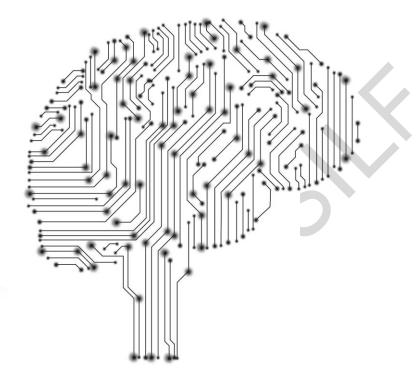


Rising from Service to Partner: A Team Science Model to Redefining Digital Scholarship Centers in Libraries



Xuemao Wang Dean and University Librarian University of Cincinnati

> James Lee Academic Director Digital Scholarship Center



More Than Just a Name

"Digital Humanities":

- Transforming an Entire Area of Academic Inquiry
- A Recognized Field / A Critical Mass Forming

"Digital Scholarship":

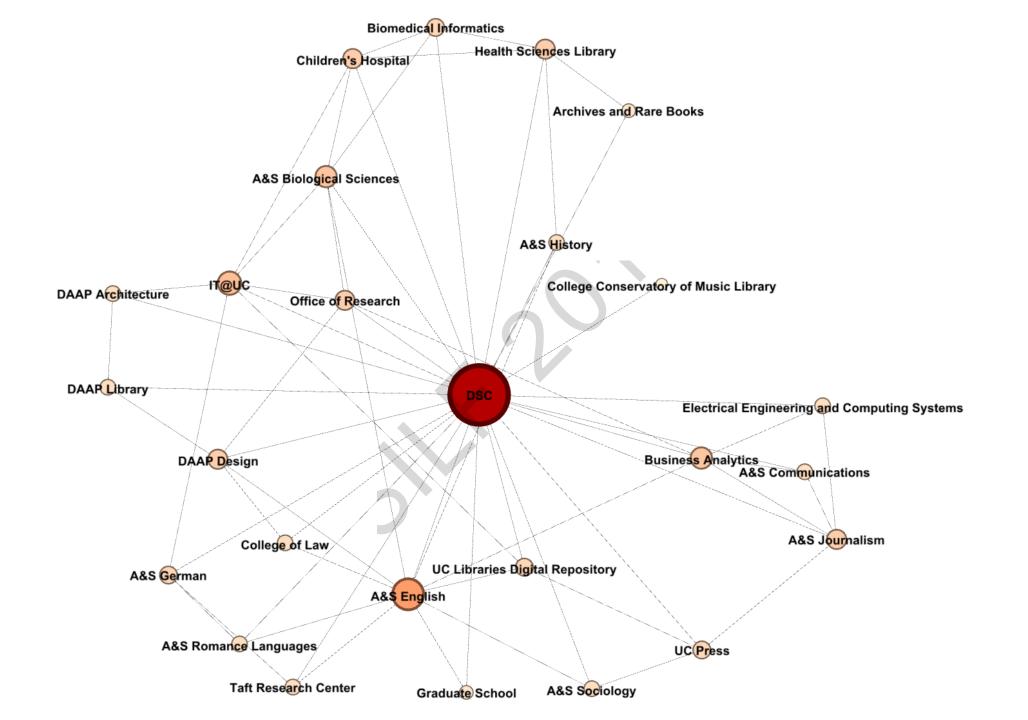
- Producing New Knowledge using Digital Techniques
- New Publications and Venues



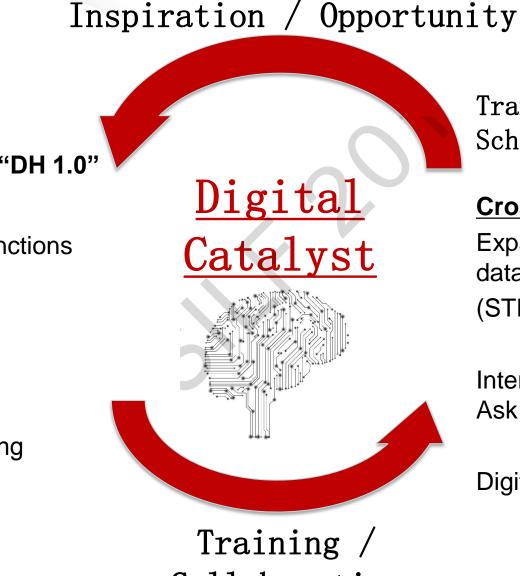
From Initiative to Center

- Co-directorship: Spirit of Partnership between A&S and the Libraries
 - Groundwork for Deep Collaborations between Center and Academic Departments
- An Academic Center: Learning from Precedents

Existing Model 1: Service Provider / "Digital Dry Cleaner"
 Existing Model 2: Pure Research Lab
 Our Hybrid Model: R&D and Catalyst







Digital Humanities: "DH 1.0"

Services: Library Functions

•Omeka

- Text Encoding
- •Tableau

•"Intro to DH" Teaching Modules

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Transdisciplinary Digital Scholarship: "DH 2.0"

Cross-Disciplinary Pipeline:

Expand DH techniques to unconventional datasets

(STEM / Applied Data / Archives)

Interactive Tools to Allow Collaborators to Ask Questions of Data

Digital Pedagogy across the Disciplines



Model: Catalyst vs. Concierge

- 6 Digital Centers/Studios supported by Mellon initiative.
- Leaders defining a new type of "digital integrator" collapsing silos.
- First wave: UIUC, UConn, Brown, Emory.
- Now: UC's DSC and Duke.
- Spectrum from "concierge" to "catalyst."
- Digital integrators as hubs in the academic research ecosystem.



Transdisciplinary Teams in Digital Scholarship

- What are Digital Scholarship Centers / Studios?
- The DSC has assembled research groups that genuinely span multiple disciplines, with people trained to think very differently about every step in the research process.
- Teams are composed of true partners across entire research lifecycle:
 - Formulation of research questions
 - Pitching grant proposals
 - Dataset cleanup and manipulation
 - Data analysis and visualization
 - o Argument formation
 - Publication of findings



Not Just a Feel-Good Story

- Multiple publications in a range of fields content area, methodology, popular press.
- Grants from multiple bodies agencies, foundations, industry.
 Example: "Iowa Digital Bridges" Mellon and Gates Foundations, NIH, NSF, NEH, NEA.
- A new perspective on teaching and doctoral training.



HOME ABOUT US WHAT IS DH NEWS VISUALIZATIONS PUBLICATIONS CONTACT US

UC DIGITAL SCHOLARSHIP CENTER

A catalyst for collaborative, trans-disciplinary forms of research and teaching, bringing together humanistic methods with technical innovations.



Andrew W. Mellon Foundation Grant

- \$900,000 over 30 months from the Andrew W. Mellon Foundation.
- Specific goal: Advance our "catalyst" model of Digital Scholarship.
- The long view: Mellon supports culture change.
- Goals:

 Model new transdisciplinary strategies and practices for digital scholarship centers to overcome challenges in the transition from a service-oriented model to a more active model of intellectual partnership in the research enterprise.

 Transdisciplinary computational tools / Human interpretable research products

Machine Learning and Historical Archives



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Building Bridges: Data Structures



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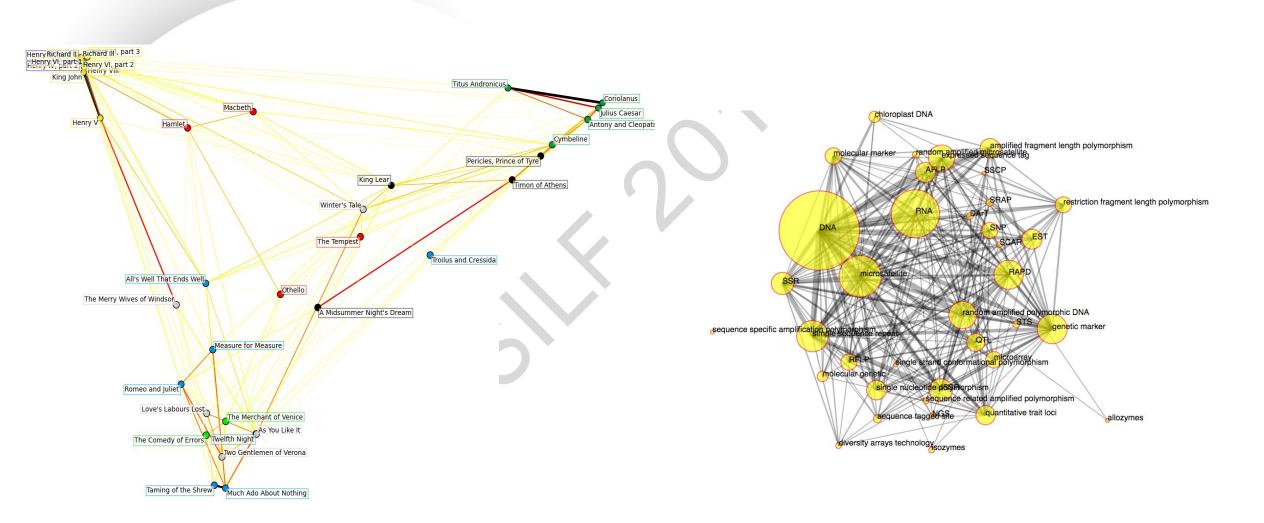
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Building Bridges: Data Structures

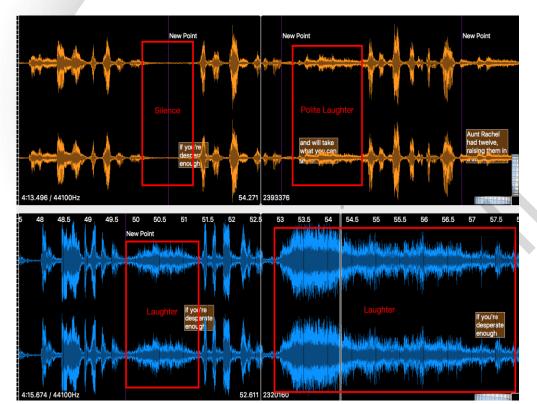


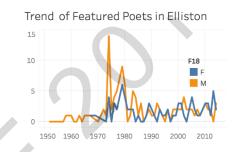


Building Bridges: Data Visualization

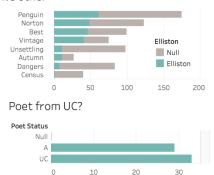


• Different visual frameworks for analysis and interpretability



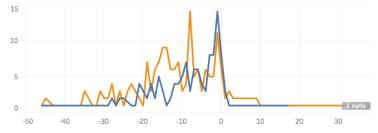




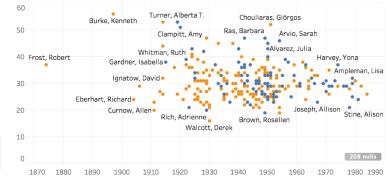


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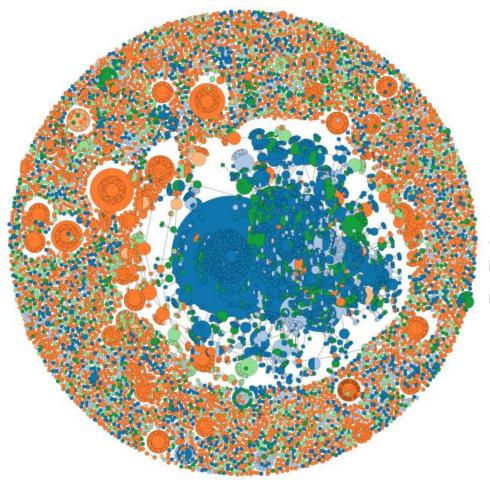


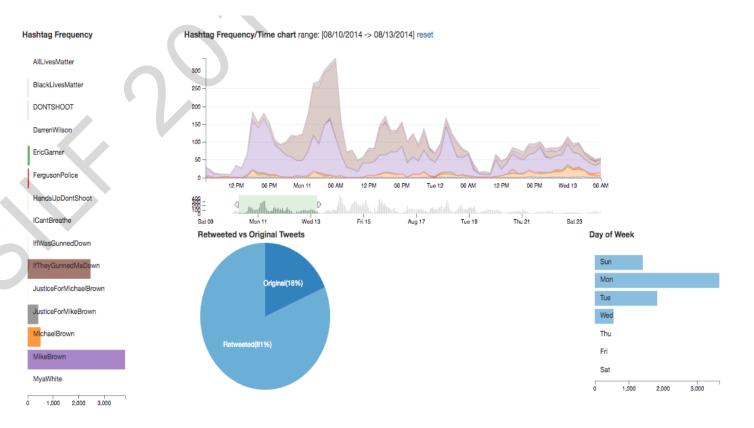
Age when first book is released



Shared Motivations, Different Languages CINCINNATI LIBRARIES

- Twitter Social Networks: Social network analysis and visualization of social movements.
- Team: DSC. A&S Tournalism. DAAP. CoM, CEAS EECS, CECH.

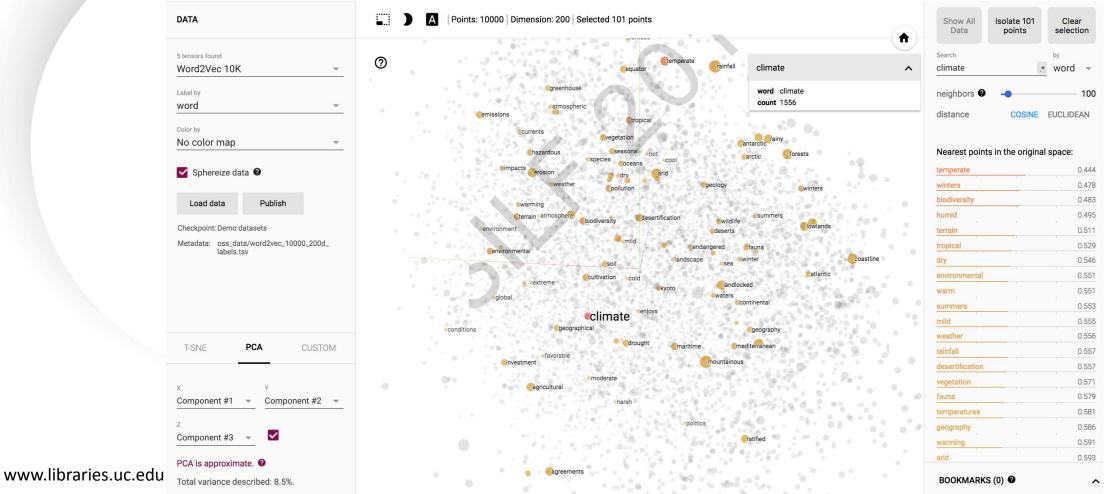




Shared Motivations, Different Languages



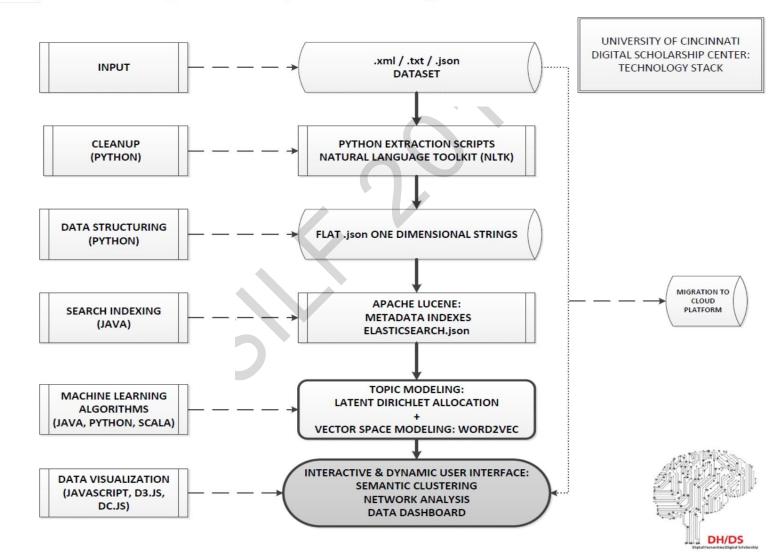
- Using machine learning to parse, extract salient features, and analyze scientific literature.
- Team: A&S Biological Sciences, UC CoM, CCHMC Foster Care Team, Visual Systems Group.



Cloud Platform for Collaboration



University of Cincinnati Digital Scholarship Center Technology Stack



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Topic model: +plant +biodiversity-bow [50t,1 + | Term:

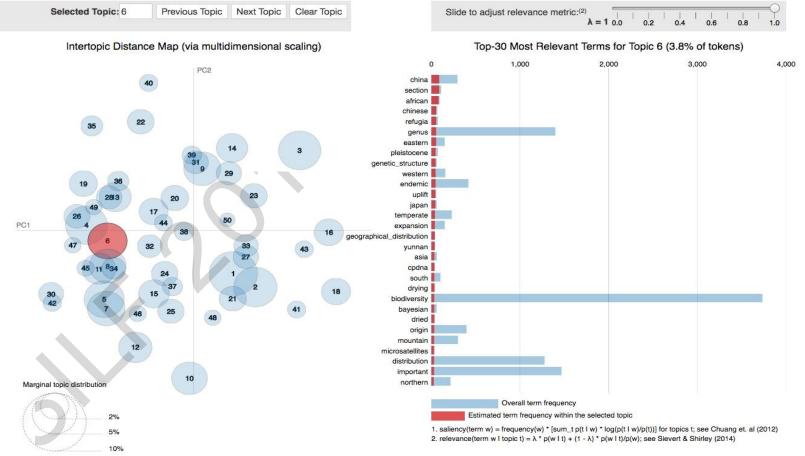
Pollen [D011058]

Check Models

Topic models are trained on selected searches from the Pubmed corpus. Visualization based on the Python port of the LDAvis package.

+plant +biodiversity-bow [50t,100p,2017-08-05,03.18.18] (7036 articles)

Select a	a topic to see the related documents.	
Topic 6		
197232	248] Phylogenetic origin of Phyllolobium with a further implicati	0.64
230716	663] Genetic diversity and population structure of cucumber (Cucu	0.54
166227	792] Biodiversity of Streptomyces of high-mountainous ecosystems	0.39
264676	618] Phylogeography of Phytophagous Weevils and Plant Species in	0.35
239624	109] Phylogeography sheds light on the central-marginal hypothesi	0.34
[240651	[81] Contemporary pollen-mediated gene immigration reflects the h	0.31
[171918	376] Biologically active ibogan and vallesamine derivatives from	0.30
[182062	283] Reduced nitrogen has a greater effect than oxidised nitrogen	0.28
278862	271] Speciation and genetic diversity in Centaurea subsect. Phalo	0.28
[220814	12] Establishing the phylogenetic origin, history, and age of th	0.26
225460	007] Phylogeographic analysis reveals significant spatial genetic	0.26
24498	03] Genetic differentiation and genetic diversity of Castanopsis	0.26
176383	329] Topoisomerase-II-inhibitory principles from the stems of Spa	0.25
	228] Prenylated benzophenone peroxide derivatives from Hypericum	0.25
-	146] Linking patterns and processes of species diversification in	0.24
	346] Diversity of viruses in Cryphonectria parasitica and C. nits	0.24
	258] Ectomycorrhizal characterization of an American chestnut (Ca	0.24
	178) Forest refugia revisited: nSSRs and cpDNA sequences support	0.24
	278] Effect of degradation intensity on grassland ecosystem servi	0.24
	944] Post-Boreotropical dispersals explain the pantropical disjun	0.24
	324] The evolutionary history of Eugenia sect. Phyllocalyx (Myrta	0.24
	783] Temperate pine barrens and tropical rain forests are both ri	0.24
	994] A phylogeny of Delphinieae (Ranunculaceae) shows that Aconit	0.23
		0.22
	542] Phylogeographic evidence for a link of species divergence of	
-	582] Large-scale pattern of genetic differentiation within Africa	0.22
	022] Range expansion of a selfing polyploid plant despite widespr	0.21
	053] Diversification of plant species in arid Northwest China: sp	0.21
	070] Tertiary origin and pleistocene diversification of dragon bl	0.20
PMID	20854478	
Article Title	Forest refugia revisited: nSSRs and cpDNA sequences support historica in a wide-spread African tree with high colonization capacity, Milicia exc (Moraceae). ar 2010	
	Africa [D000349]	
	Bayes Theorem [D001499]	
	Cluster Analysis [D016000]	
	DNA, Chloroplast [D018742]	
	genetics [Q000235]	
	DNA, Plant [D018744]	
	genetics [Q000235]	
	Evolution, Molecular [D019143] Gene Flow [D051456]	
Mach	Gene Pool [D005788]	
Mesh	Genetics, Population [D005828]	
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	Models, Genetic [D008957]	
	Moraceae [D029586]	
	genetics [Q000235]	



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Topic 10	
A07602,5,699	1.000000
A26373,24,54	1.000000
A29216,4,158	1.000000
A29216,4,171	1.000000
A37163,1,3	1.000000
A39127,18,160	1.000000
A46270,5,528	1.000000
A52865,7,2198	1.000000
A63414,10,275	1.000000
A63439,12,274	1.000000
A77565,28,2215	1.000000
B05011.0.17	1.000000

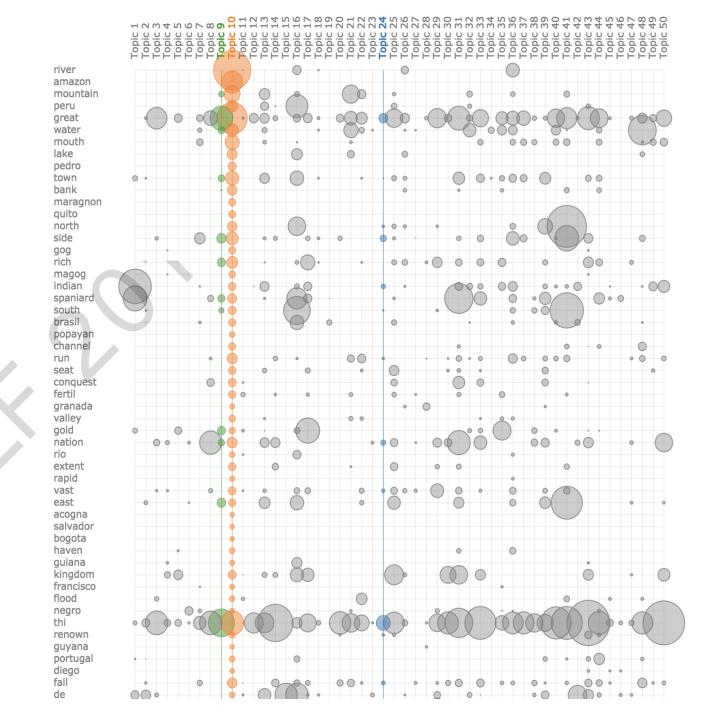
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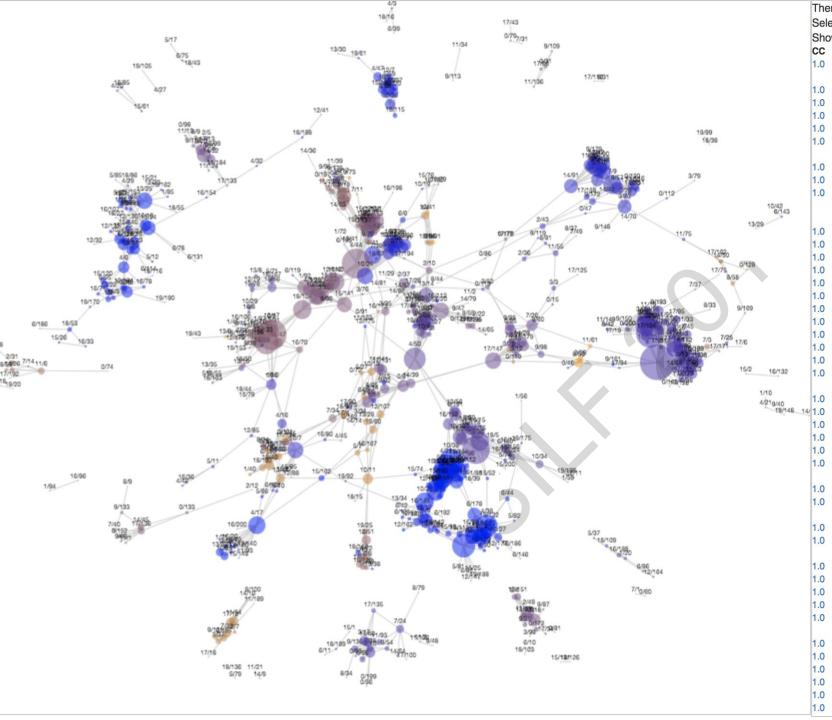
Topic Score: >0 >1 >10 >25 >50 >100

The works of Josephus with great diligence revised and [A46286,13,37]

The Hangings were also of the same **length**, being a Babylonian Vail, wrought with Violet, and Purple Silk and Scarlet, admirable to behold: the permixtion of which colours had a mystical meaning, The Babylonians Vail of admirable workmanship. bearing as it were the signification of the whole **World**. For the Scarlet seemed to express the Fire, the Silk the Earth, the Violet the Air, and the Purple the **Sea**; partly in their colours resembling them, partly also as having their beginning from them: The signification of the Vail. for the Purple is ingendred in the **Sea**, and the Silk is produced by the Earth. In this Tapestry **work** was curiously wrought, and deciphered all the Speculations of the Heavens, only the Celestial Signs excepted. Being entred within, you come into a lower **place** of the Temple, which was sixty Cubits **high**, and as many in **length**, and 20 in breadth. Which **place** was

divided into two parts, **whereof** first contained fourty Cubits,Three admirable works: The Candlestick, the Table and Censer. having in it three most admirable things, famous throughout the **World**, to wit, a Candlestick, a Table, and the Altar of Incense. Upon the Candelstick seven Lamps were placed, signifying the seven Planets, (for so many did there come all out of one stem of the Candelstick). Upon the Table were standing twelve loaves of





here a	are 69 labels	s, including -1.
		# Edges: 43
	By Cc / By N	
C		Positive Terms
.0	6/42	expression 0.07, gene 0.04, stress 0.03, tissue 0.02, response 0.02, promoter 0.02, regulate 0.02
.0	13/48	evolution 0.03, specie 0.02
.0	13/37	
.0	1/62	gene 0.11, arabidopsis 0.02, expression 0.02
.0	4/5	expression 0.02, mutant 0.02, function 0.02
.0	18/178	function 0.07, mutant 0.06, control 0.03, arabidopsis 0.03, yeast 0.02, signal 0.02, cellular 0.02
.0	12/166	gene 0.06, development 0.05, function 0.03, expression 0.02
.0	12/189	protein 0.13, domain 0.04, family 0.02, function 0.02
.0	15/139	evolution 0.08, lineage 0.05, clade 0.04, evolutionary 0.04, origin 0.03, loss 0.03, phylogenetic 0.03, evolve 0.03, phylogeny 0.03, angiosperm 0.03, ancient 0.02, suggest 0.02, early 0.02
.0	19/122	protein 0.25, domain 0.09, sequence 0.03, conserve 0.03, terminal 0.03, motif 0.02
.0	19/142	mutant 0.07, arabidopsis 0.04, mutation 0.03, function 0.03, phenotype 0.03
.0	10/39	gene 0.05, specie 0.03, evolution 0.02
.0	12/59	expression 0.07, promoter 0.04, gene 0.04, regulate 0.02
.0	5/14	gene 0.09, expression 0.04, study 0.02, identify 0.02
.0	12/147	pathway 0.05, signal 0.04, response 0.04, mechanism 0.03, mediate 0.03, stress 0.02
.0	16/197	gene 0.14, intron 0.02
.0	1/9	protein 0.1, domain 0.03
.0	6/178	protein 0.26, domain 0.07, family 0.04, identify 0.02
.0	6/71	gene 0.19, identify 0.03, analysis 0.03, expression 0.02, study 0.02, arabidopsis 0.02
.0	19/188	enzyme 0.07, pathway 0.06, signal 0.04, bacterial 0.02
.0	12/177	protein 0.07, subunit 0.02, terminal 0.02, complex 0.02, show 0.02, sequence 0.02, form 0.02, conservation 0.02
.0	1/73	mutant 0.05, function 0.03, arabidopsis 0.03, cell 0.03, expression 0.02
.0	18/122	protein 0.08, domain 0.05, bind 0.03, structure 0.03
.0	15/93	protein 0.04, yeast 0.03, arabidopsis 0.03, function 0.03, show 0.02, cell 0.02
.0	4/22	gene 0.08
.0	5/84	protein 0.25, domain 0.06
.0	19/136	evolution 0.06, arabidopsis 0.04, gene 0.04, conserve 0.03, divergence 0.02, specie 0.02, function 0.02
.0	15/182	gene 0.13, expression 0.04, arabidopsis 0.04, function 0.03
.0	12/151	evolution 0.07, lineage 0.03, evolve 0.03, evolutionary 0.02, angiosperm 0.02, divergence 0.02, origin 0.02
.0	6/90	yeast 0.04, complex 0.03, protein 0.03, subunit 0.02, mammalian 0.02
.0	16/143	gene 0.08, expression 0.06, mutant 0.04, function 0.03, development 0.03, regulate 0.02, show 0.02, express 0.02
.0	10/46	protein 0.06
.0	4/38	protein 0.08, domain 0.02
.0	6/64	evolution 0.06, gene 0.04, angiosperm 0.02, family 0.02
.0	18/69	gene 0.19, expression 0.06, show 0.03, function 0.03, express 0.03, arabidopsis 0.02
.0	5/86	function 0.06, arabidopsis 0.04, pathway 0.03, development 0.03, regulate 0.03, signal 0.03, control 0.02, role 0.02
.0	5/100	gene 0.09
.0	15/159	protein 0.26, domain 0.08
.0	19/113	protein 0.08, yeast 0.03, show 0.02
.0	10/27	protein 0.04, domain 0.03, family 0.02, sequence 0.02
.0	10/26	gene 0.06, expression 0.03, arabidopsis 0.02
.0	16/98	protein 0.13

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table	cloud	timeline	json mo	ors:china m	noors:turks	america:chi	ina america	othello	china moor	rs moor	
1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680
turks	turks	moors	turks	turks	moors	turks	saracens	moors 100%, 69%	moors	moors 100%, 69%	turks 71%, 100%
turkes	turkes	turks	moors	moors	turks	moors	parthians	turks 69%, 100%	turks 75%, 100%	turks	moors
saracens	saracens	turkes	turkes	turkes	turkes	turkes	moors	saracens	tartars 69%, 74%	tartars 70%, 71%	spaniards
assyrians	persians	tartars	spaniards	saracens	saracens	barbarians	turks	tartars	spaniards	saracens	saracens 74%, 72%
nunnes	pagans	hungarians	hungarians	moores	moores	saracens	turkes	spaniards	saracens	persians	tartars
oersians	barbarians	tartarians	67% romans	pagans	tartarians	tartars	80% pagans	67%, 70% tartarians	66%, 68% turkes	indians	indians
vandales	armenians	67% saracens	portugals	mahumetans	arabians	moores	vandals	68%, 67% scythians	63%, 67% sarazens	64%, 68% sarazens	barbarian
saracenes	65% assyrians	66% spaniards	barbarians	tartars	62% parthians	68% scythians	70% gothes	66%, 66%	65%, 64% portugals	63%, 66% arabians	66%, 71% persians
	64%	65%	66%	64%	61%		67%	83%	68%, 61%	63%, 64%	65%, 72%
artarians	egyptians 62%	dalmatians 64%	tartars 65%	arabians 64%	vandales	persians 64%	67%	78%	muscovites 62%, 64%	tartarians 61%, 65%	germans 68%, 68%
arabians	arabians 61%	nomades 64%	sarazins	barbarians 64%	portugals	romans 63%	tartars 65%	sarmatians	hungarians	armenians 67%	venetians
spanyards	infidels 61%	persians	moores	infidels 64%	visigothes	tartarians	persians	pagans 70%	moores 67%	mahometans	imperialis
othes	gothes	gaules	sicilians	armenians	pagans	danes	moores	huns 69%	carthaginians	scythians	hungariar
medes	scythians	moores	britans	mahometans	spaniards	indians	arabians	mahometans	venetians	mahumetans	romans 67%
normans	romans	scythians	sarasins	persians	persians	venetians	carthaginians	infidels	portuguez	barbarians	arabians
noores	sarasins	lombardes	persians	grecians	infidells	hungarians	danes	vandals	indians	moscovites	scythians
19.30	59%	parthians		61% aethiopians	58% indians	polonians	heathens	mahumetans	65% castilians	infidels	muscovit
		gothes	61% sirians	pomerania	alani	getes	grecians	sarazens	persians	moores	islanders
		60% sacrata	52% mahumetists	epire	58% tartars	57% spartan	61% tartarians	goths	64% germans	63% goths	65%
		60% florentia	52% perspicua	58% benin	58% goths	54% patricians	60% scythians	67% persians	63% pyrates	63% portugals	65% numidian
		60%	51%	57%	57%	54%	59%	67%	63%	62%	64%
		aider 60%	longi 50%	aria 57%	infidels 57%	scithians	turkish 59%	turk 67%	mamalukes	spaniards 61%	swedes 64%
		celtiberians	bramas	abassia	herules	libyan	goths	barbary	arabians	chineses	gauls

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opic model:	+plant +biodiversity-bow [50t,1 \$	Term:	
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Topic 6		
[1972324	48] Phylogenetic origin of Phyllolobium with a further implicati	0.64
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N	78] Effect of degradation intensity on grassland ecosystem servi	0.24
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	22] Range expansion of a selfing polyploid plant despite widespr	0.21
	53] Diversification of plant species in arid Northwest China: sp	0.21
	70] Tertiary origin and pleistocene diversification of dragon bl	0.20
PMID	20854478	
Article	Forest refugia revisited: nSSRs and cpDNA sequences support historic	
Title	in a wide-spread African tree with high colonization capacity, Milicia ex	celsa
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Pub Yea		
	Africa [D000349]	
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	Cluster Analysis [D016000]	
	DNA, Chloroplast [D018742]	
	genetics [Q000235]	
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	genetics [Q000235]	
	Evolution, Molecular [D019143] Gene Flow [D051456]	
	Gene Plow [D051456] Gene Pool [D005788]	
Mesh		
	Genetics, Population [D005828]	
neading	sMicrosatellite Repeats [D018895] Models, Genetic [D008957]	
	Models, Genetic [D008957] Moraceae [D029586]	
	genetics [Q000235]	
	Pollen [D011058]	

