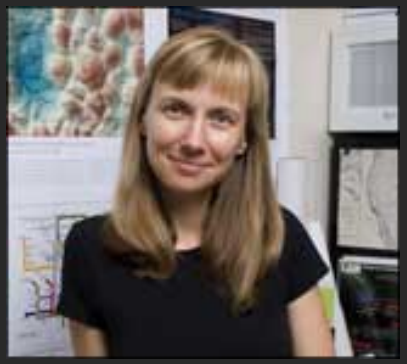
Descriptive and Process Models of Scientific Structure and Evolution



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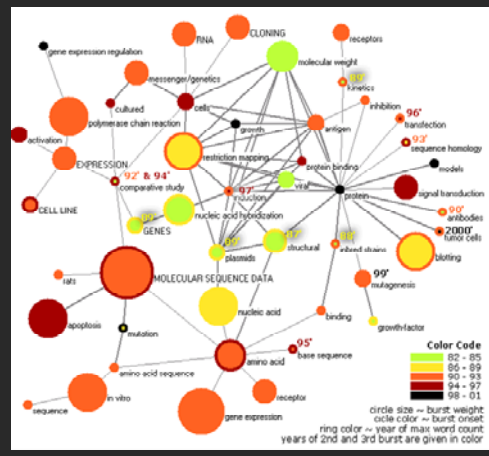
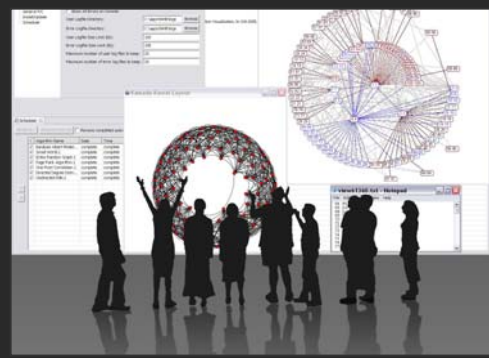
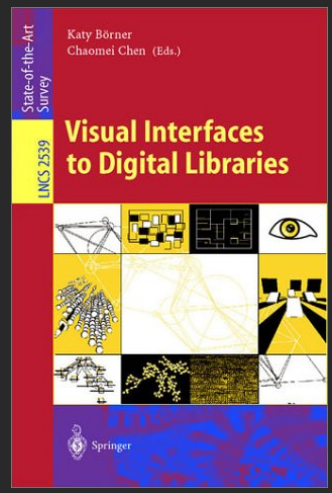
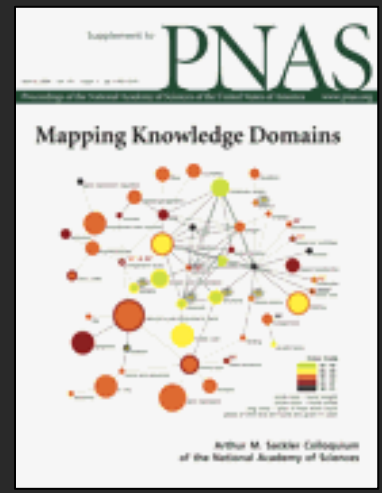
NESCent Seminar
February 20th, 2008





Computational Scientometrics: Studying Science by Scientific Means





- *Börner, Katy, Chen, Chaomei, and Boyack, Kevin. (2003).* ***Visualizing Knowledge Domains.*** *In Blaise Cronin (Ed.), Annual Review of Information Science & Technology, Medford, NJ: Information Today, Inc./American Society for Information Science and Technology, Volume 37, Chapter 5, pp. 179-255.* http://ivl.slis.indiana.edu/km/pub/2003-borner-arist.pdf
- *Shiffrin, Richard M. and Börner, Katy (Eds.) (2004).* ***Mapping Knowledge Domains.*** *Proceedings of the National Academy of Sciences of the United States of America, 101(Suppl_1).* http://www.pnas.org/content/vol101/suppl_1/
- *Börner, Katy, Sanyal, Soma and Vespignani, Alessandro (2007).* ***Network Science.*** *In Blaise Cronin (Ed.), Annual Review of Information Science & Technology, Information Today, Inc./American Society for Information Science and Technology, Medford, NJ, Volume 41, Chapter 12, pp. 537-607.* http://ivl.slis.indiana.edu/km/pub/2007-borner-arist.pdf

- ***Places & Spaces: Mapping Science*** *exhibit, see also* *http://scimaps.org*.

Process of Analyzing and Mapping Knowledge Domains

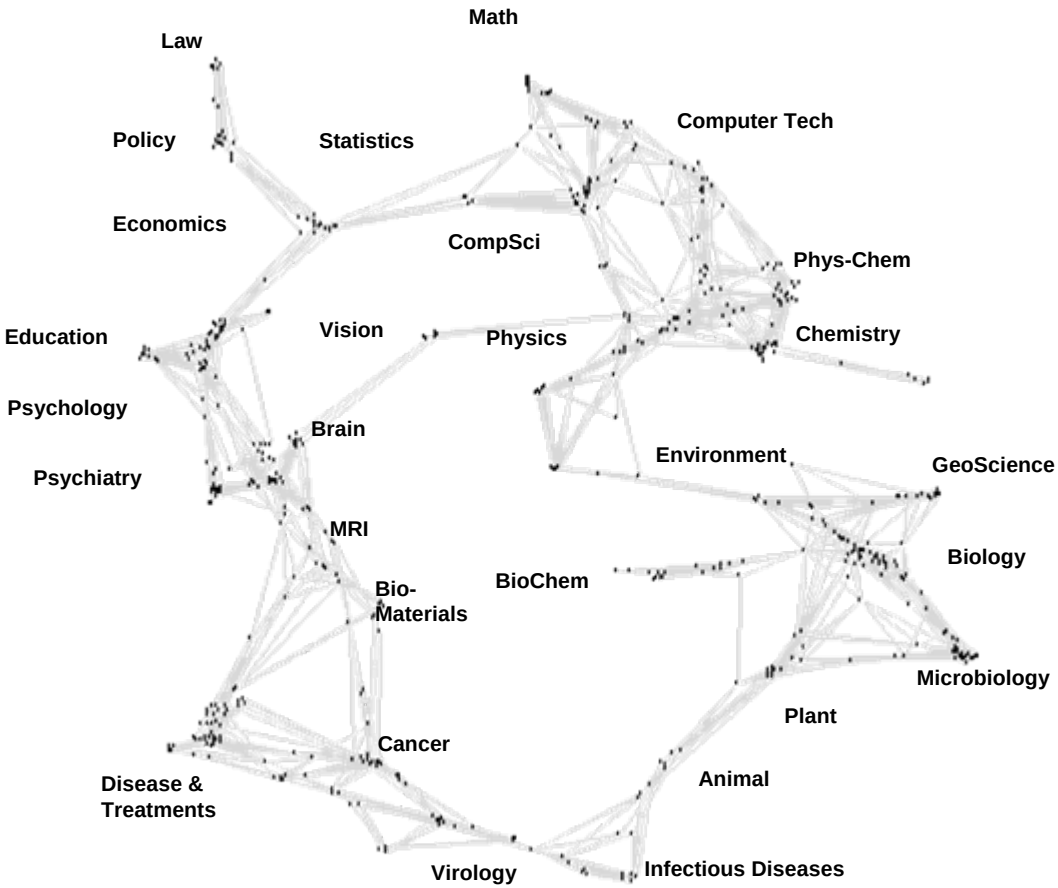
DATA EXTRACTION	UNIT OF ANALYSIS	MEASURES	LAYOUT (often one code does both similarity and ordination steps)		DISPLAY
			SIMILARITY	ORDINATION	
SEARCHES ISI INSPEC Eng Index Medline ResearchIndex Patents etc. BROADENING By citation By terms	COMMON CHOICES Journal Document Author Term	COUNTS/FREQUENCIES Attributes (e.g. terms) Author citations Co-citations By year THRESHOLDS By counts	SCALAR (unit by unit matrix) Direct citation Co-citation Combined linkage Co-word / co-term Co-classification VECTOR (unit by attribute matrix) Vector space model (words/terms) Latent Semantic Analysis (words/terms) incl. Singular Value Decomp (SVD) CORRELATION (if desired) Pearson's R on any of above	DIMENSIONALITY REDUCTION Eigenvector/ Eigenvalue solutions Factor Analysis (FA) and Principal Components Analysis (PCA) Multi-dimensional scaling (MDS) LSA, **Topics** Pathfinder networks (PFNet) Self-organizing maps (SOM) includes SOM, ET-maps, etc. CLUSTER ANALYSIS SCALAR Triangulation Force-directed placement (FDP)	INTERACTION Browse Pan Zoom Filter Query Detail on demand ANALYSIS

Börner, Katy, Chen, Chaomei, and Boyack, Kevin. (2003) Visualizing Knowledge Domains. In Blaise Cronin (Ed.), Annual Review of Information Science & Technology, Volume 37, Medford, NJ: Information Today, Inc./American Society for Information Science and Technology, chapter 5, pp. 179-255.

Latest 'Base Map' of Science

Kevin W. Boyack, Katy Börner, & Richard Klavans (2007). Mapping the Structure and Evolution of Chemistry Research. 11th International Conference on Scientometrics and Informetrics. pp. 112-123.

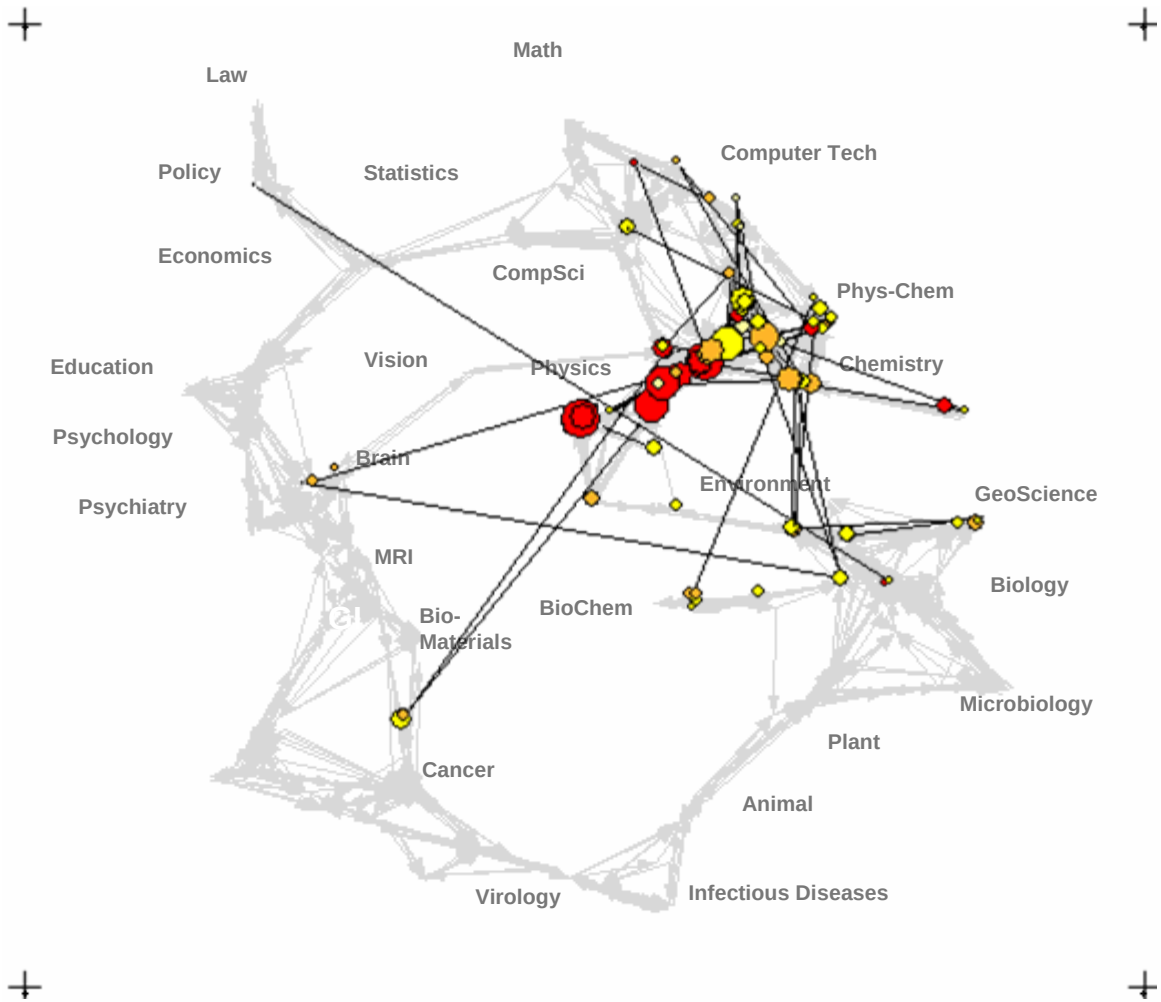
- Uses combined SCI/SSCI from 2002
  - 1.07M papers, 24.5M references, 7,300 journals
  - Bibliographic coupling of papers, aggregated to journals
- Initial ordination and clustering of journals gave 671 clusters
- Coupling counts were reaggregated at the journal cluster level to calculate the
  - (x,y) positions for each journal cluster
  - by association, (x,y) positions for each journal



Science map applications: Identifying core competency

Kevin W. Boyack, Katy Börner, & Richard Klavans (2007).

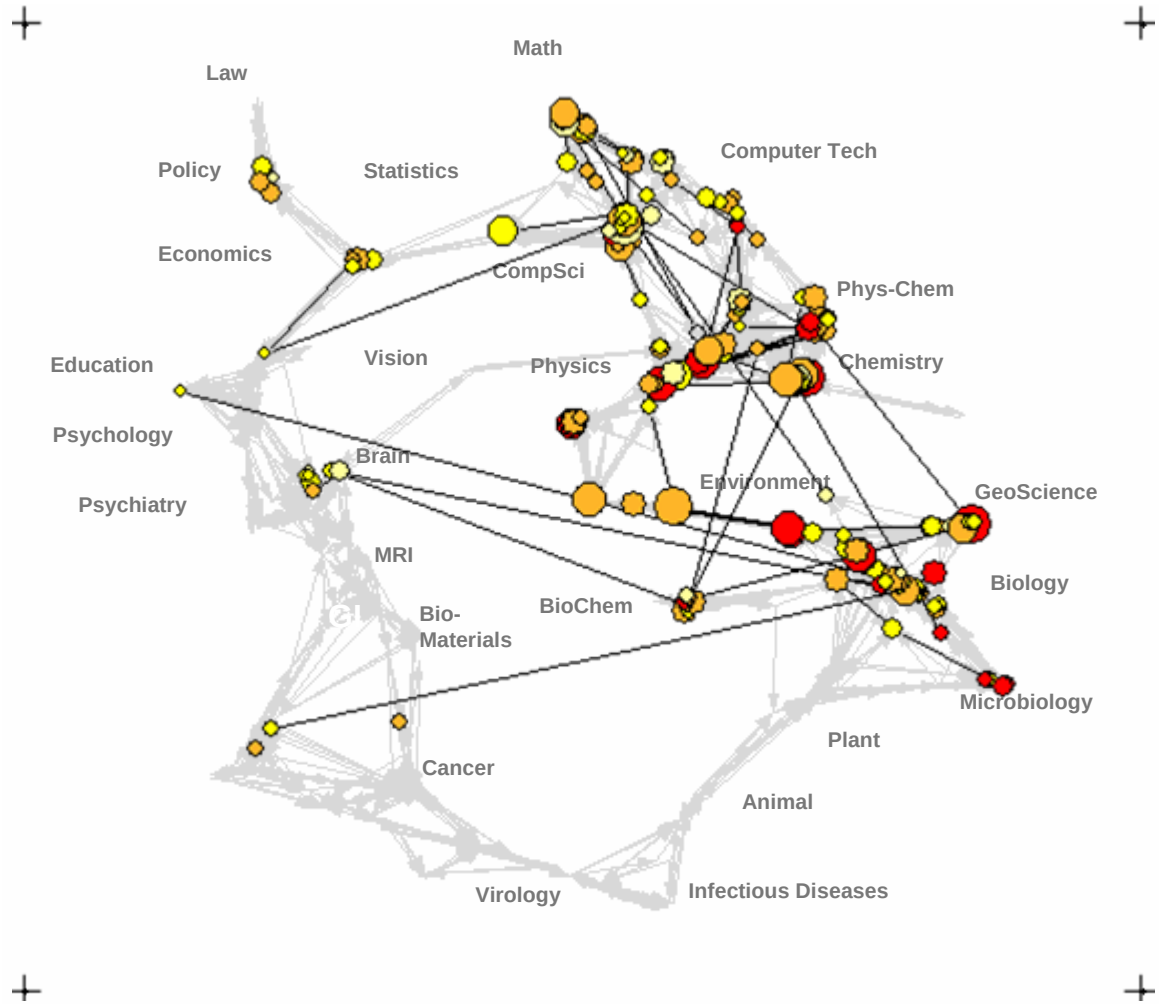
Funding patterns of the US Department of Energy (DOE)



Science map applications: Identifying core competency

Kevin W. Boyack, Katy Börner, & Richard Klavans (2007).

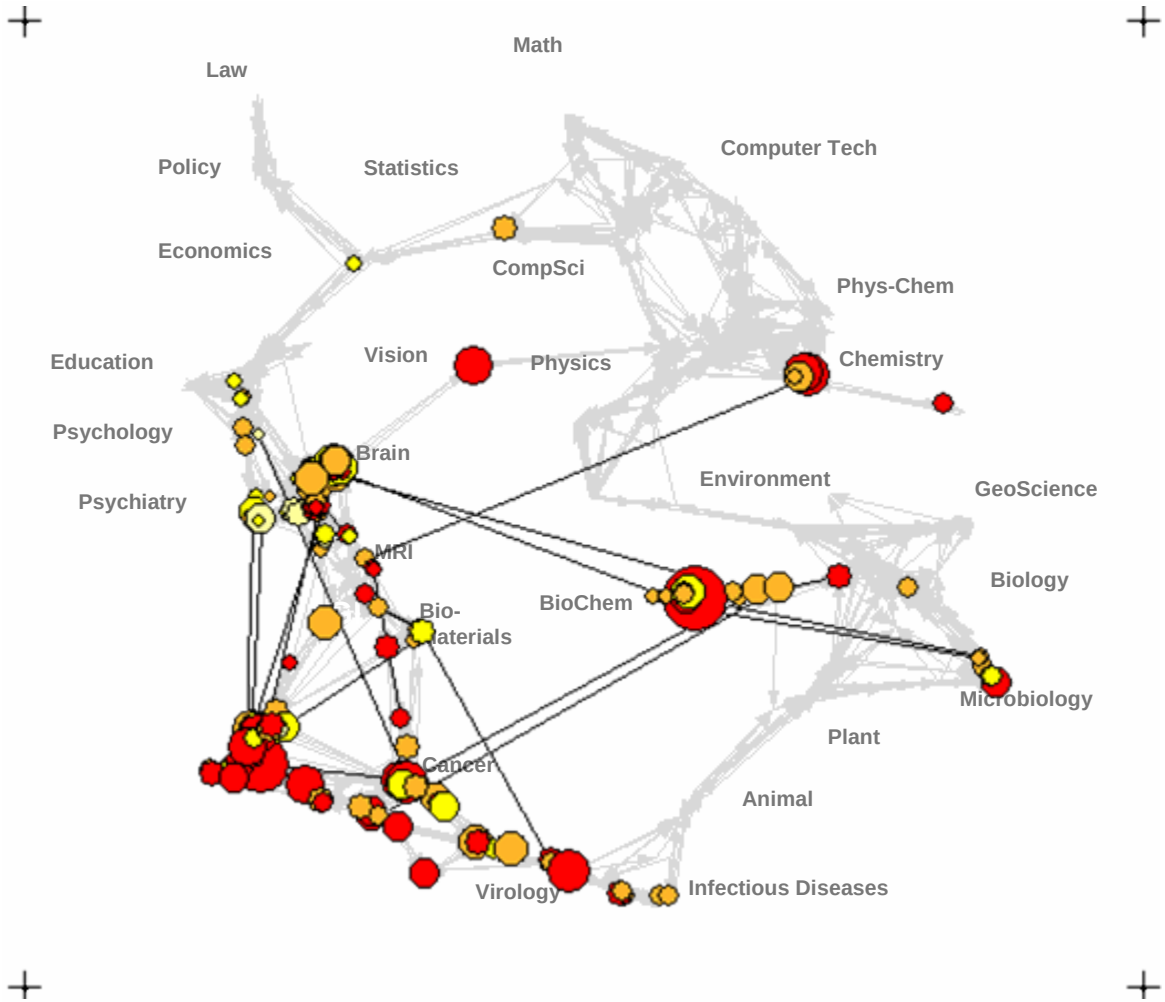
Funding Patterns of the National Science Foundation (NSF)



Science map applications: Identifying core competency

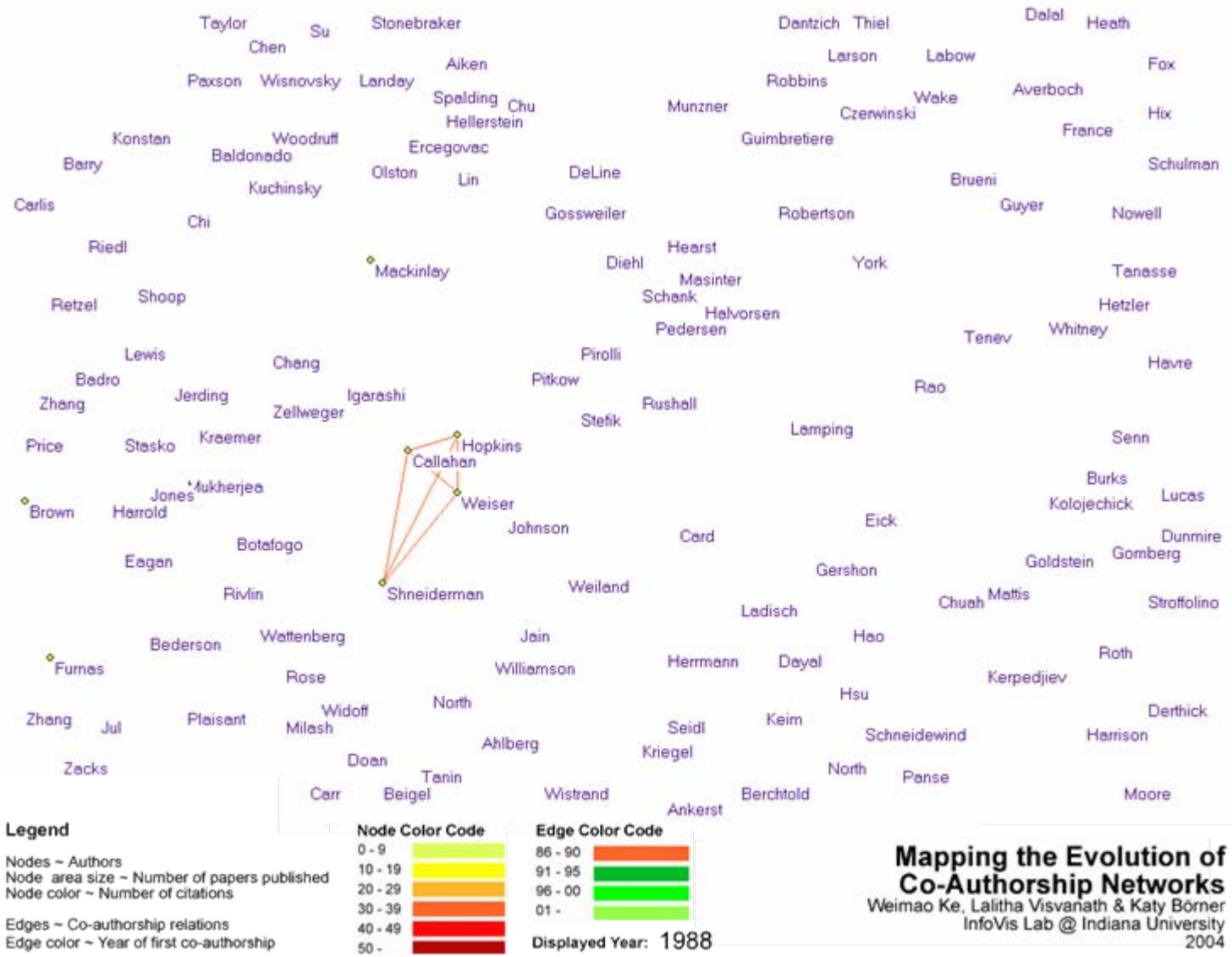
Kevin W. Boyack, Katy Börner, & Richard Klavans (2007).

Funding Patterns of the National Institutes of Health (NIH)



Mapping the Evolution of Co-Authorship Networks

Ke, Visvanath & Börner, (2004) Won 1st price at the IEEE InfoVis Contest.



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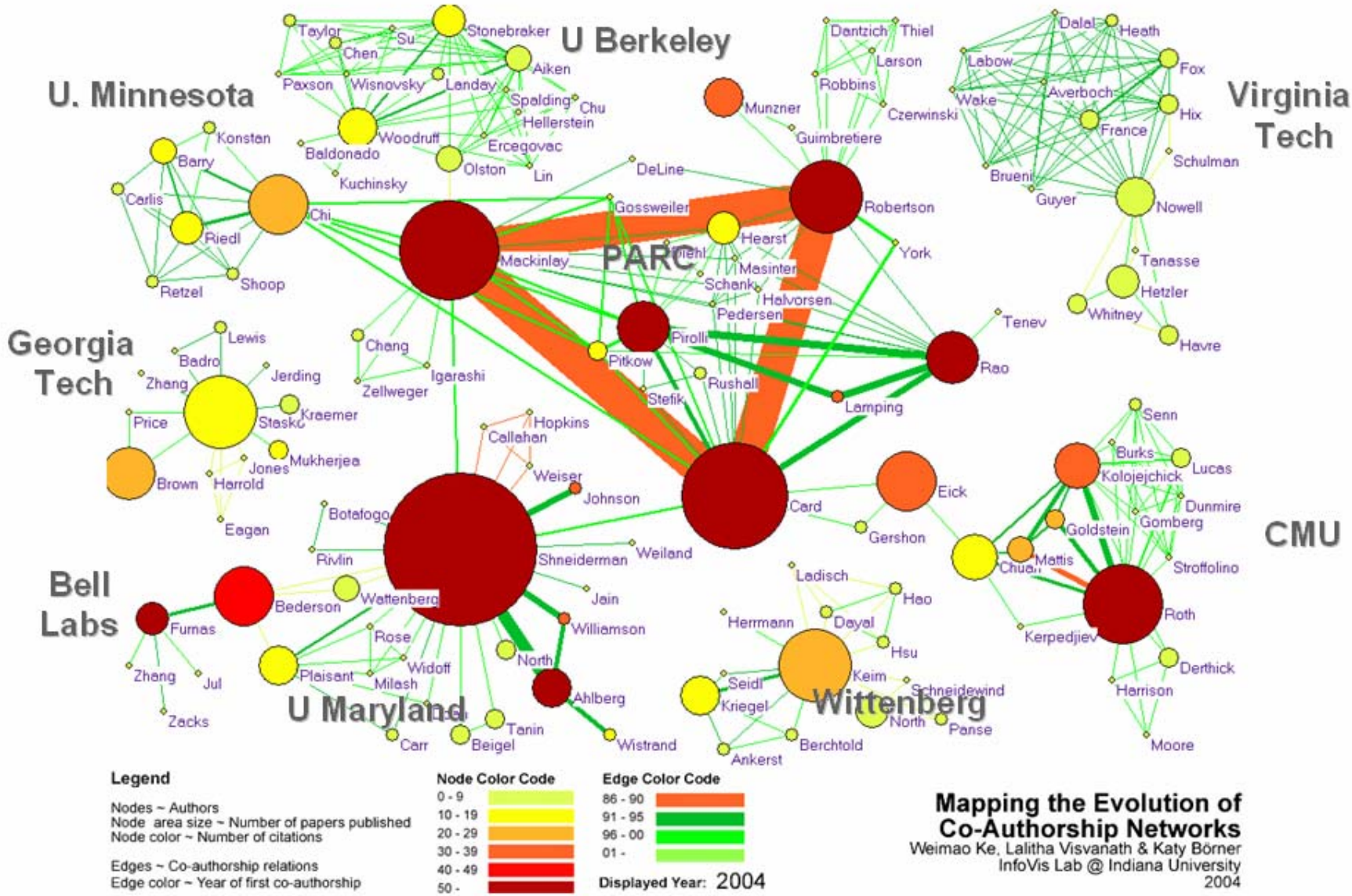
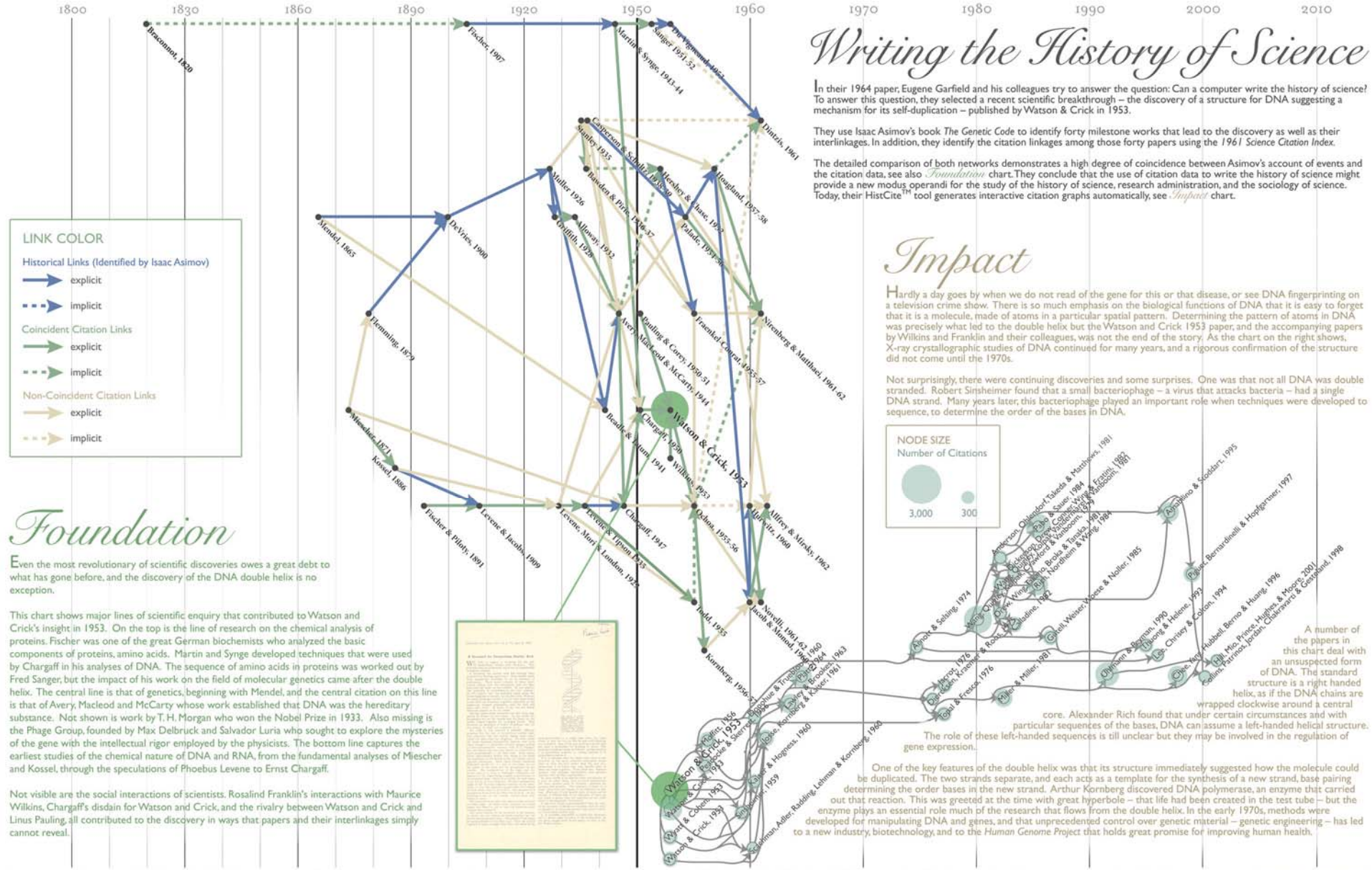


Writing the History of Science

In their 1964 paper, Eugene Garfield and his colleagues try to answer the question: Can a computer write the history of science? To answer this question, they selected a recent scientific breakthrough – the discovery of a structure for DNA suggesting a mechanism for its self-duplication – published by Watson & Crick in 1953.

They use Isaac Asimov's book *The Genetic Code* to identify forty milestone works that lead to the discovery as well as their interlinkages. In addition, they identify the citation linkages among those forty papers using the *1961 Science Citation Index*.

The detailed comparison of both networks demonstrates a high degree of coincidence between Asimov's account of events and the citation data, see also *Foundation* chart. They conclude that the use of citation data to write the history of science might provide a new modus operandi for the study of the history of science, research administration, and the sociology of science. Today, their HistCite™ tool generates interactive citation graphs automatically, see *Impact* chart.



LINK COLOR

Historical Links (Identified by Isaac Asimov)
- explicit
- implicit

Coincident Citation Links
- explicit
- implicit

Non-Coincident Citation Links
- explicit
- implicit

NODE SIZE
Number of Citations
3,000
300

Foundation

Even the most revolutionary of scientific discoveries owes a great debt to what has gone before, and the discovery of the DNA double helix is no exception.

This chart shows major lines of scientific enquiry that contributed to Watson and Crick's insight in 1953. On the top is the line of research on the chemical analysis of proteins. Fischer was one of the great German biochemists who analyzed the basic components of proteins, amino acids. Martin and Synge developed techniques that were used by Chargaff in his analyses of DNA. The sequence of amino acids in proteins was worked out by Fred Sanger, but the impact of his work on the field of molecular genetics came after the double helix. The central line is that of genetics, beginning with Mendel, and the central citation on this line is that of Avery, Macleod and McCarty whose work established that DNA was the hereditary substance. Not shown is work by T. H. Morgan who won the Nobel Prize in 1933. Also missing is the Phage Group, founded by Max Delbruck and Salvador Luria who sought to explore the mysteries of the gene with the intellectual rigor employed by the physicists. The bottom line captures the earliest studies of the chemical nature of DNA and RNA, from the fundamental analyses of Miescher and Kossel, through the speculations of Phoebus Levene to Ernst Chargaff.

Not visible are the social interactions of scientists. Rosalind Franklin's interactions with Maurice Wilkins, Chargaff's disdain for Watson and Crick, and the rivalry between Watson and Crick and Linus Pauling, all contributed to the discovery in ways that papers and their interlinkages simply cannot reveal.

Impact

Hardly a day goes by when we do not read of the gene for this or that disease, or see DNA fingerprinting on a television crime show. There is so much emphasis on the biological functions of DNA that it is easy to forget that it is a molecule, made of atoms in a particular spatial pattern. Determining the pattern of atoms in DNA was precisely what led to the double helix but the Watson and Crick 1953 paper, and the accompanying papers by Wilkins and Franklin and their colleagues, was not the end of the story. As the chart on the right shows, X-ray crystallographic studies of DNA continued for many years, and a rigorous confirmation of the structure did not come until the 1970s.

Not surprisingly, there were continuing discoveries and some surprises. One was that not all DNA was double stranded. Robert Sinsheimer found that a small bacteriophage – a virus that attacks bacteria – had a single DNA strand. Many years later, this bacteriophage played an important role when techniques were developed to sequence, to determine the order of the bases in DNA.

A number of the papers in this chart deal with an unsuspected form of DNA. The standard structure is a right handed helix, as if the DNA chains are wrapped clockwise around a central core. Alexander Rich found that under certain circumstances and with particular sequences of the bases, DNA can assume a left-handed helical structure. The role of these left-handed sequences is till unclear but they may be involved in the regulation of gene expression.

One of the key features of the double helix was that its structure immediately suggested how the molecule could be duplicated. The two strands separate, and each acts as a template for the synthesis of a new strand, base pairing determining the order bases in the new strand. Arthur Kornberg discovered DNA polymerase, an enzyme that carried out that reaction. This was greeted at the time with great hyperbole – that life had been created in the test tube – but the enzyme plays an essential role much of the research that flows from the double helix. In the early 1970s, methods were developed for manipulating DNA and genes, and that unprecedented control over genetic material – genetic engineering – has led to a new industry, biotechnology, and to the *Human Genome Project* that holds great promise for improving human health.


1947 A. Mirsky & I. Goodman


1947 J. Monod


1947 E. Chargaff

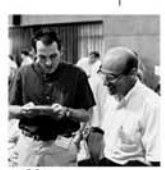

1948 A. Mirsky & P.C. Koller


1950 R. Franklin


1953 J. D. Watson & F. H. C. Crick

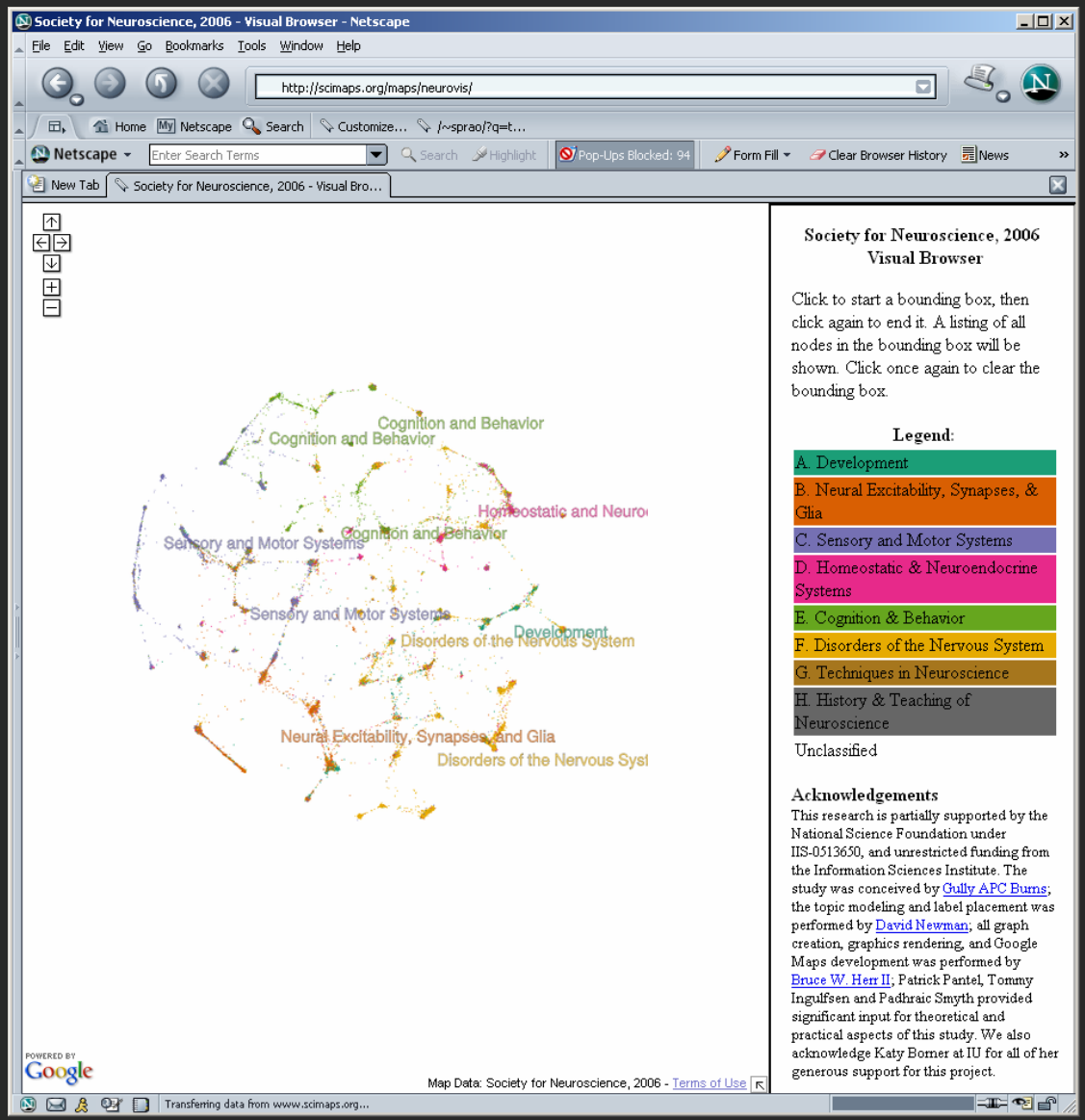

1963 V. Ingram, M. Nirenberg & M. Staehelin


1963 J. Speyer & M. Nirenberg

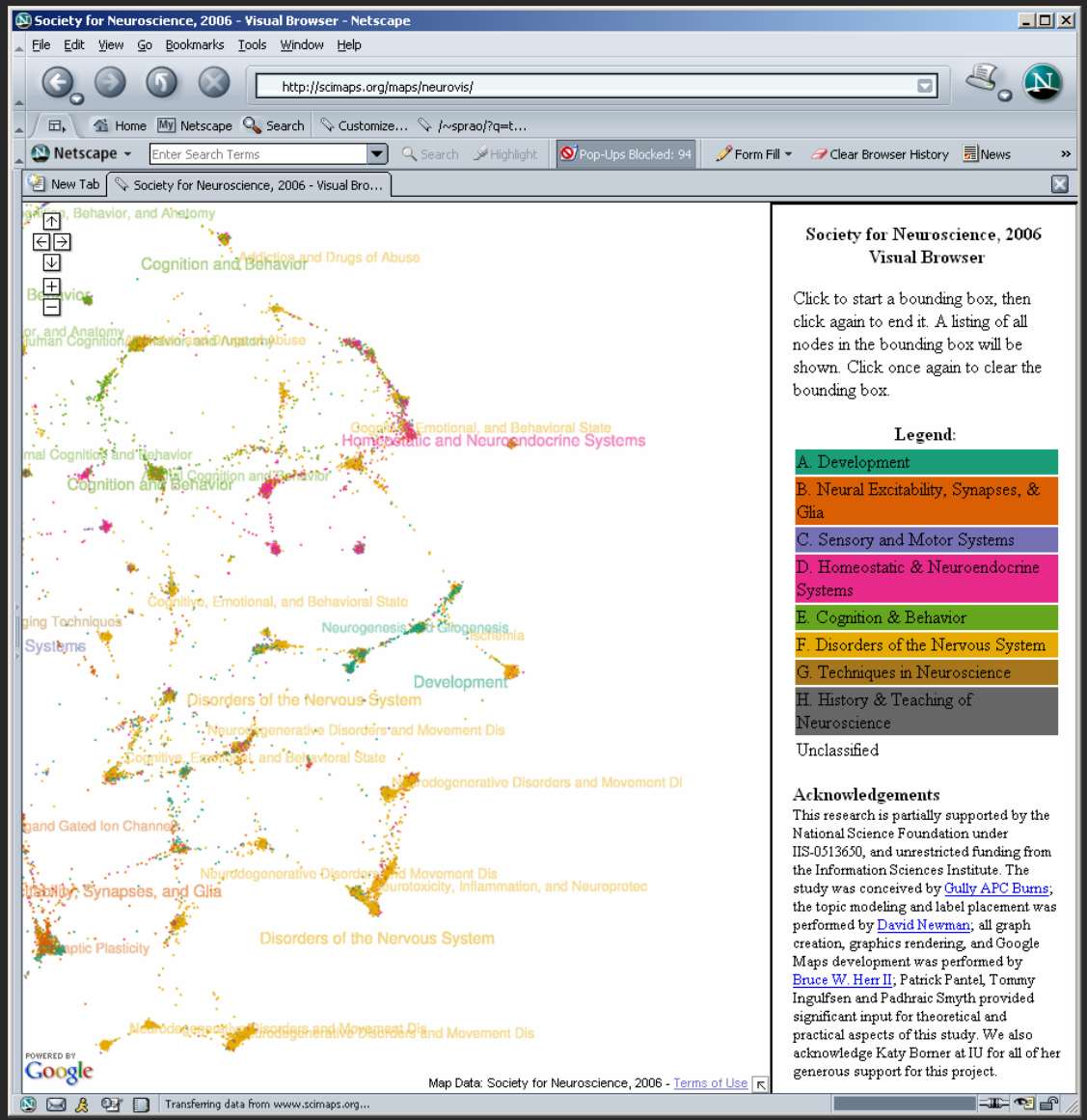

1968 C. Thomas & A. Kornberg


1974 Participants


1978 A. Kornberg



Bruce W. Herr II, Gully Burns (USC), David Newman (UCI), Society for Neuroscience, 2006 Visual Browser, 2007, http://scimaps.org/maps/neurovis/



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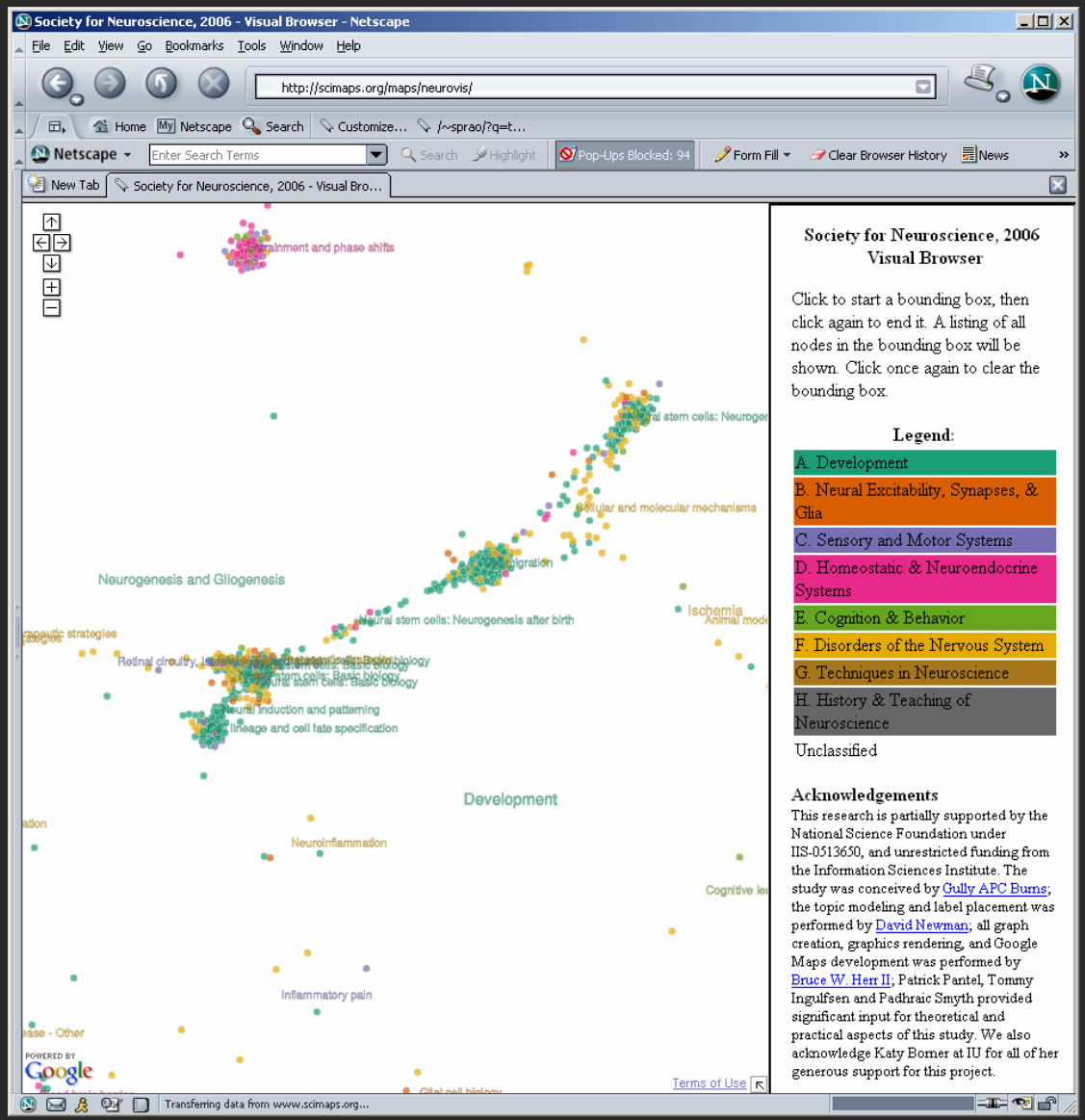

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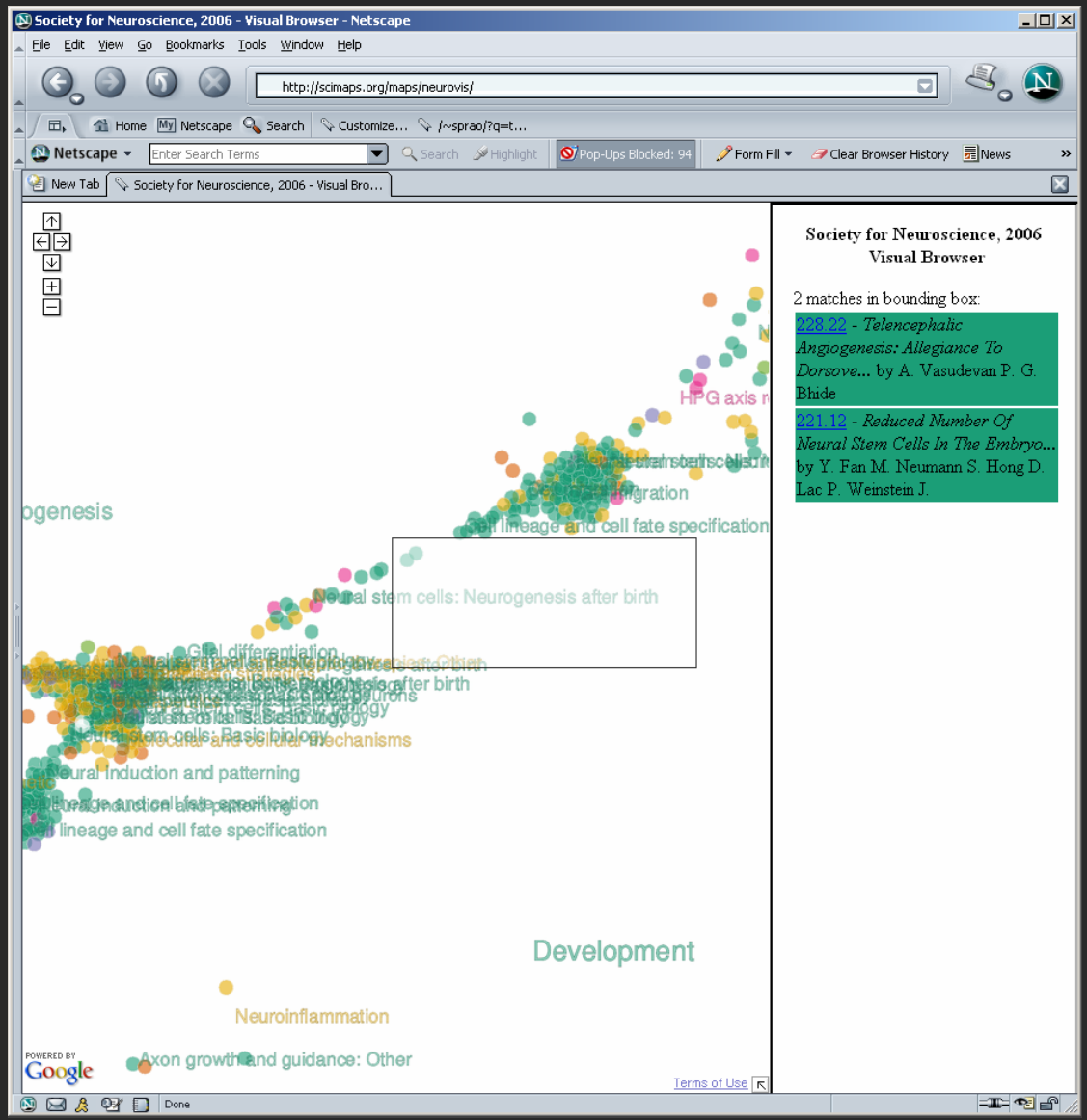

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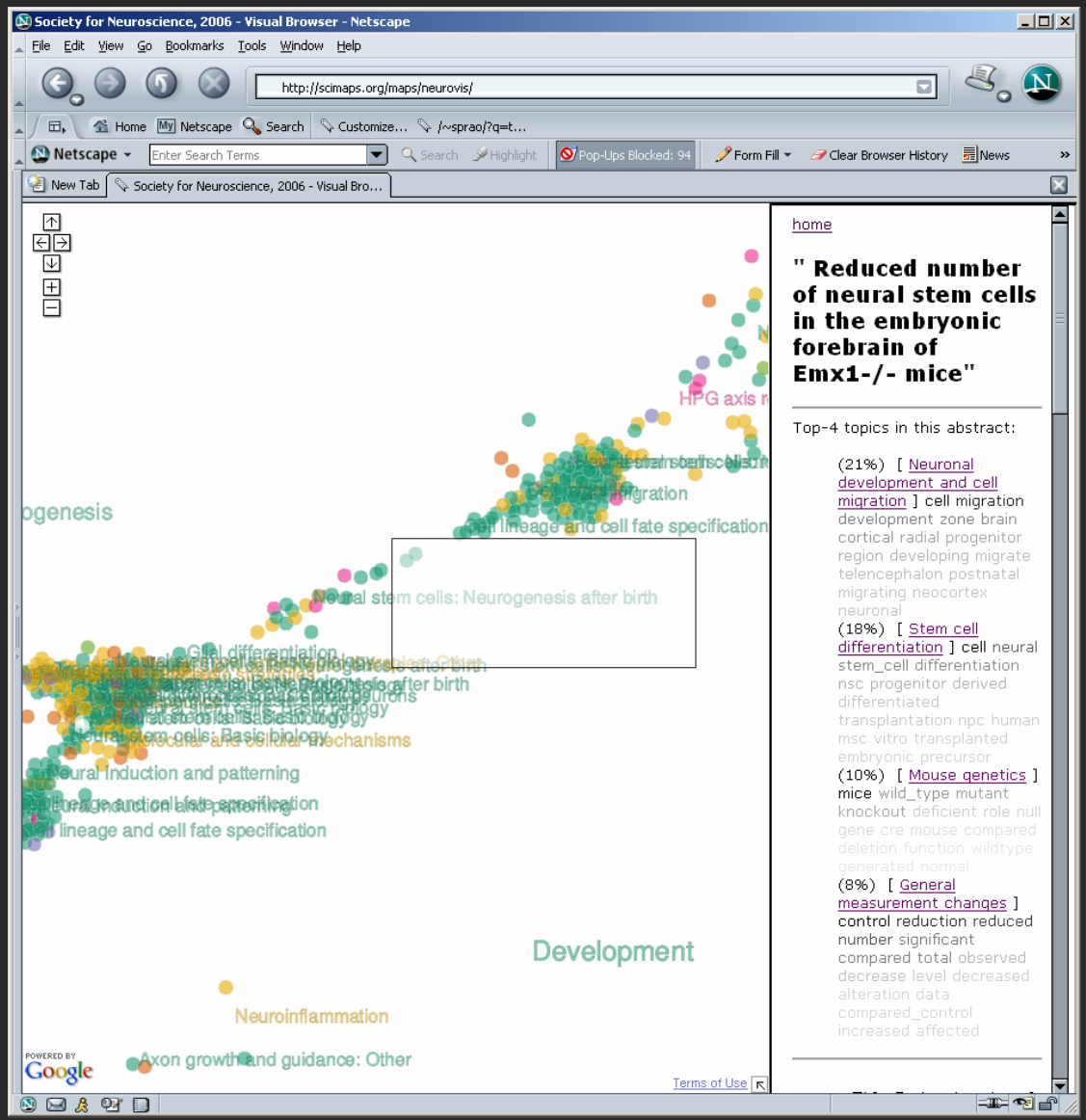
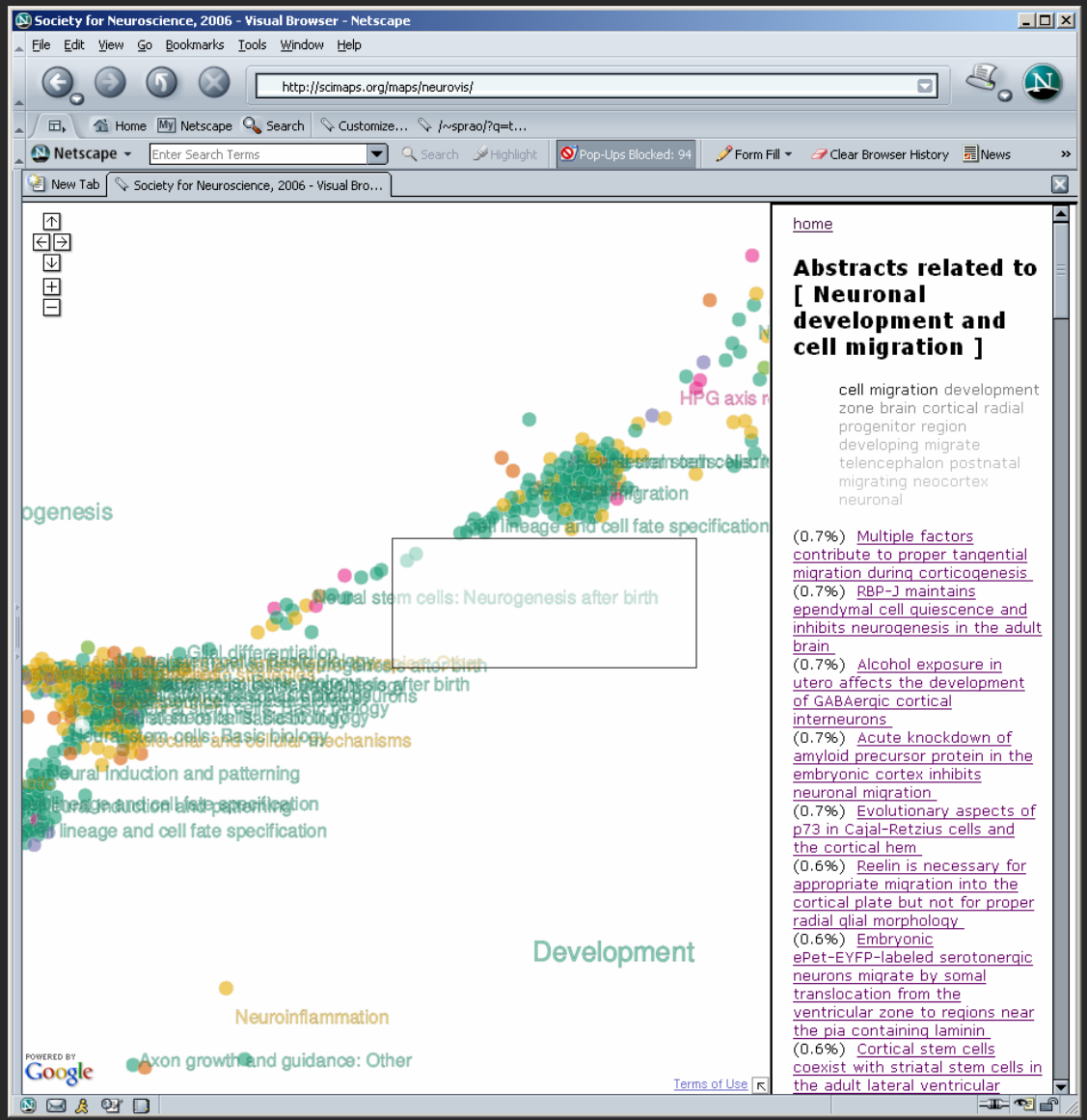


Bruce W. Herr II, Gully Burns (USC), David Newman (UCI), Society for Neuroscience, 2006
Visual Browser, 2007, http://scimaps.org/maps/neurovis/



Bruce W. Herr II, Gully Burns (USC), David Newman (UCI), Society for Neuroscience, 2006 Visual Browser, 2007, http://scimaps.org/maps/neurovis/

Wikipedian Activity

Studying large scale social networks such as Wikipedia

Vizzards 2007 Entry

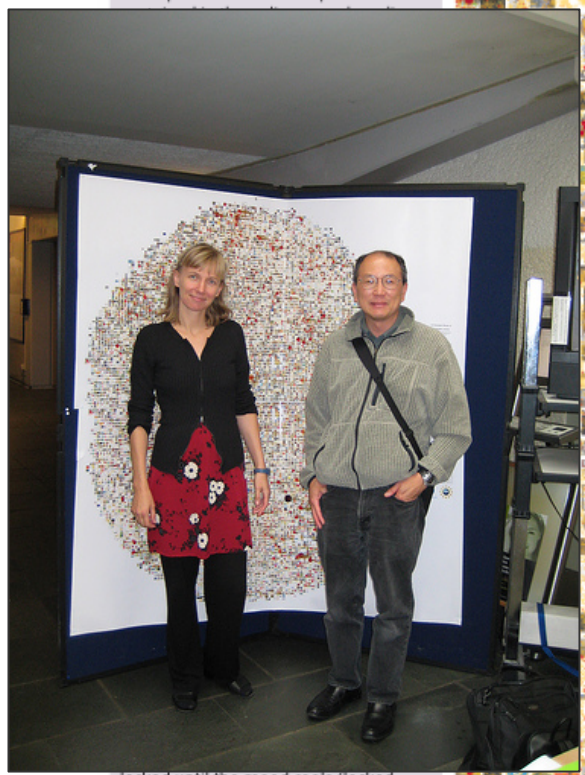
Second Sight: An Emergent Mosaic of Wikipedian Activity, The NewScientist, May 19, 2007

Second sight

Image: Bruce W. Herr and Todd M. Holloway

Power struggle

How do you keep track of the bubbling mass of information that is Wikipedia? This chaotic-looking mosaic is one attempt to show which topics are



locked until the mood cools (locked pages at the time of writing include entries on Sheffield Wednesday football club, Mikhail Gorbachev and pigs).

The mosaic has been commended in a competition for images that visualise network dynamics, coinciding with this week's International Workshop and Conference on Network Science in Bloomington.

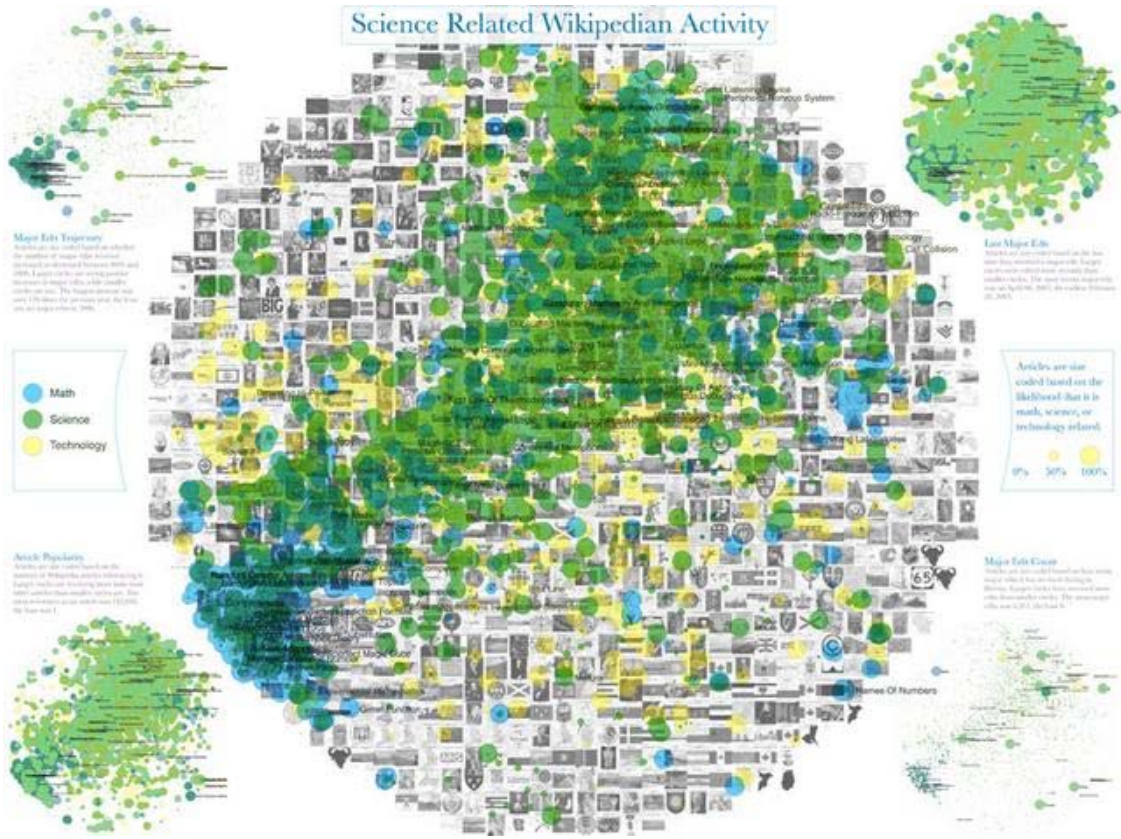
Science Related Wikipedian Activity

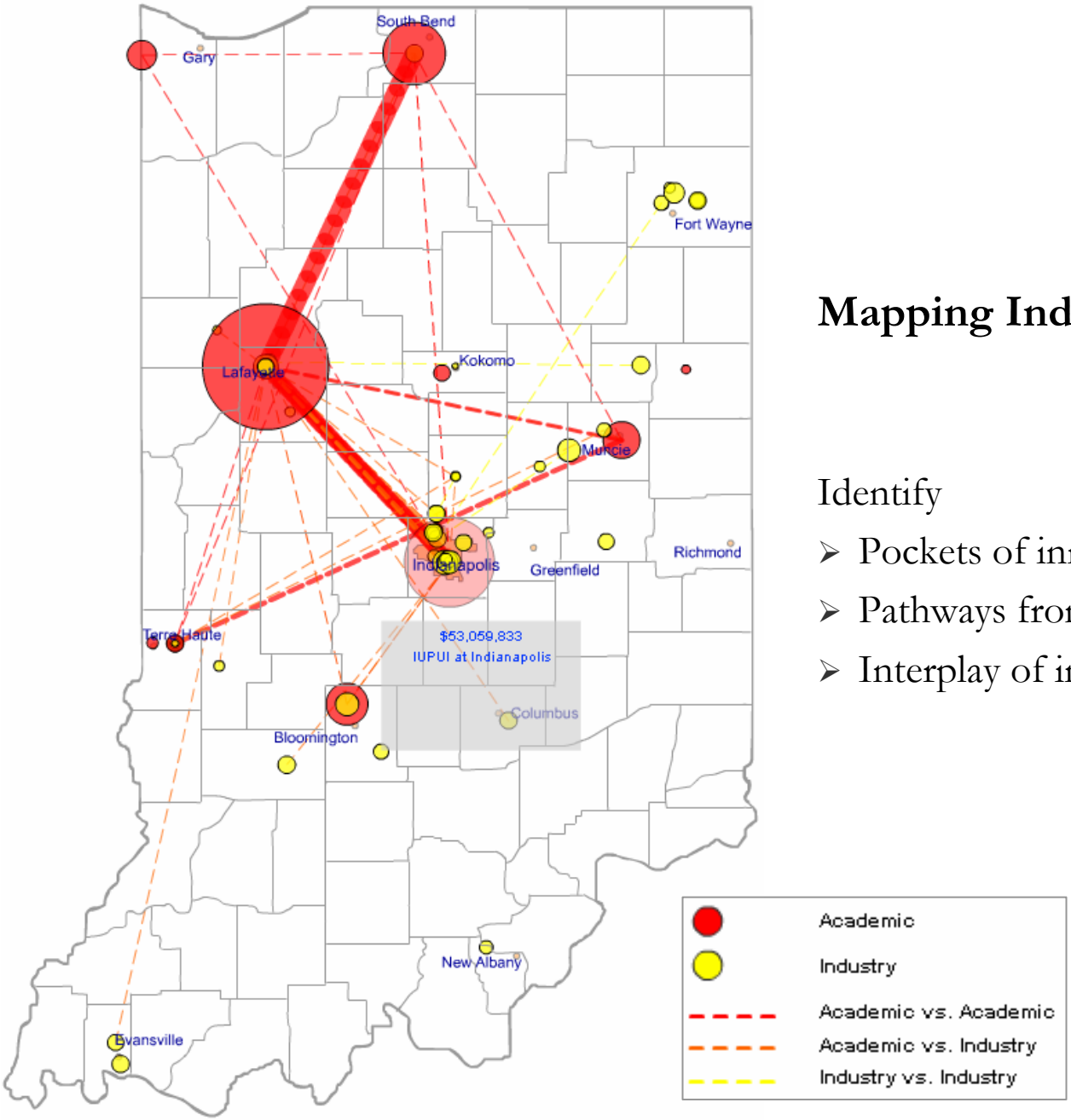
http://scimaps.org/dev/map_detail.php?map_id=165

Same base map.

Overlaid are 3,599 math (blue), 6,474 science (green), and 3,164 technology relevant articles (yellow).
All other articles are given in grey.

Corners show articles size coded according to
-article edit activity (top left),
- number of major edits (top right),
- number of bursts in edit activity (bottom, right)
- indegree (bottom left).





Mapping Indiana's Intellectual Space

Identify

- Pockets of innovation
- Pathways from ideas to products
- Interplay of industry and academia

Mapping Topic Bursts

Co-word space of the top 50 highly frequent and bursty words used in the top 10% most highly cited PNAS publications in 1982-2001.

Mane & Börner. (2004) PNAS, 101(Suppl. 1): 5287-5290.

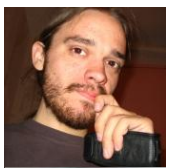
RNA
CLONING
receptors
gene expression regulation
molecular weight
messenger/genetics
89' kinetics
cultured
cells
inhibition
96' transfection
polymerase chain reaction
growth
antigen
activation
93' sequence homology
EXPRESSION
restriction mapping
protein binding
models
92' & 94' comparative study
viral
97' induction
protein
signal transduction
CELL LINE
nucleic acid hybridization
90' antibodies
89' GENES
2000' tumor cells
87' structural
88' inbred strains
89' plasmids
blotting
rats
MOLECULAR SEQUENCE DATA
99' mutagenesis
nucleic acid
binding
apoptosis
mutation
growth-factor
95' base sequence
amino acid
amino acid sequence
in vitro
receptor
sequence
gene expression

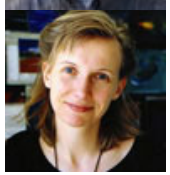
Color Code
82 - 85
86 - 89
90 - 93
94 - 97
98 - 01

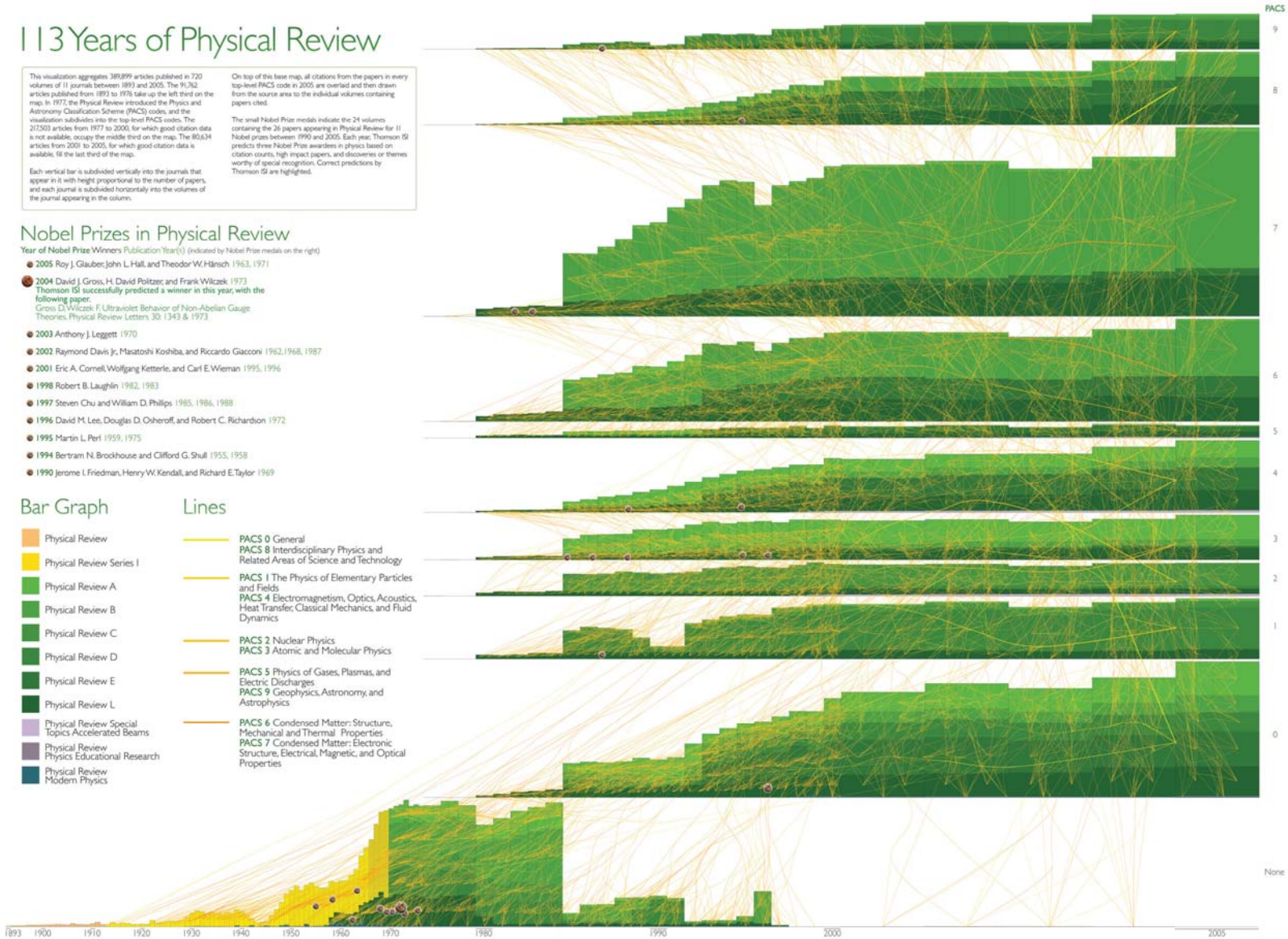
circle size ~ burst weight
cicle color ~ burst onset
ring color ~ year of max word count
years of 2nd and 3rd burst are given in color

113 Years of Physical Review

Bruce W. Herr II and Russell Duhon (Data Mining & Visualization), Elisha F. Hardy (Graphic Design), Shashikant Penumarthy (Data Preparation) and Katy Börner (Concept)







Places & Spaces: Mapping Science

a science exhibit that introduces people to maps of sciences, their makers and users.

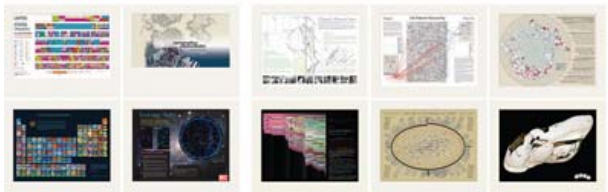
http://scimaps.org.

Exhibit Curators: Dr. Katy Börner & Elisha Hardy

Mapping Science Exhibit – 10 Iterations in 10 years

The Power of Maps (2005)

The Power of Reference Systems (2006)



The Power of Forecasts (2007)

Science Maps for Economic Decision Makers (2008)

Science Maps for Science Policy Makers (2009)
Science Maps for Scholars (2010)
Science Maps as Visual Interfaces to Digital Libraries (2011)
Science Maps for Kids (2012)
Science Forecasts (2013)

How to Lie with Science Maps (2014)

scimaps.org

Illuminated Diagram Display

W. Bradford Paley, Kevin W. Boyack, Richard Kalvans, and Katy Börner (2007) Mapping, Illuminating, and Interacting with Science. SIGGRAPH 2007, San Diego, CA.

YouTube Video:
http://www.youtube.com/watch?v=bXABcOABG4E

The TARL Model (Topics, Aging, and Recursive Linking)

Börner, Katy, Maru, Jeegar & Goldstone, Robert. (2004). The Simultaneous Evolution of Author and Paper Networks. PNAS. Vol. 101(Suppl. 1), 5266-5273.

The TARL model incorporates

- A partitioning of authors and papers into topics,
- Aging, i.e., a bias for authors to cite recent papers, and
- A tendency for authors to cite papers cited by papers that they have read resulting in a rich get richer effect.

The model attempts to capture the roles of authors and papers in the production, storage, and dissemination of knowledge.

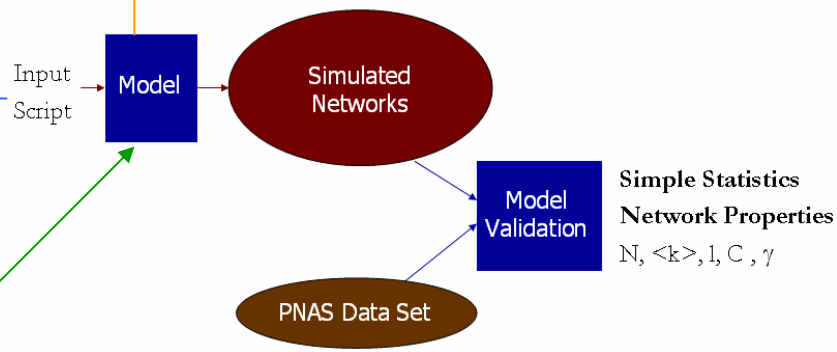
Model Assumptions

- Co-author and paper-citation networks co-evolve.
- Authors come and go.
- Papers are forever.
- Only authors that are 'alive' are able to co-author.
- All existing (but no future) papers can be cited.
- Information diffusion occurs directly via co-authorships and indirectly via the consumption of other authors' papers.

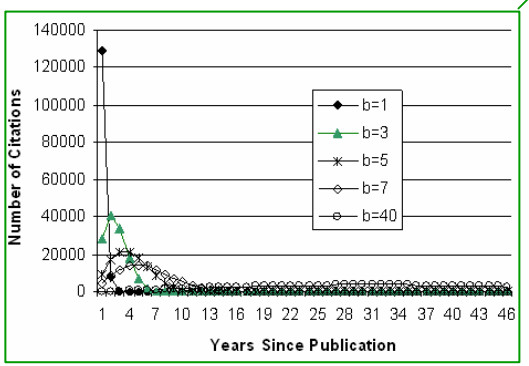
- Preferential attachment is modeled as an emergent property of the elementary, local networking activity of authors reading and citing papers, but also the references listed in papers.

```
// Initialization
generate #_papers papers and assign a random topic to each paper;
generate #_authors authors and assign a random topic to each author;
randomly assign #_co-authors+1 authors to papers of the same topic;
// Simulation
for each year do {
    add #_new_authors new authors, deactivate authors older than #_author_age;
    for each topic do {
        randomly partition set of authors into author_groups of size #_co-authors+1;
        for each author_group do {
            for each new_paper to be produced, do {
                generate new_paper;
                randomly select #_read_ papers from existing papers;
                get all references of read_ papers up to #_reference_path_length;
                for each new_paper_reference do {
                    select a time_slice from (start year to curr_year-1) with probability given in aging_function;
                    randomly select a paper published or cited in this time_slice; as a new_paper_reference;
                    add the new_paper_reference to new_paper;
                }
            }
        }
    }
    add all new papers to the set of existing papers;
    add new links to author and paper information;
}
```

```
-------------------------------------------
Model Parameters (0=without, 1=with)
-------------------------------------------
0/1  Topics
0/1  Co-Authors
0/1  Consider References
0    Aging Function
-------------------------------------------
Model Initialization Values
-------------------------------------------
2  # Years
5  # Authors in Start Year
5  # Papers in Start Year
2  # Papers Consumed (Referenced) per Paper
1  # Papers Produced per Author each Year
5  # Topics
1  # Co-Author(s) per Author
1   # Levels References are Considered
```



Aging function



Model Validation

The properties of the networks generated by this model are validated against a 20-year data set (1982-2001) of documents of type article published in the Proceedings of the National Academy of Science (PNAS) – about 106,000 unique authors, 472,000 co-author links, 45,120 papers cited within the set, and 114,000 citation references within the set.

Table 3 Statistics for SIM data

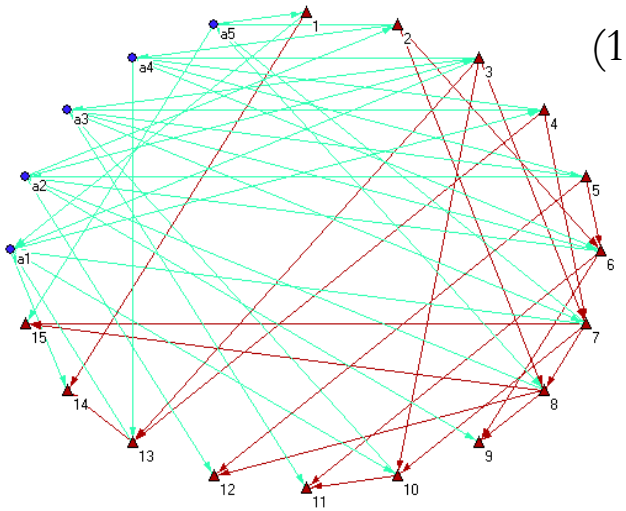
Year	#p	#a	#r	#c	a#ca
1981	1624	3953	0	756	8.21
1982	1040	5200	31200	112161	4
1983	1118	5590	33540	21397	4
1984	1197	5985	35910	10224	4
1985	1275	6375	38250	6184	4
1986	1353	6765	40590	4687	4
1987	1432	7160	42960	3573	4
1988	1510	7550	45300	2816	4
1989	1589	7945	47670	2219	4
1990	1667	8335	50010	1853	4
1991	1745	8725	52350	1634	4
1992	1824	9120	54720	1431	4
1993	1902	9510	57060	1167	4
1994	1981	9905	59430	1040	4
1995	2059	10295	61770	767	4
1996	2137	10685	64110	632	4
1997	2216	11080	66480	522	4
1998	2294	11470	68820	400	4
1999	2373	11865	71190	265	4
2000	2451	12255	73530	125	4
2001	2529	12645	75870	0	4
Total	**37316**		**1070760**	**173853**	

Table 2. PNAS Statistics

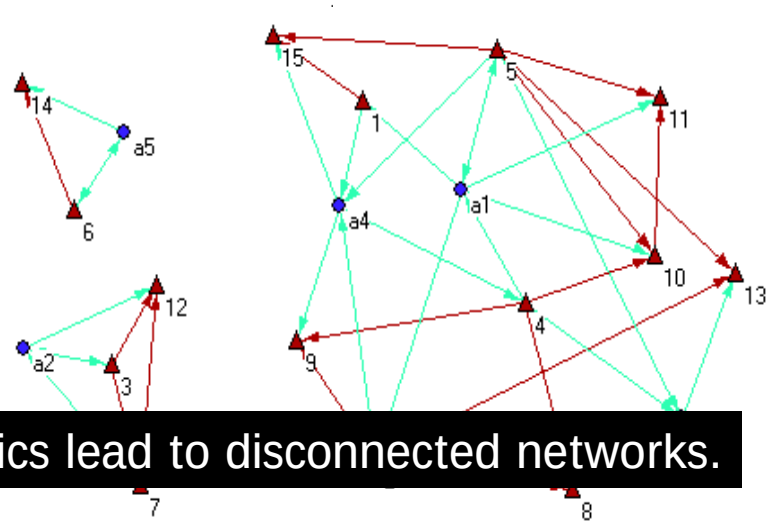
Year	#p	#a	#r	#c	a#ca
1982	1669	5201	46665	156690	3.92
1983	1611	5142	46685	161437	3.98
1984	1695	5583	49834	174161	4.22
1985	1846	6325	55662	191750	4.38
1986	2042	7209	64379	218229	4.76
1987	1924	7061	59110	207729	4.88
1988	2035	7471	63116	215227	4.8
1989	2088	7959	65883	215437	5.01
1990	2066	8031	66019	207138	5.15
1991	2382	9559	77740	223102	5.25
1992	2500	9812	80949	211238	5.29
1993	2413	9770	79848	193867	5.55
1994	2600	10656	86176	187353	5.56
1995	2476	10429	82021	151249	5.66
1996	2765	11803	99061	148622	5.96
1997	2618	11255	96788	122908	6.12
1998	2711	12328	100973	107764	6.48
1999	2603	12182	97018	76080	6.69
2000	2501	12201	94181	44131	7.6
2001	2575	13038	97450	16357	8.4
Total	**45120**		**1509558**	**3230469**	

The TARL Model: The Effect of Parameters

(0000)

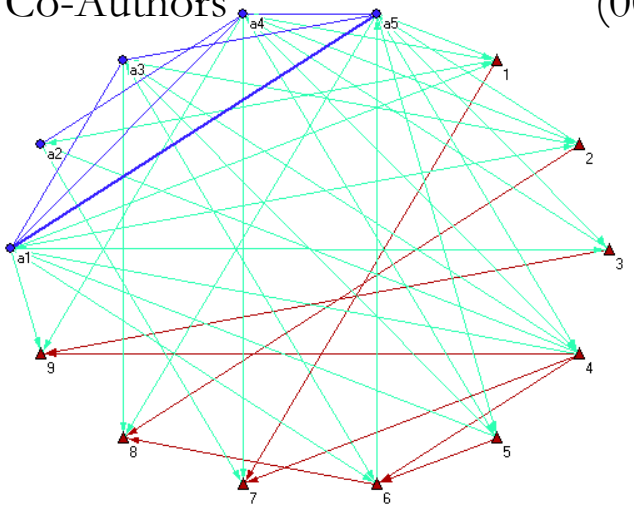


(1000) Topics

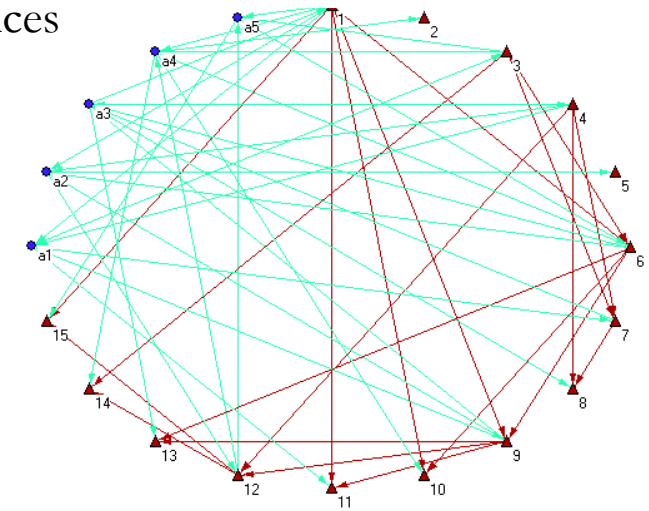


Topics lead to disconnected networks.

(0100) Co-Authors



(0010) References



Co-authoring leads to fewer papers.

```
// Initialization
generate #_papers papers and assign a random topic to each paper;
generate #_authors authors and assign a random topic to each author;
randomly assign #_co-authors+1 authors to papers of the same topic;
// Simulation
for each year do {
    add #_new_authors new authors, deactivate authors older than #_author_age;
    for each topic do {
        randomly partition set of authors into author_groups of size #_co-authors+1;
        for each author_group do {
            for each new_paper to be produced, do {
                generate new_paper;
                randomly select #_read_ papers from existing papers;
                get all references of read_ papers up to #_reference_path_length;
                for each new_paper_reference do {
                    select a time_slice from (start year to curr_year-1) with probability given in aging_function;
                    randomly select a paper published or cited in this time_slice; as a new_paper_reference;
                    add the new_paper_reference to new_paper;
                }
            }
        }
    }
    add all new papers to the set of existing papers;
    add new links to author and paper information;
}
```

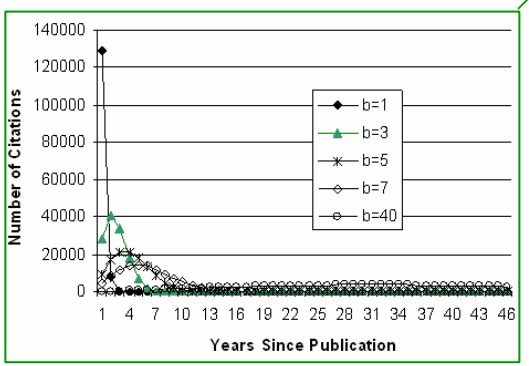
```
-------------------------------------------
Model Parameters (0=without, 1=with)
-------------------------------------------
0/1  Topics
0/1  Co-Authors
0/1  Consider References
0    Aging Function
-------------------------------------------
Model Initialization Values
-------------------------------------------
2  # Years
5  # Authors in Start Year
5  # Papers in Start Year
2  # Papers Consumed (Referenced) per Paper
1  # Papers Produced per Author each Year
5  # Topics
1  # Co-Author(s) per Author
1   # Levels References are Considered
```

Input Script → Model → Simulated Networks → Model Validation

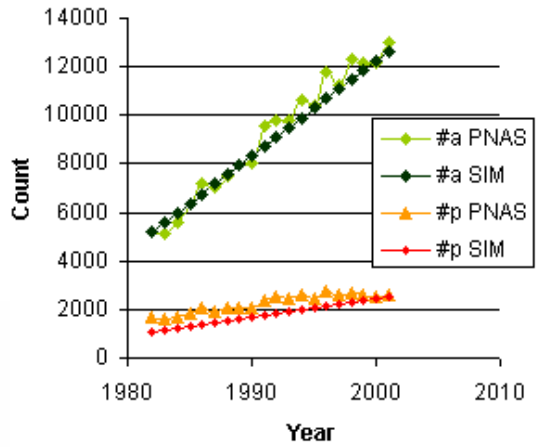
PNAS Data Set → Model Validation

Simple Statistics
Network Properties
N, <k>, l, C , γ

Aging function



Counts for Papers and Authors



Counts for Citations

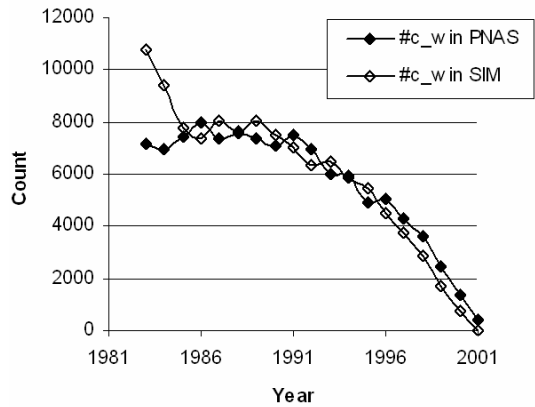


Table 2. Properties of co-author & paper citation networks comprising number of nodes n, average node degree <k>, path length l, cluster coefficient C, and power law exponent γ. Source references are given in the left column.

Network	n	<k>	l	C	γ	Reference
Co-authorship networks						
LANL	52,909	9.7	5.9	0.43	--	Newman, (2001a; 2001b; 2001c)
MEDLINE	1,520,251	18.1	4.6	0.066	--	
SPIRES	56,627	1.73	4.0	0.726	1.2	
NCSTRL	11,994	3.59	9.7	0.496	--	
Math.	70,975	3.9	9.5	0.59	2.5	Barabasi et al., (2002)
Neurosci.	209,293	11.5	6	0.76	2.1	
PNAS	105,915	8.97	5.89	0.399	2.54	
Paper-citation networks						
ISI	783,339	8.57	--	--	3	Redner, (1998)
PhysRev	24,296	14.5	--	--	3	
PNAS	45,120	3.53	--	0.081	2.29	
SIM	37,114	2.13	--	0.074	2.05	

```
// Initialization
generate #_papers papers and assign a random topi
generate #_authors authors and assign a random to
randomly assign #_co-authors+1 authors to papers o
// Simulation
for each year do {
    add #_new_authors new authors, deactivate aut
    for each topic do {
        randomly partition set of authors into autho
        for each author_group do {
            for each new_paper to be produced,
                generate new_paper;
                randomly select #_read_paper
                get all references of read_pap
                for each new_paper_reference
                    select a time_slice from (s
                    randomly select a paper p
                    add the new_paper_refere
                }
            }
        }
    }
    add all new papers to the set of existing papers;
    add new links to author and paper information;
}
```

```
-------------------------------------------
Model Parameters (0=without, 1=with)
-------------------------------------------
0/1  Topics
0/1  Co-Authors
0/1  Consider References
0    Aging Function
-------------------------------------------
Model Initialization Values
-------------------------------------------
2  # Years
5  # Authors in Start Year
5  # Papers in Start Year
2  # Papers Consumed (Referenced) per Paper
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5  # Topics
1  # Co-Author(s) per Author
1   # Levels References are Considered
```

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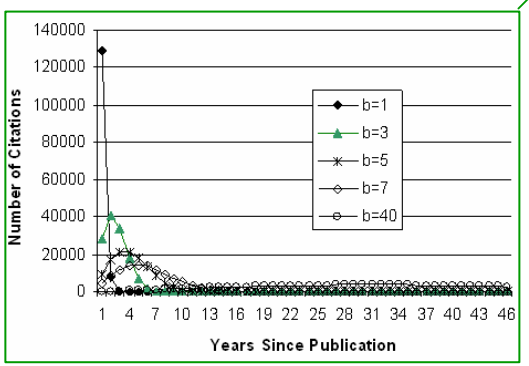
PNAS Data Set → Model Validation

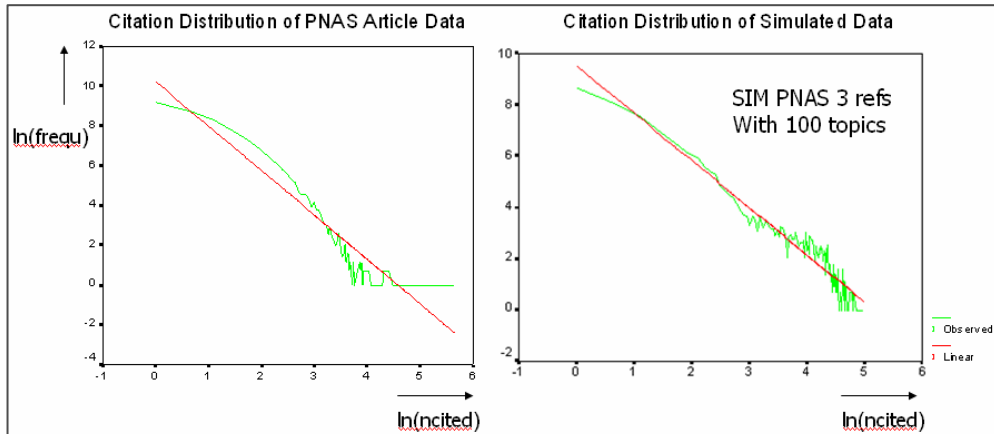
Simple Statistics
Network Properties
N, <k>, l, C , γ

Co-Author and Paper-Citation Network Properties

Aging function



Power Law Distributions



Rsq	d.f.	F	Sigf	b0	b1
.877	70	497.88	.000	10.2251	**-2.2978**

Rsq	d.f.	F	Sigf	b0	b1
.842	114	1572.51	.000	9.5196	**-2.054**

```
// Initialization
generate #_papers papers and assign a random topic to each paper;
generate #_authors authors and assign a random topic to each author;
randomly assign #_co-authors+1 authors to papers of the same topic;
// Simulation
for each year do {
    add #_new_authors new authors, deactivate authors older than #_author_age;
    for each topic do {
        randomly partition set of authors into author_groups of size #_co-authors+1;
        for each author_group do {
            for each new_paper to be produced, do {
                generate new_paper;
                randomly select #_read_ papers from existing papers;
                get all references of read_ papers up to #_reference_path_length;
                for each new_paper_reference do {
                    select a time_slice from (start year to curr_year-1) with probability given in aging_function;
                    randomly select a paper published or cited in this time_slice; as a new_paper_reference;
                    add the new_paper_reference to new_paper;
                }
            }
        }
    }
    add all new papers to the set of existing papers;
    add new links to author and paper information;
}
```

```
-------------------------------------------
Model Parameters (0=without, 1=with)
-------------------------------------------
0/1  Topics
0/1  Co-Authors
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0    Aging Function
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Model Initialization Values
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2  # Years
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```

Input Script

Model

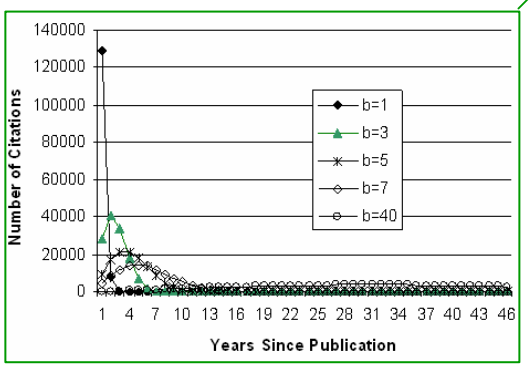
Simulated Networks

Model Validation

Simple Statistics
Network Properties
N, <k>, l, C , γ

PNAS Data Set

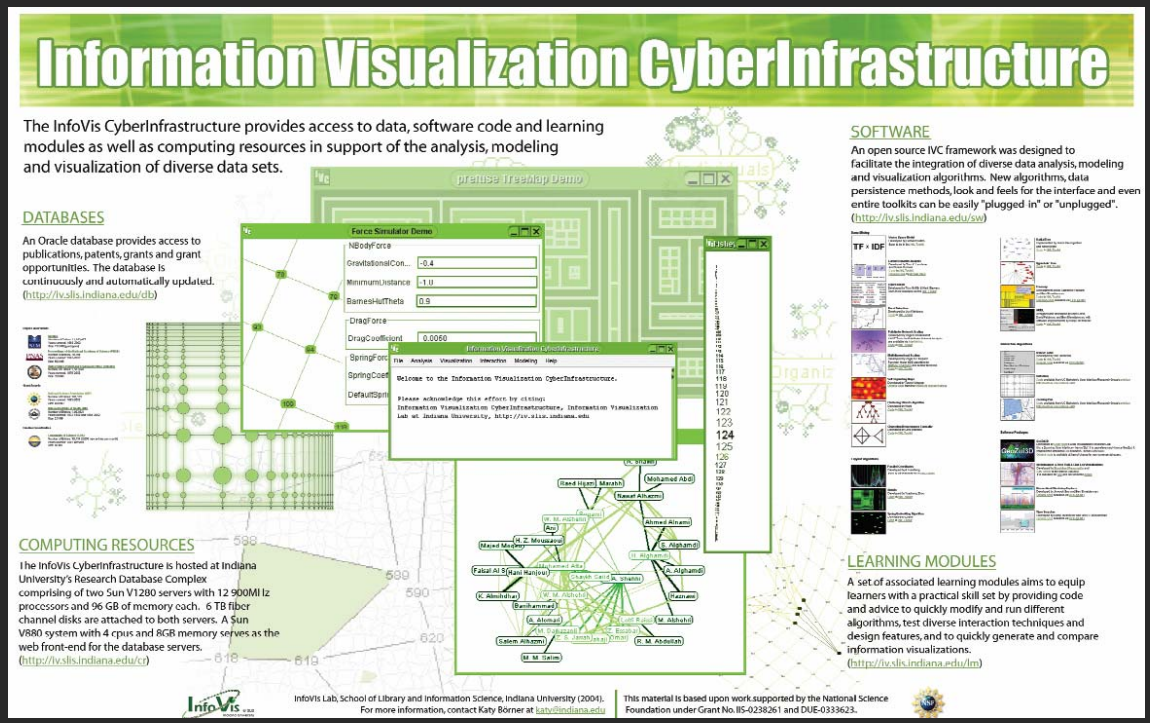
Aging function



Topics: The number of topics is linearly correlated with the clustering coefficient of the resulting network: C= 0.000073 * #topics. Increasing the number of topics increases the power law exponent as authors are now restricted to cite papers in their own topics area.

Aging: With increasing b, and hence increasing the number of older papers cited as references, the clustering coefficient decreases. Papers are not only clustered by topic, but also in time, and as a community becomes increasingly nearsighted in terms of their citation practices, the degree of temporal clustering increases.

References/Recursive Linking: The length of the chain of paper citation links that is followed to select references for a new paper also influences the clustering coefficient. Temporal clustering is ameliorated by the practice of citing (and hopefully reading!) the papers that were the earlier inspirations for read papers.



CAREER: Visualizing Knowledge Domains. NSF IIS-0238261 award (Katy Börner, $451,000) Sept. 03-Aug. 08.
http://iv.slis.indiana.edu/

CIShell
cyberinfrastructure shell

SDB | SCHOLARLY DATABASE

Scholarly Database
http://sdb.slis.indiana.edu

NetworkWorkbench
A Workbench for Network Scientists

SEI: Network Workbench: A Large-Scale Network Analysis, Modeling and Visualization Toolkit for Biomedical, Social Science and Physics Research. NSF IIS-0513650 award (Katy Börner, Albert-Laszlo Barabasi, Santiago Schnell, Alessandro Vespignani & Stanley Wasserman, Eric Wernert (Senior Personnel), $1,120,926) Sept. 05 - Aug. 08. http://nwb.slis.indiana.edu

NSF SBC Sun microsystems
HPNAP High Performance Network Applications Program
INDIANA 21st Century Research & Technology Fund

The End.