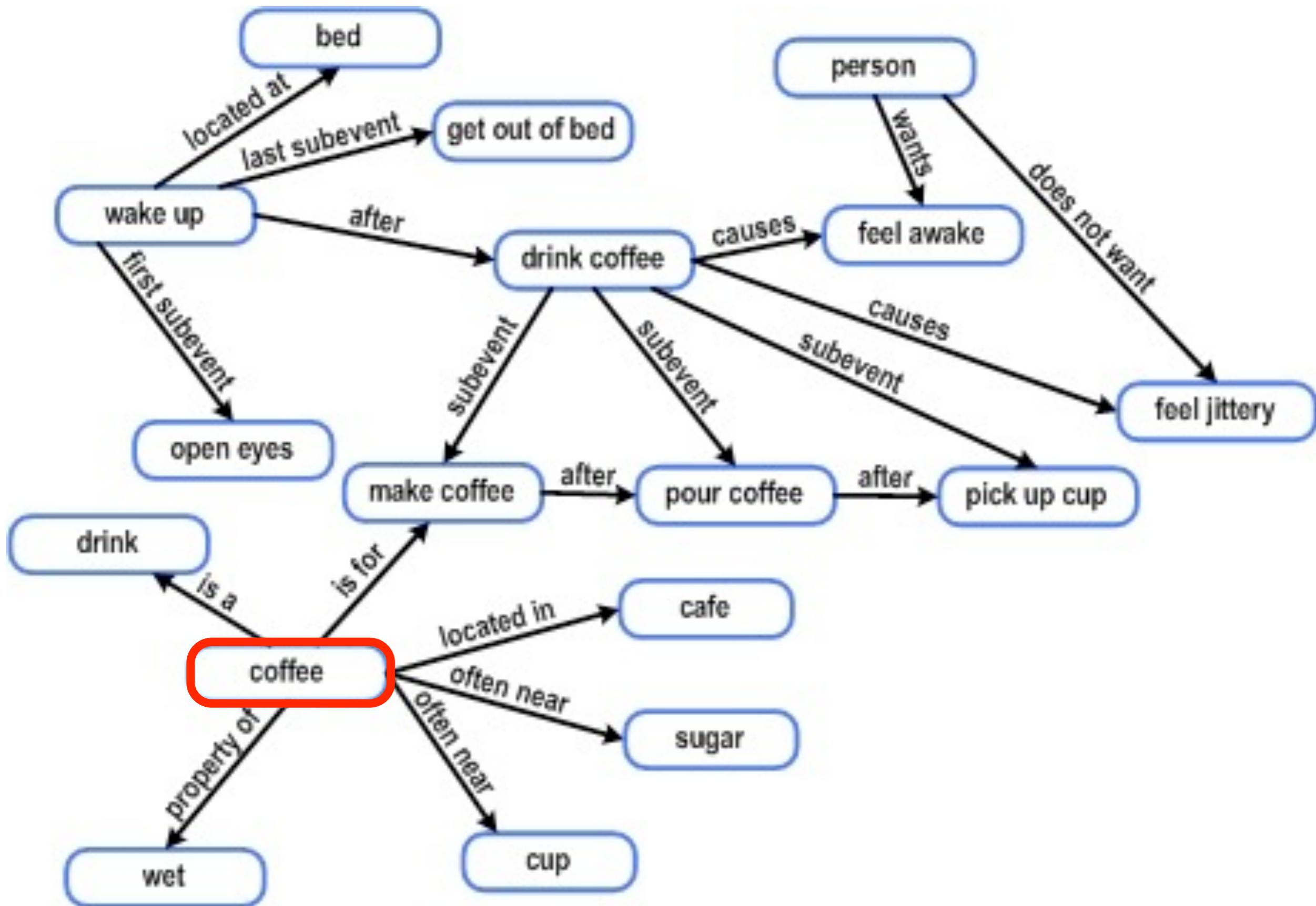
“read 189,000 papers” is *not* the ideal answer.

social* and *semantics

agreement
is hard.







espresso

coffee

cafe

kopi

cafezinho

latte

koffee

mocha

americano

“choice” or interoperability.

(pick one)

converge on common names



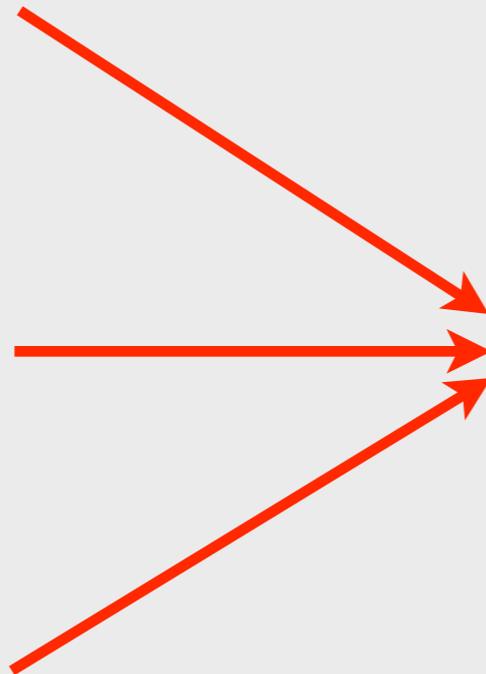
“coffee”



“cafe”



“kopi”



<http://ontology.foo.org/1234567>

Shared Names

Introduction

Community-wide use of shared names for records from public databases could have a significant effect on the practice of bioinformatics by making it easier to share and link data sets and tools across projects. While publishing data in RDF is appealing to many organizations, the mechanics of selecting and maintaining identifiers is a major obstacle to deployment. A growing body of experience emphasizes that for any solution to be generally adopted it must not only be technically sound, but also serve the practical needs of curators and other users. The Shared Names initiative has as its mission to assign URIs as names for publicly available biomedical information records and establish a community managed shared infrastructure for providing durable access to documentation about these names, as described in a set of requirements. The scope of resources under consideration is initially limited to records in databases, such as those mentioned in the external links (dbxrefs) from the Gene Ontology (GO), for records from Enzyme or Pfam. A proposed implementation uses federated PURL servers that provide RDF-encoded metadata that clearly specifies what the URI denotes and that links the shared names to alternative encodings and associated information about the records.

- [Project overview](#)
- [Public discussion group](#)
- [Steering committee](#)
- [Steering committee process](#)
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- [Discussion pages](#)

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About Shared Names

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Diabetes and tuberculosis: the impact of the diabetes epidemic on tuberculosis incidence

Catherine R Stevenson, Nita G Forouhi, Gojka Roglic, Brian G Williams, Jeremy A Lauer, Christopher Dye, Nigel Unwin

BMC Public Health. 2007; 7:234

Background

Tuberculosis (TB) remains a major cause of death in many developing countries. In many countries diabetes prevalence is increasing. Our aim was to assess the potential impact of diabetes on tuberculosis incidence, using India as an example.

Methods

We constructed an epidemiological model using data on tuberculosis incidence, diabetes prevalence, population structure, and relative risk of tuberculosis associated with diabetes. We evaluated the contribution made by diabetes to both tuberculosis incidence, and to the difference between tuberculosis incidence in urban and rural areas.



[IngentaConnect Gene expression in developing rat hippocampal ...](#)

In the absence of mossy fiber input, the CA3 **pyramidal neurons** exhibit ... of a number of **genes** involved in activity-dependent **signal transduction**, ...

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Signal Transduction and **Genes-to-Behaviors**. Pathways in Psychiatric Diseases frontal cortical **pyramidal neurons** in schizophrenia: Differential effects ...

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Signal transduction and **gene** expression regulated by calcium release from presynaptic long-term potentiation in hippocampal CA1 **pyramidal neurons**. ...

www.scielo.cl/scielo.php?pid=S0716-97602004000400028&script=sci_arttext - 83k -

better answers through better formats:

Mesh: Pyramidal Neurons



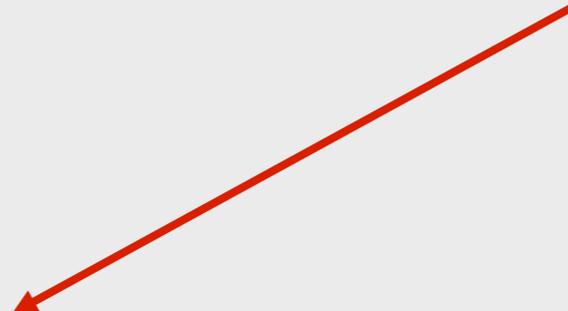
Pubmed: Journal Articles



Entrez Gene: Genes



GO: Signal Transduction

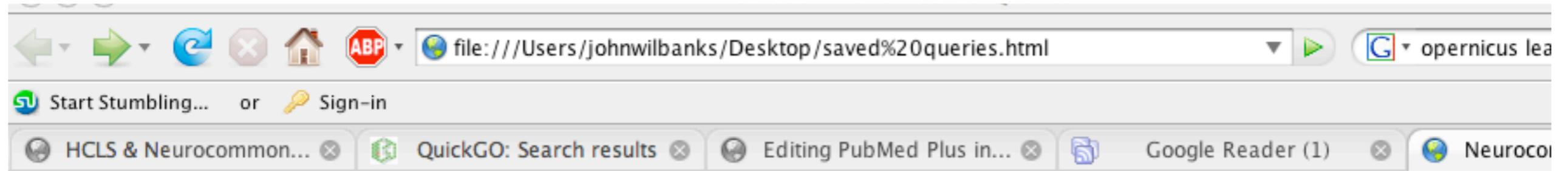


```
select ?gene_name ?process_name
where
{ PropertyValue(?pubmed_record, ?p, mesh:D017966)
  PropertyValue(?article, sc:identified_by_pmid, ?pubmed_record)
  PropertyValue(?gene_record, sc:describes_gene_or_gene_product_mentioned_by, ?article)
  SubClassOf(?protein, some(ro:has_function, some(ro:realized_as, ?process)))
  SubClassOf(?process, or(go:GO_0007166, some(ro:part_of, go:GO_0007166))
  SubClassOf(?protein, some(sc:is_protein_gene_product_of_dna_described_by, ?gene_record))
  Annotation(?gene_record, rdfs:label, {?gene_name})
  Annotation(?process, rdfs:label, ?process_name)
}
```

DRD1, 1812
ADRB2, 154
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DRD1IP, 50632
DRD1, 1812
DRD2, 1813
GRM7, 2917
GNG3, 2785
GNG12, 55970
DRD2, 1813
ADRB2, 154
CALM3, 808
HTR2A, 3356
DRD1, 1812
SSTR5, 6755
MTNR1A, 4543
CNR2, 1269
HTR6, 3362
GRIK2, 2898
GRIN1, 2902
GRIN2A, 2903
GRIN2B, 2904
ADAM10, 102
GRM7, 2917
LRP1, 4035
ADAM10, 102
ASCL1, 429
HTR2A, 3356
ADRB2, 154
PTPRG, 5793
EPHA4, 2043
NRTN, 4902
CTNND1, 1500

adenylate cyclase activation
adenylate cyclase activation
arrestin mediated desensitization of G-protein coupled receptor protein signaling pathway
dopamine receptor signaling pathway
dopamine receptor, adenylylase activating pathway
dopamine receptor, adenylylase inhibiting pathway
G-protein coupled receptor protein signaling pathway
G-protein signaling, coupled to cyclic nucleotide second messenger
glutamate signaling pathway
glutamate signaling pathway
glutamate signaling pathway
glutamate signaling pathway
integrin-mediated signaling pathway
negative regulation of adenylylase activity
negative regulation of Wnt receptor signaling pathway
Notch receptor processing
Notch signaling pathway
serotonin receptor signaling pathway
transmembrane receptor protein tyrosine kinase activation (dimerization)
transmembrane receptor protein tyrosine kinase signaling pathway
transmembrane receptor protein tyrosine kinase signaling pathway
transmembrane receptor protein tyrosine kinase signaling pathway
Wnt receptor signaling pathway

turn ugly query code into a link



Saved Queries: Neurocommons

[Show me all signal transduction genes on the cell surface in pyramidal neurons](#)

social barriers:

protection instinct / culture of control

quality control, ***integrity*** concerns

“my data”, ***interpretation*** issues

fear, uncertainty, doubt (***FUD***)

the data “*rights*” conundrum...

implications of FLOSS toggles

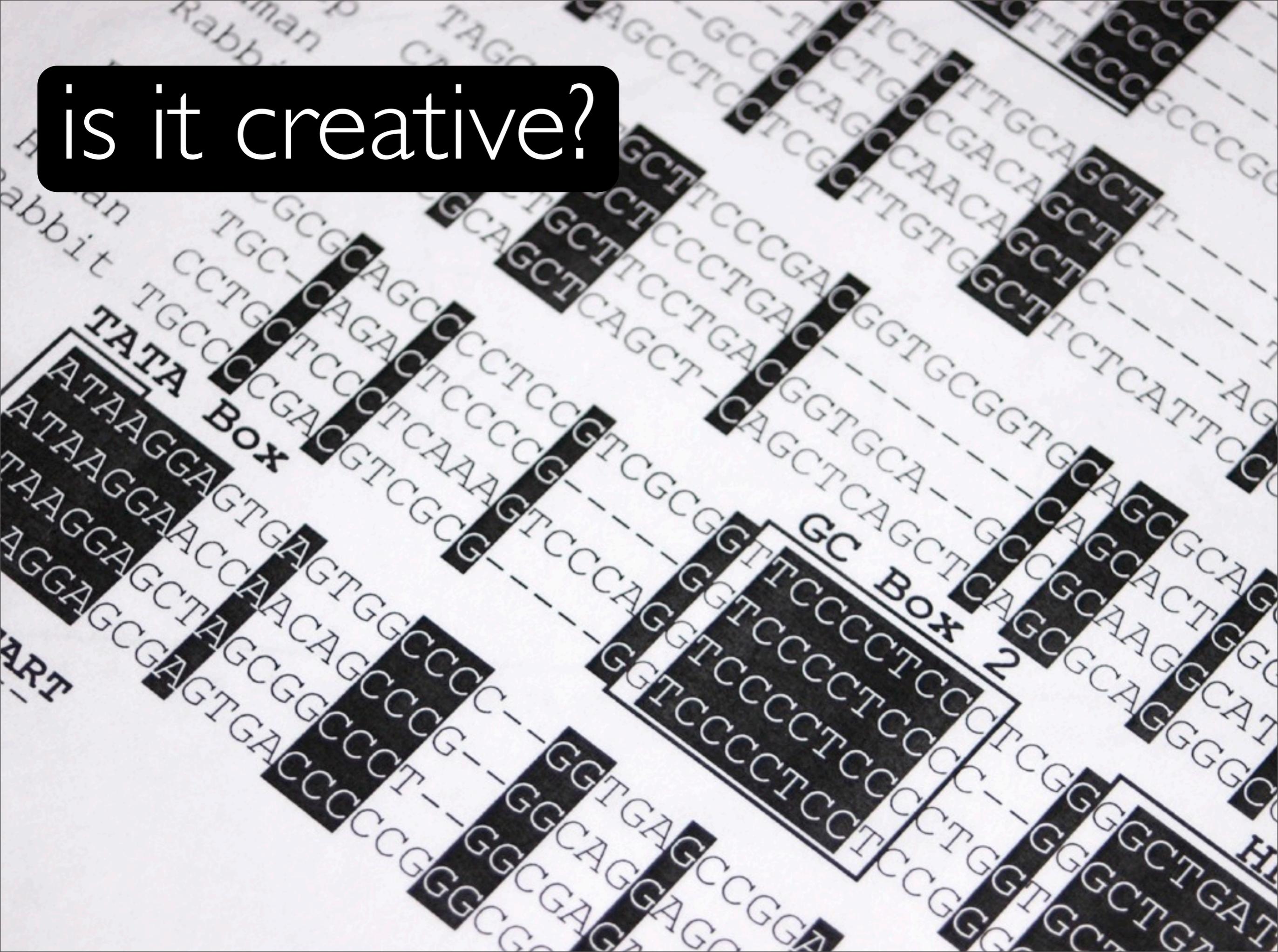


“creative expression”

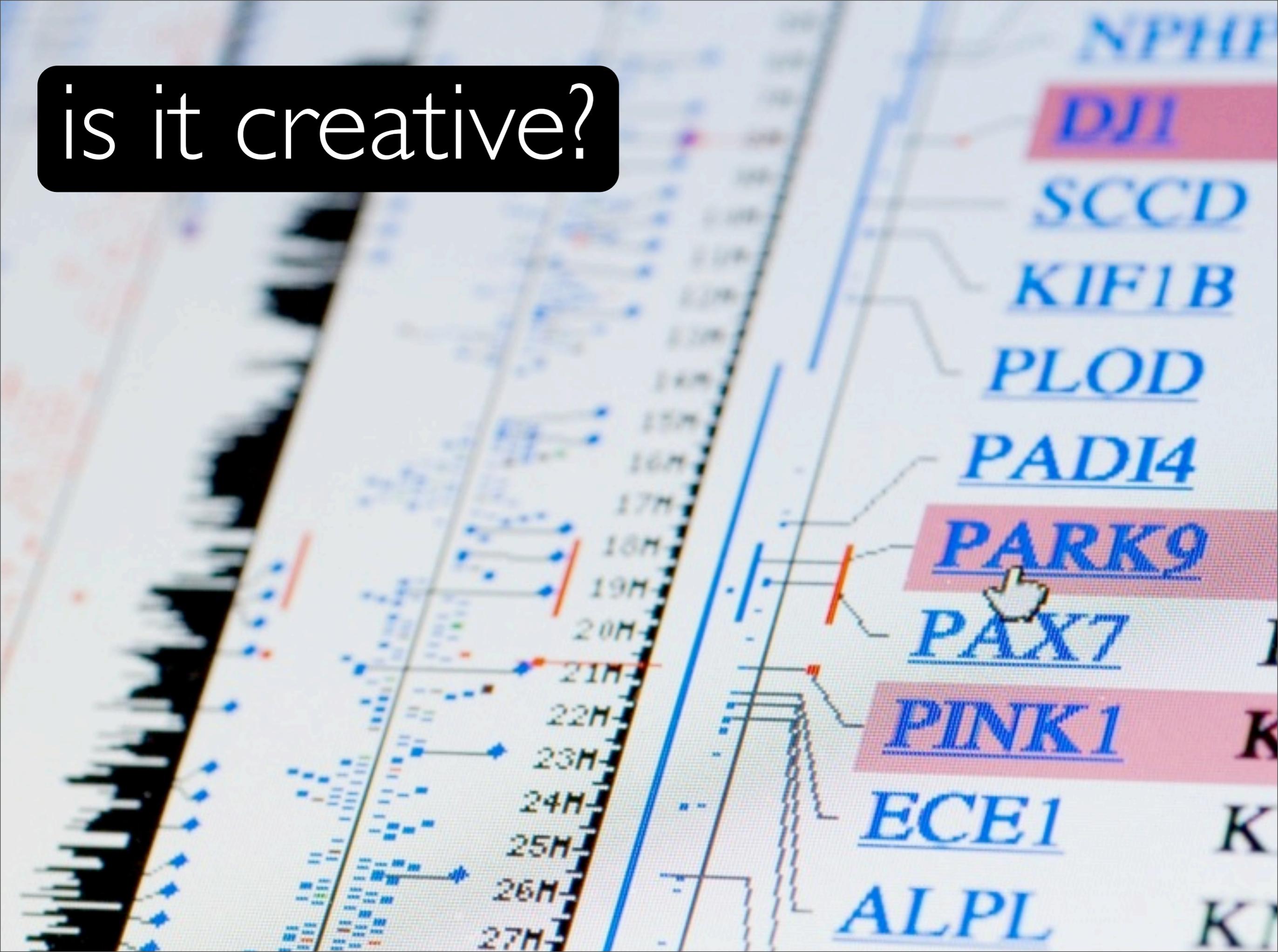
is it creative?



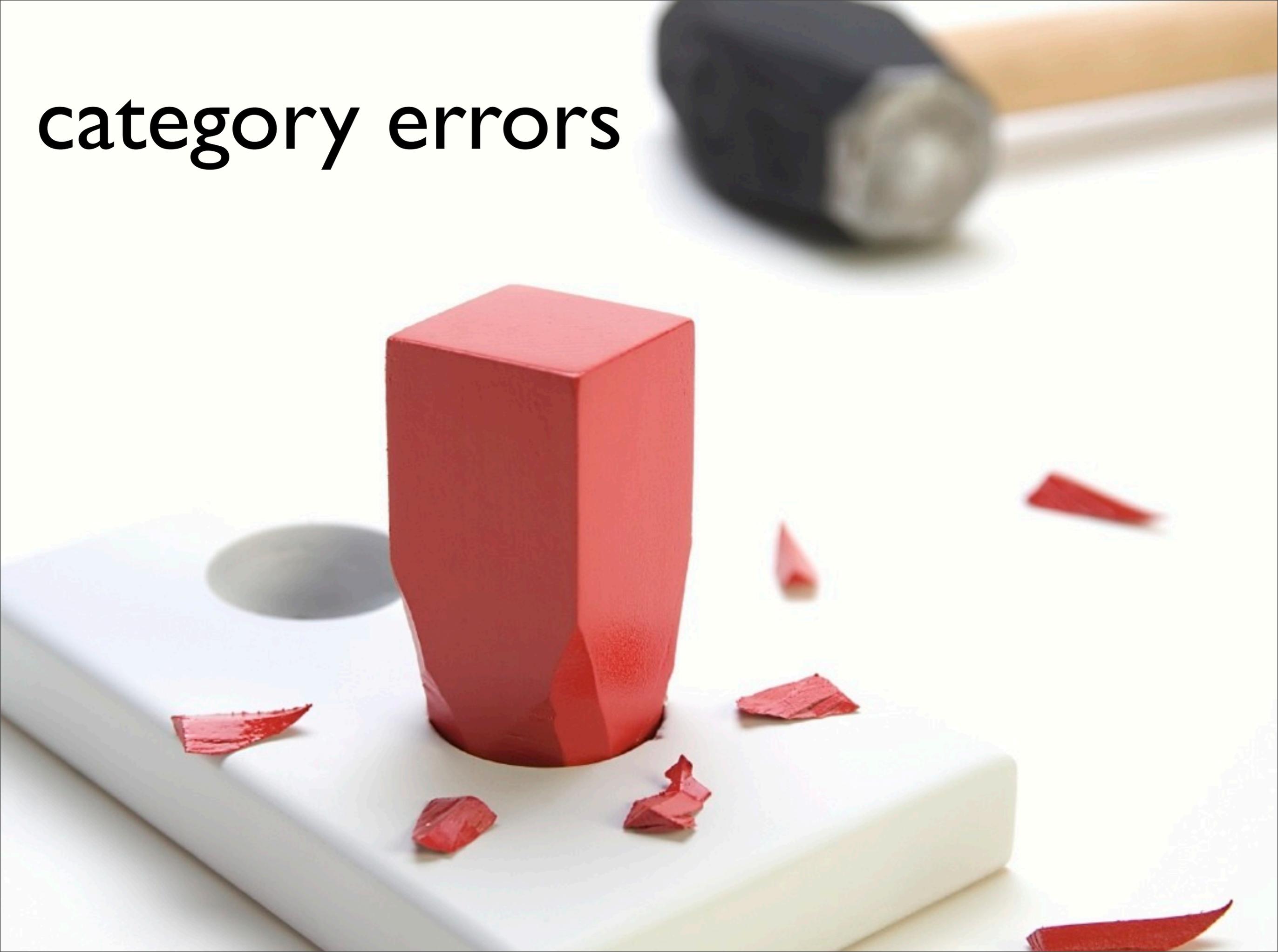
is it creative?



is it creative?



category errors



the problem of...



Non-Commercial

for data



Non-Commercial

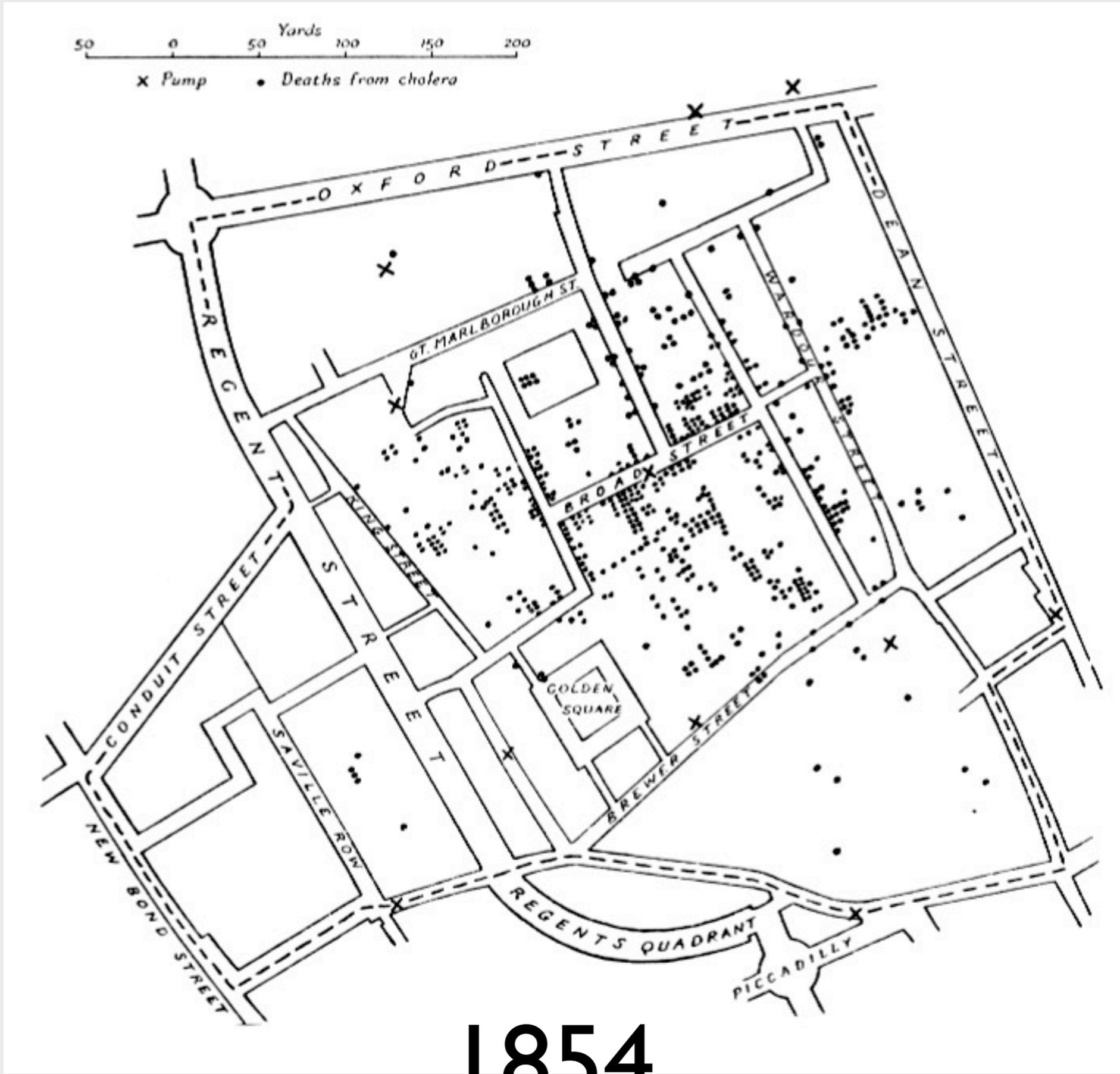
**what's a commercial use
of the data web?**

the problem of...



Share Alike

for data



1854

issue of ***license proliferation***

whatever you do to the least of the
databases, you do to the integrated system

(the most restrictive wins)

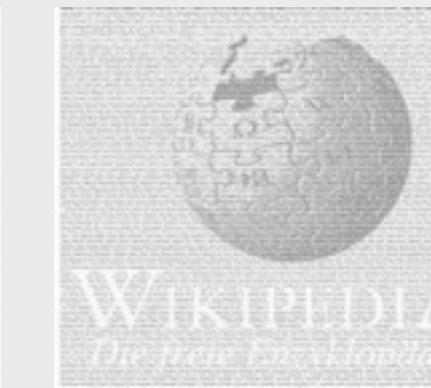
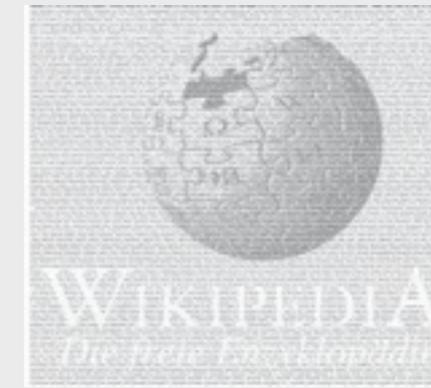
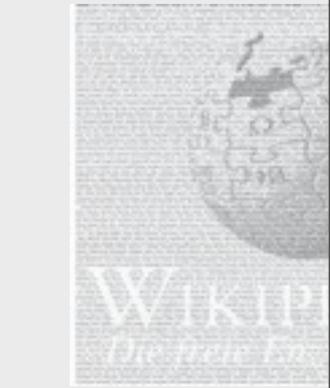
risk for unintended consequences

the problem of...



Attribution

for data



the problem of...

any license

for data

national law / jurisdiction-based hurdles

sui generis,
“sweat of the brow”
Crown copyright
“level of skill”

***how internat'l data sharing efforts
are affected?***

attribution vs. citation

which one applies? which is best fit?
what's the difference?

“credit where credit is due”

attribution:
(*legal entity*)

“triggered by making of a copy”

does it apply to facts?

how to attribute? (papers, ontologies, data)

“in a manner specified by ...”

attribution stacking

citation:
(gentle(wo)man's club)

legal requirement?
interoperability?
credit where credit is due
entrenched scientific norm

we ***shouldn't*** use the law to make it
hard to do the ***wrong*** thing ...

need for a ***legally accurate*** and
simple solution

reducing or eliminating the need to
make the distinction of what's protected

requires modular, ***standards based***
approach to licensing

Licenses that can be used for derivative work or adaptation

	Licenses that can be used for derivative work or adaptation						
Original Work	by	by-nc	by-nc-nd	by-nc-sa	by-nd	by-sa	pd
pd	Green	Green	Green	Green	Green	Green	Green
by	Green	Green	Green	Green	Green	Green	
by-nc		Green	Green	Green			
by-nc-nd							
by-nc-sa				Green			
by-nd							
by-sa						Green	

Licenses that can be used for derivative work or adaptation

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Original Work	by	by-nc	by-nc-nd	by-nc-sa	by-nd	by-sa	pd
pd	Green	Green	Green	Green	Green	Green	Green
by	Green	Green	Green	Green	Green	Green	
by-nc		Green	Green	Green			
by-nc-nd							
by-nc-sa				Green			
by-nd							
by-sa						Green	



converge on the public domain

Protocol for Implementing Open Access Data

Status of this Memo

This memo provides information for the Internet community interested in distributing data or databases under an "open access" structure. There are several definitions of "open" and "open

1. Intellectual foundation for the protocol

The motivation behind this memorandum is interoperability of scientific data.

The volume of scientific data, and the interconnectedness of the systems under study, makes integration of data a necessity. For example, life scientists must integrate data from across biology and chemistry to comprehend disease and discover cures, and climate change scientists must integrate data from wildly diverse disciplines to understand our current state and predict the impact of new policies.

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The technical challenge of such integration is significant, although emerging technologies appear to be helping. But the forest of terms and conditions around data make integration difficult to legally perform in many cases. One approach might be to develop and recommend a single license: any data with this license can be integrated with any other data under this

... must promote **legal predictability** and **certainty**.

... must be **easy to use** and **understand**.

... must impose the **lowest possible** transaction costs on users.

full text:

<http://sciencecommons.org/projects/publishing/open-access-data-protocol/>

norms approach

set of principles (not license)

open, accessible, interoperable

create legal zones of certainty

calls for data providers to ***waive*** all rights necessary for ***data extraction*** and ***re-use***

requires provider place ***no additional*** obligations (like share-alike) to limit downstream use

request behavior (like attribution) through ***norms*** and ***terms of use***

the Tropical Disease Initiative

an open source drug discovery project



Kernel 1.0

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Dihydrofolate reductase-thymidylate synthase. predicted to bind 6 ligands [LYD LYA DUR UFP DDU SUL]

UniPort id: **A7UD81** [*P. falciparum*]

Target keywords: Anti-Arrhythmia Agents; ; Antimetabolites; Calcium Channel Blockers; Analgesics; Antineoplastic Agents; A7UD81; Antiviral Agents;

Antineoplastics; Anesthetics; Enzyme Inhibitors; Methyltransferase; Transferase.; Anticonvulsants; Folic Acid Antagonists; Tocolytic Agents

Do you consider this target suitable for drug discovery: ★★★★★ (1 votes, average: 5.00 out of 5)

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Binding site prediction to approved drugs (need help reading this page?):

PDB	Ⓞ	Template	Ⓞ	Model	↔	Ligand	Exact	SupStr	SubStr	Similar
+ 1dduB	100.00/100.00	1qzfA	42.00/1.29	PFD0830w.1.pdb	92.31/100.00	DDU			DB00322 DB00432	DB00322 DB00432
+ 2tdd	93.33/100.00	1qzfA	42.00/1.29	PFD0830w.1.pdb	95.45/100.00	UFP		DB00322		DB00322
+ 1jutB	86.67/100.00	1qzfA	42.00/1.29	PFD0830w.1.pdb	92.86/100.00	LYD				DB00642
+ 1tduA	94.12/100.00	1qzfA	42.00/1.29	PFD0830w.1.pdb	88.24/100.00	DUR			DB00322 DB00432	DB00322 DB00432

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• [A7UD81](#) (5.00 out of 5)

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Personal Genome Project

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Volunteers from the general public working together with researchers to advance personal genomics.

We believe individuals from the general public have a vital role to play in making personal genomes useful. We are recruiting volunteers who are willing to share their genome sequence and many types of personal information with the research community and the general public, so that together we will be better able to advance our understanding of genetic and environmental contributions to human traits and to improve our ability to diagnose, treat, and prevent illness. Learn more about how to [participate](#) in the Personal Genome Project.



Project Overview. The PGP hopes to make personal genome sequencing more affordable, accessible, and useful for humankind. Learn more about our [mission](#).



Want to participate? We aim to enroll 100,000 informed participants from the general public. Learn more about [participation](#) in the PGP and how you can get involved.



Meet our volunteers. Participants may volunteer to publicly share their DNA sequence and other personal information for research and education. Meet the "[PGP-10](#)".

Project News

Welcome readers of [Wired Magazine](#)! This month's issue features an [article](#) about the PGP.



[Enrollment](#) begins soon, [register now](#) to be notified by email.

April 15, 2008: IRB approval obtained from Harvard Medical School to scale project from ten volunteers to 100,000.

[Read about our first ten](#)

Our Tranche Network

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Tranche and the Open Access Database Protocol: Tranche Hashes



The Science Commons has **formally recommended** how resources such as Tranche can mark data as either open-access or restricted. Please see the [main documentation page](#) for more information. This page summarizes how Tranche's hashes reflects the licensing terms specified on an uploaded data set.

The key point: Tranche adds value to **CCo** licensed data sets because it provides a proper citation that formally verifies the data is **CCo** licensed, verifies that the data hasn't changed since publication, and allows access to the data from any computer without worrying about 'link rot'.

The following FAQ help elaborate these points.

- [What does Tranche provide compared to using a license such as the CCo license on its own?](#)
- [Why does my Tranche hash change depending on my licensing terms?](#)
- [How do I properly cite a Tranche hash to show that the data is open access?](#)

What does Tranche provide compared to using a license such as the CCo

SIDER Side Effect Resource

Downloading data

Mapping of labels

The package inserts contain information about the common and/or brand names of the drugs they describe. Based on this information, labels were mapped to [STITCH](#) compound identifiers, which in turn are derived from [PubChem](#) compound identifiers. (These compound identifiers might change between major versions of STITCH, which happen every one or two years.)

File	Size	License
README	1.5 KB	
label_mapping.tsv.gz	369.6 KB	

COSTART side effects

We used the [COSTART](#) dictionary to extract side effects from drug labels. The results of this mapping are available under a [Creative Commons Attribution-Noncommercial-Share Alike 3.0 License](#). For commercial use, please contact [biobyte solutions GmbH](#).

OPINION

Post-publication sharing of data and tools

Despite existing policies on sharing source data and bioresources, good practice is not widespread. A meeting of mouse researchers in Rome propose ways to promote a culture of sharing.

Sharing scientific data through publication has long underpinned the cycle of discovery and is the dominant means by which scientists earn credit for their work. More recently, technologies generating very large data sets and novel biological materials have given rise to principles under which communities share data and materials (pre- and post-publication), and to a new sharing infrastructure — large public databases and repositories. While much attention has been given to practical and ethical guidelines for prepublication data release from large scale 'community resource projects', summarized in the Bermuda Principles¹ and the Fort Lauderdale report², sharing of data and resources from hypothesis-driven research has largely been addressed piecemeal by individual communities, journals and funding agencies.

We report here the efforts of one such community to address issues of particular relevance to the free sharing of data and resources for mouse biology, genetics and functional genomics. Our community has had more than six decades experience with strategies for sharing mice, and more recently for cell lines. When it comes to resource sharing, the two greatest impediments to fully exploiting global research using the mouse

as a model organism are the barriers created by material transfer agreements and the underuti-

research community despite the existence of publicly-funded mouse repositories provided for this purpose (see International Mouse Strain Resource (IMSR), www.findmice.org). Comparison of the number of knockout mice recorded by the international Mouse Genome Informatics (MGI) database (<http://www.informatics.jax.org/>) with those deposited in IMSR repositories suggests that currently only 35% are available in this way. This is an encouraging doubling of the percentage available since last assessed in a 2006 NIH survey. To further improve this figure, however, it is important that the sharing ethos is consistently observed by the mouse community and investment in repositories continues to keep pace with the generation of new strains.

Experiences shared at the meeting indicated that enforcement of existing policies regarding data and resource deposition is variable, and that despite increased emphasis on the importance of sharing by journals and funding organizations in recent years, there is evidence that geneticists and genomic researchers are withholding data and research materials with

increasing frequency³. It is one thing to encourage data deposition and resource sharing through guidelines and policy statements, and

quite another to ensure that it happens in practice as a recent informal survey of proteomics

the ready exchange of data and resources and to share good practices already implemented by some organisations and journals.

Access to publication-associated data

Prepublication data release is comprehensively discussed in an accompanying paper from the Toronto group³ whose conclusions were broadly supported in Rome. For publication-associated data, the meeting strongly endorsed the recommendations of the National Academy of Sciences UPSIDE report⁷, which lays out detailed guidelines for data sharing, not least the principle that data on which publications are based should be made available immediately on publication.

Currently, funding bodies rarely require investigators to deposit their mice in public repositories, although many encourage it, with the consequence that mutant lines may be lost or not fully exploited. The meeting strongly recommended that, at least on publication, journals should insist that mice and embryonic stem cells be deposited in a public repository within a specified time frame, the length of which still requires community consensus. Additionally, funders should be willing explicitly to cover the costs of deposition of mice arising from projects into public repositories.

We recommend that it becomes mandatory for scientific papers to explain where and how to access data and resources generated as part of the investigation. We are aware that some

"Enforcement of existing policies regarding data and resource deposition is variable."

at best, we're partially right.

at worst, we're really wrong.

infrastructure for a data web

the ***digital commons***

law + content + technology +
community

**resist the temptation to treat
as property**

**embrace the potential to treat instead
as a network resource**

early days of WWW

no licenses (even free)

debate over code

CERN's decision

view/edit source

network effects



the right to fix our mistakes.

thank you.

kaitlin@creativecommons.org

sciencecommons.org

creativecommons.org

slideshare.net/kaythaney