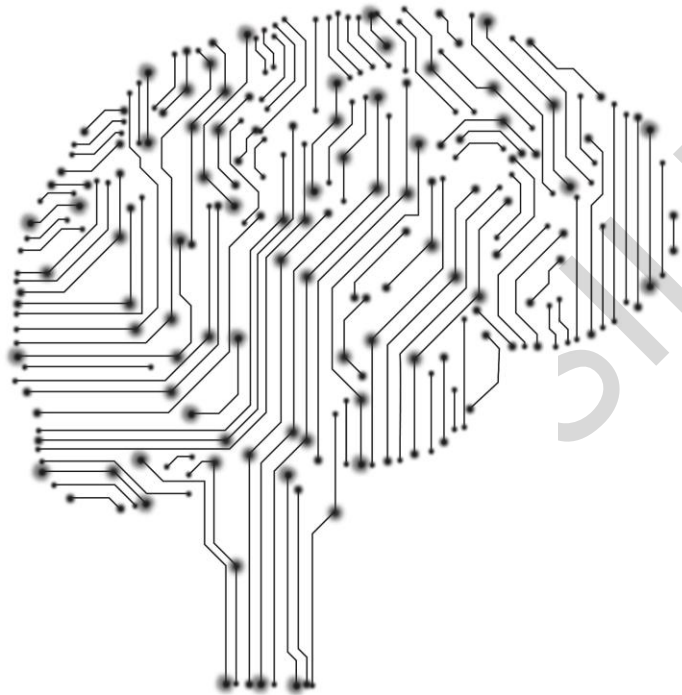# Rising from Service to Partner: A Team Science Model to Redefining Digital Scholarship Centers in Libraries

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~~
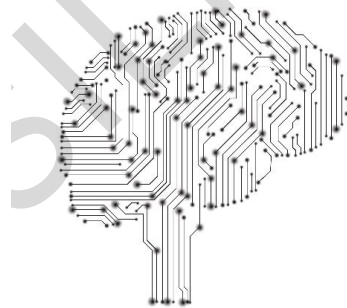 ➢ Our Hybrid Model: R&D and Catalyst
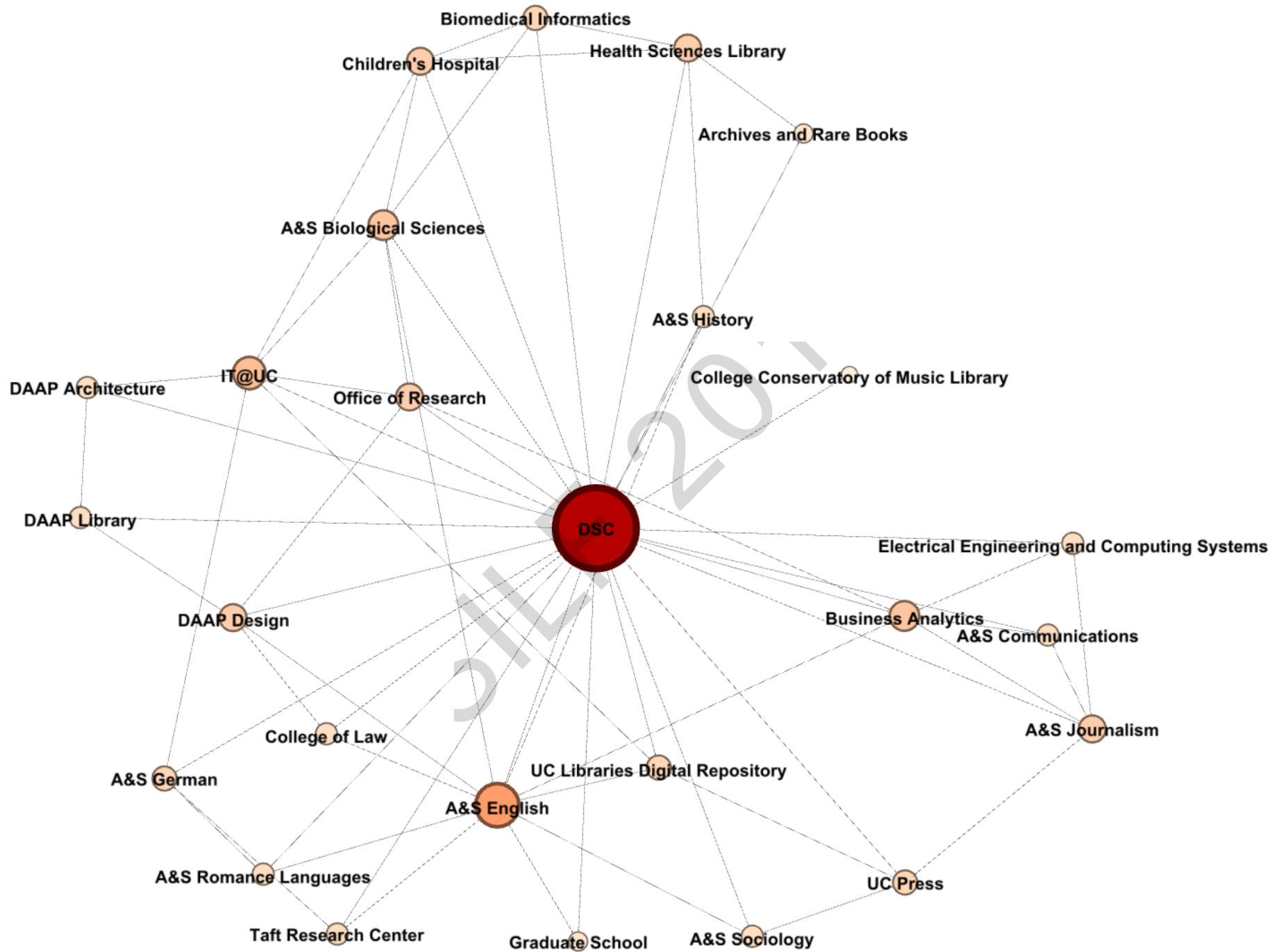
Inspiration / Opportunity

Digital Humanities:"DH 1.0"

Services: Library Functions

•Omeka

•Text Encoding

•Tableau

•"Intro to DH" Teaching Modules

Digital Catalyst

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

Training /

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
  - 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.

University of
CINCINNATI

UC DIGITAL SCHOLARSHIP CENTER

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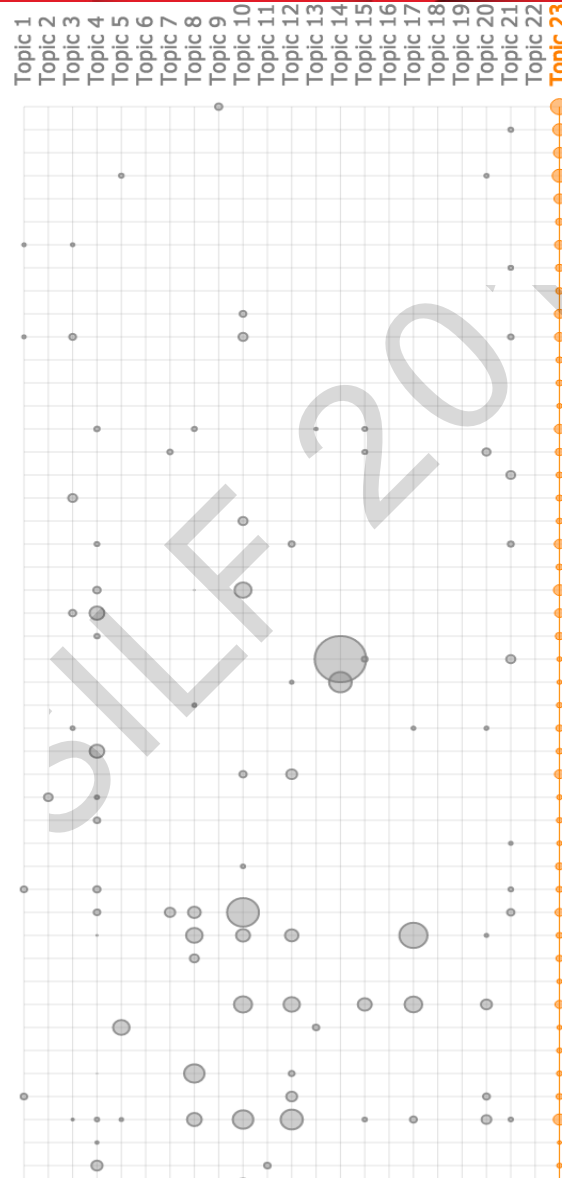
Andrew W. Mellon Foundation Grant

- $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
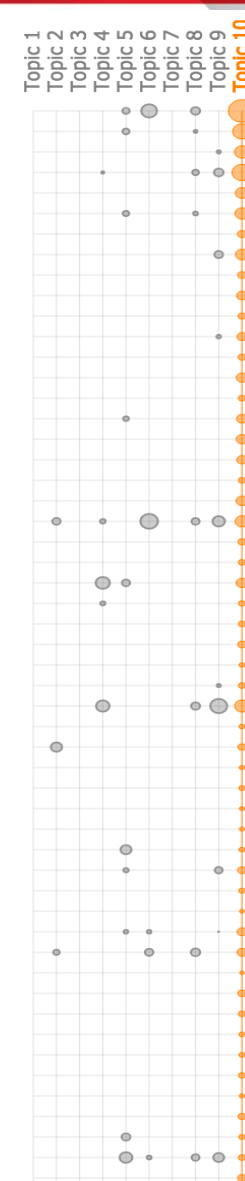
- The Shakespearean and the

13502 1000
the 0.303977 0.044844 0.306057 -0.061538 -0.052806 0.012809 0.191494 -0.300545 -0.151903 0.229944 0.108848 0.262025

```json
[ {
    "section" : "title page",
    "content" : [ "PVRCHAS his PILGRIMAGE. OR RELATIONS OF THE WORLD AND THE RELIGIONS OBSERVED IN ALL AGES
}, {
    "section" : "dedication",
    "content" : [ "TO THE MOST REVEREND FATHER IN GOD, GEORGE BY THE DIVINE PROVIDENCE, LORD ARCHBISHOP OF
}, {
    "section" : "to the reader",
    "content" : [ "TO THE READER.", "_AND now, Reader, I come vnto thee, with whom I dare bee somewhat bolde
}, {
    "section" : "encomia",
    "content" : [ "&Egr;&Igr;&Sgr; &tgr;&igr;&ohgr; &Sgr;&Agr;&Mgr;&Ogr;&Ugr;&EEgr;&Lgr;&Ogr;&Ugr; &tgr;&oug
}, {
    "section" : "table of contents",
    "content" : [ "THE CONTENTS OF THE SEVERALL CHAPTERS IN THE NINE BOOKES ENSVING.", "ASIA.", "THE FIRST E
}, {
    "section" : "bibliography",
    "content" : [ "The Catalogue of the Authors.", "A", "B", "C", "D", "E", "F", "G", "H", "I", "K", "L", "M
}, {
    "section" : "book",
    "content" : [ "THE FIRST BOOKE.", "CHAP. I.", "CHAP. II.", "CHAP. III.", "CHAP. IIII.", "CHAP. V.", "CHA
}, {
    "section" : "book",
    "content" : [ "THE FIRST PART OF THE RELATIONS OF THE WORLD, AND THE RELIGIONS OBSERVED IN ALL AGES, AND
}, {
    "section" : "book",
    "content" : [ "OF THE ARABIANS, SARACENS, TVRKES, AND OF THE ANCIENT INHABITANTS OF ASIA MINOR, AND OF T
}, {
    "section" : "book",
    "content" : [ "OF THE ARMENIANS, MEDES, PERSIANS, PARTHIANS, SCYTHIANS, TARTARIANS, CHINOIS, AND OF THEI
}, {
    "section" : "book",
    "content" : [ "OF THE EAST-INDIES: AND OF THE SEAS AND ILANDS ABOVT ASIA, WITH THEIR RELIGIONS.", "CHAP.
}, {
    "section" : "book",
    "content" : [ "RELATIONS OF THE REGIONS AND RELIGIONS IN AFRICA. OF AeGYPT, BARBARIE, NVMI, DIA, LIBYA,
}, {
    "section" : "book",
    "content" : [ "RELATIONS OF THE REGIONS AND RELIGIONS IN AFRICA. OF AeTHIOPIA, AND THE AFRICAN ILANDS; A
}, {
    "section" : "book",
    "content" : [ "RELATIONS OF THE DISCOVERIES, REGIONS, AND RELIGIONS, OF THE NEW WORLD. OF NEW FRANCE, VI
}, {
    "section" : "book",
    "content" : [ "RELATIONS OF THE DISCOVERIES, REGIONS, AND RELIGIONS, OF THE NEW WORLD. OF CVMANA, GVIANA
}, {
    "section" : "index",
    "content" : [ "A TABLE OF THE PRINCIPALL MATTERS CONTAINED IN THE FIVE FIRST BOOKES, WHICH ARE OF ASIA.
}, {
    "section" : "index",
    "content" : [ "A TABLE OF THE PRINCIPALL MATTERS IN THE FOVRE LAST BOOKES, WHICH ARE OF AFRICA AND AMERI
} ]
```

- Different visual frameworks for analysis and interpretability
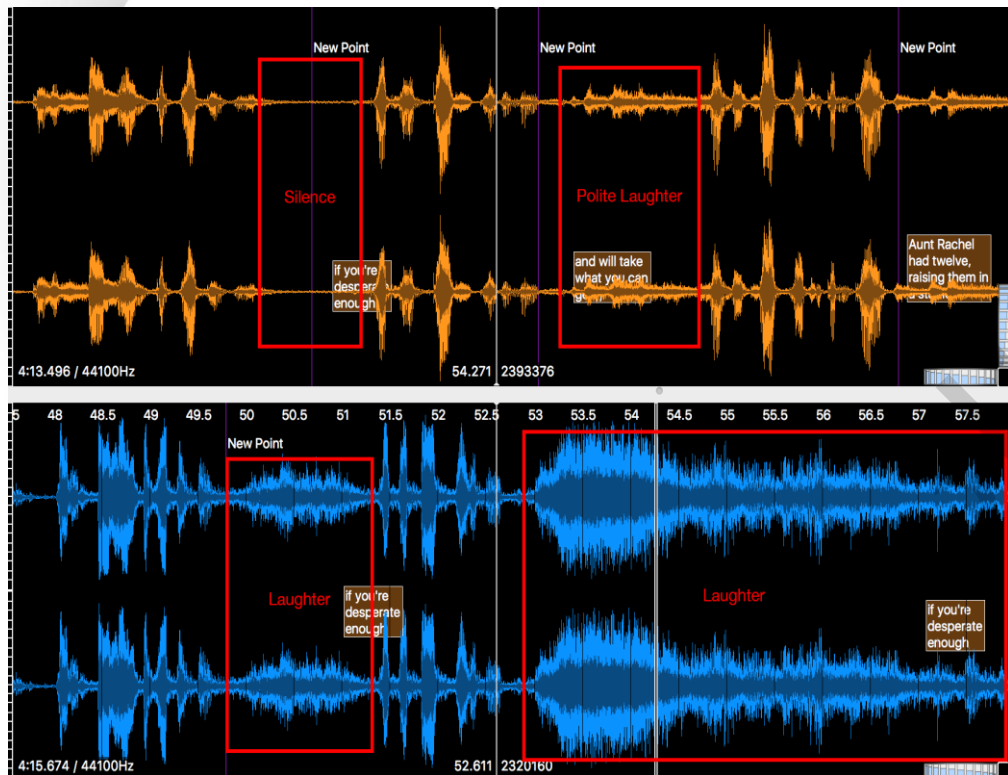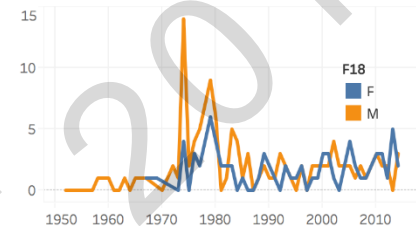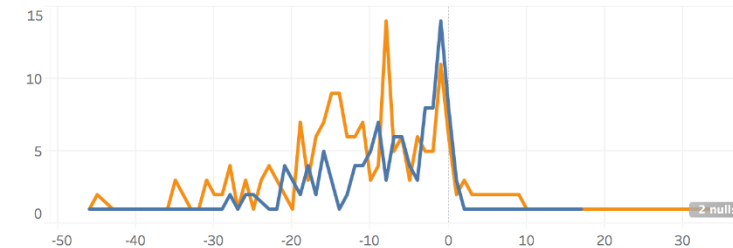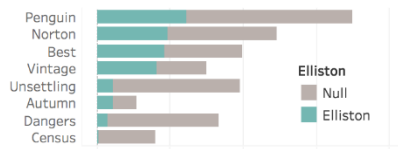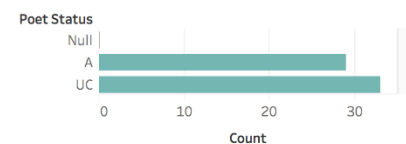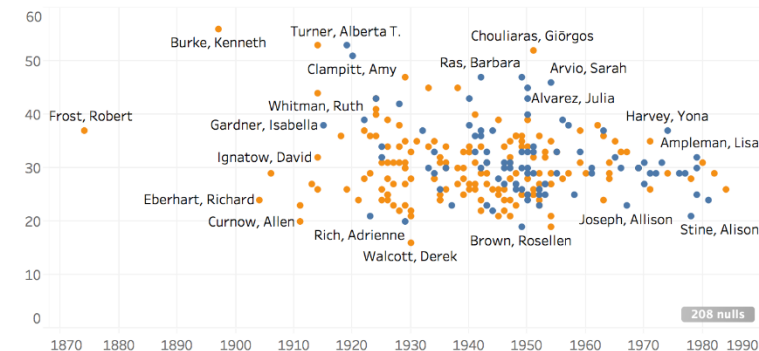
Shared Motivations, Different Languages

- Twitter Social Networks: Social network analysis and visualization of social movements.

- Team: DSC. A&S Journalism. DAAP. CoM, CEAS EECS, CECH.
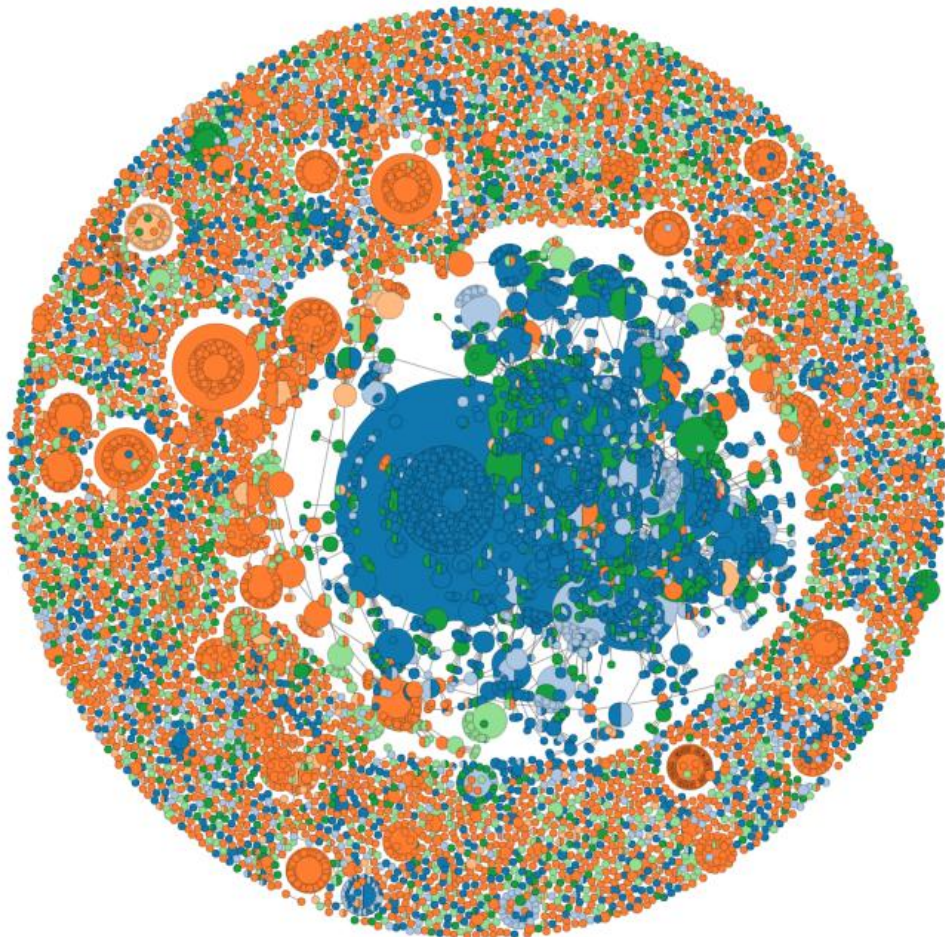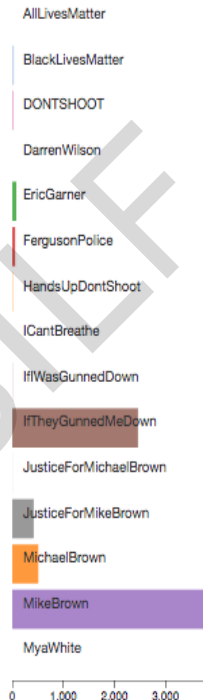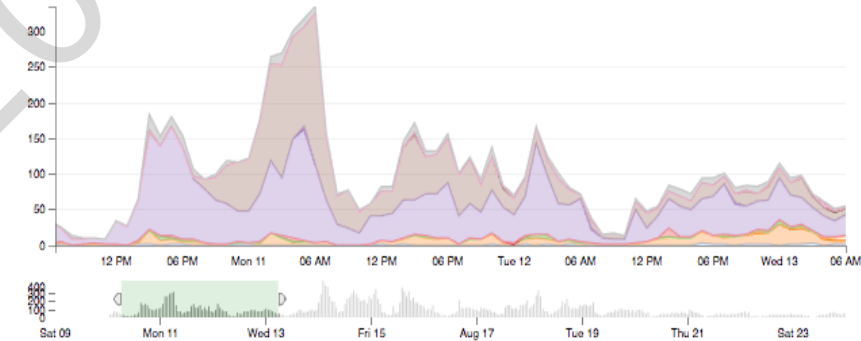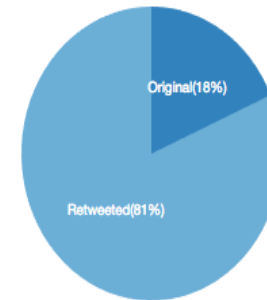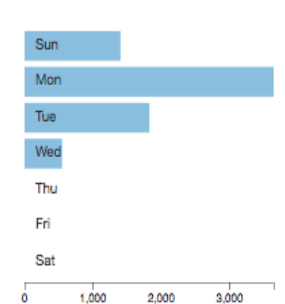
Shared Motivations, Different Languages

- 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.

University of Cincinnati Digital Scholarship Center Technology Stack

Topic model: [+plant +biodiversity-bow [50t,1 ⬍] | Term: [ ]   [Check Models]

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

Select a topic to see the related documents.

Topic 6

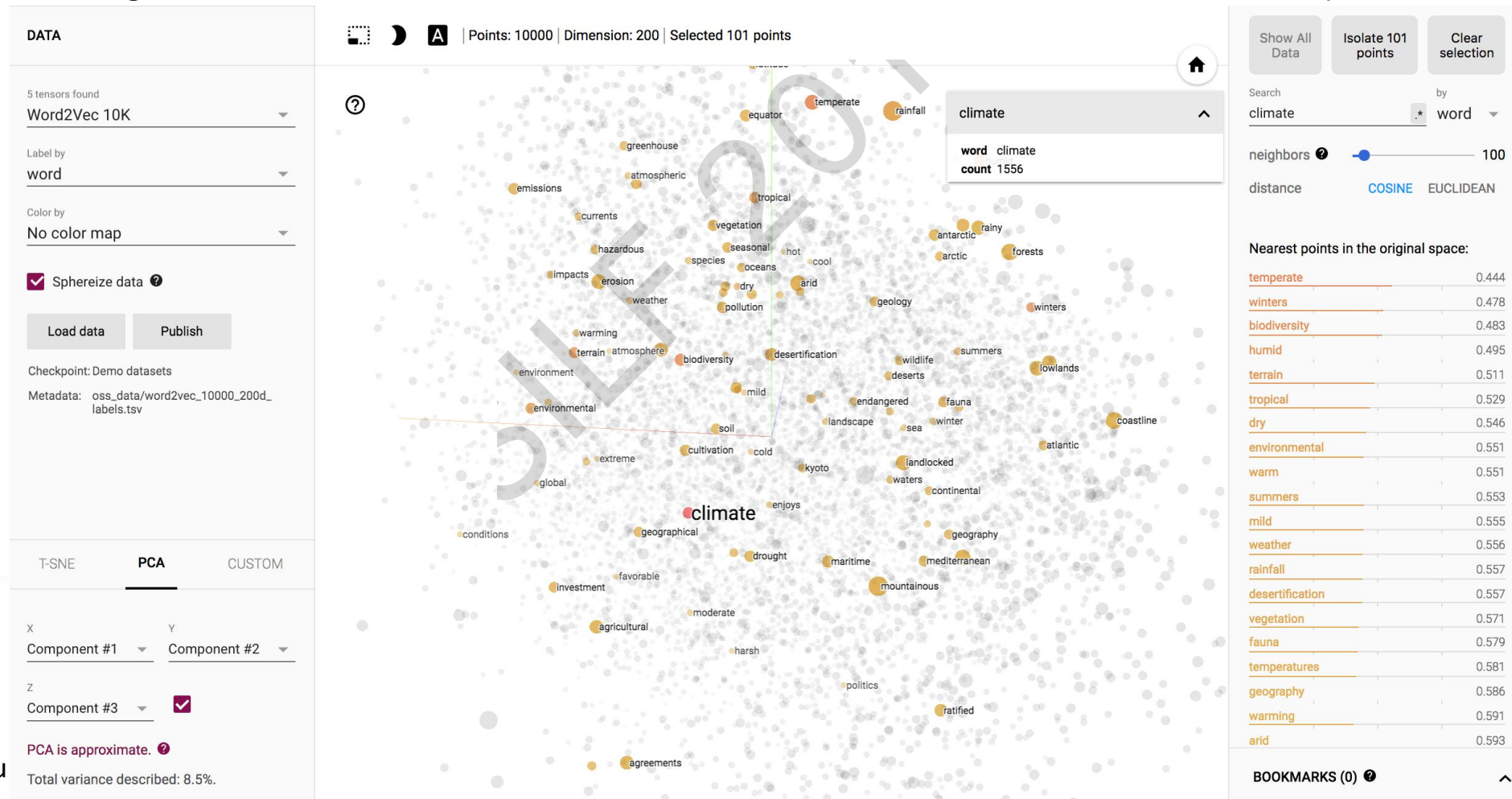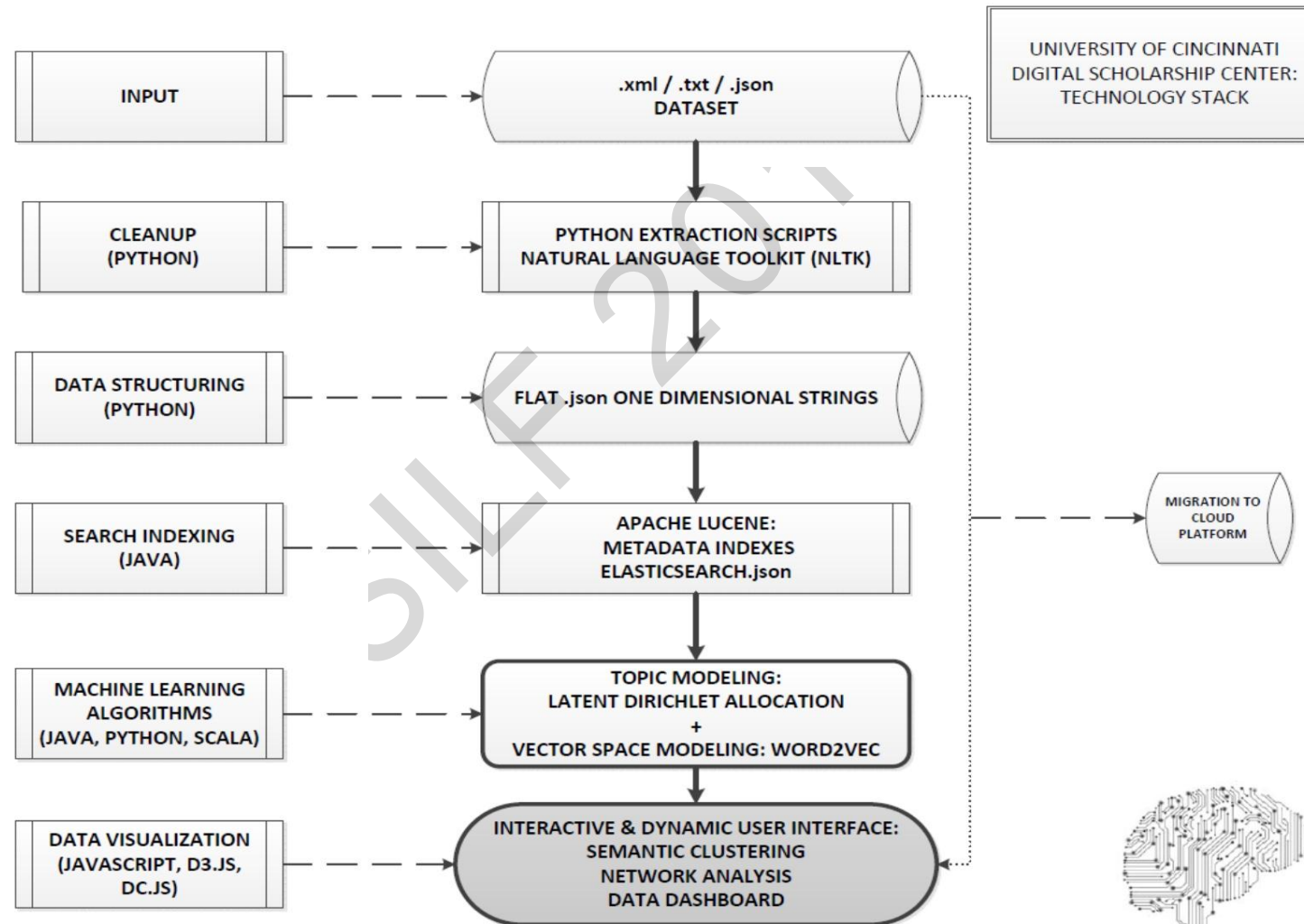|	
[19723248] Phylogenetic origin of Phyllolobium with a further implicati	0.64
[23071663] Genetic diversity and population structure of cucumber (Cucu	0.54
[16622792] Biodiversity of Streptomyces of high-mountainous ecosystems	0.39
[26467618] Phylogeography of Phytophagous Weevils and Plant Species in	0.35
[23962409] Phylogeography sheds light on the central-marginal hypothesi	0.34
[24065181] Contemporary pollen-mediated gene immigration reflects the h	0.31
[17191876] Biologically active ibogan and vallesamine derivatives from	0.30
[18206283] Reduced nitrogen has a greater effect than oxidised nitrogen	0.28
[27886271] Speciation and genetic diversity in Centaurea subsect. Phalo	0.28
[22081412] Establishing the phylogenetic origin, history, and age of th	0.26
[22546007] Phylogeographic analysis reveals significant spatial genetic	0.26
[24498103] Genetic differentiation and genetic diversity of Castanopsis	0.26
[17638329] Topoisomerase-II-inhibitory principles from the stems of Spa	0.25
[20397228] Prenylated benzophenone peroxide derivatives from Hypericum	0.25
[16876446] Linking patterns and processes of species diversification in	0.24
[17509846] Diversity of viruses in Cryphonectria parasitica and C. nits	0.24
[18807258] Ectomycorrhizal characterization of an American chestnut (Ca	0.24
[20854478] Forest refugia revisited: nSSRs and cpDNA sequences support	0.24
[23469278] Effect of degradation intensity on grassland ecosystem servi	0.24
[23478944] Post-Boreotropical dispersals explain the pantropical disjun	0.24
[27974324] The evolutionary history of Eugenia sect. Phyllocalyx (Myrta	0.24
[25072783] Temperate pine barrens and tropical rain forests are both ri	0.23
[22182994] A phylogeny of Delphinieae (Ranunculaceae) shows that Aconit	0.22
[23418542] Phylogeographic evidence for a link of species divergence of	0.22
[24028582] Large-scale pattern of genetic differentiation within Africa	0.22
[22730022] Range expansion of a selfing polyploid plant despite widespr	0.21
[23629053] Diversification of plant species in arid Northwest China: sp	0.21
[23560070] Tertiary origin and pleistocene diversification of dragon bl	0.20

PMID	20854478
Article Title	Forest refugia revisited: nSSRs and cpDNA sequences support historical isolation in a wide-spread African tree with high colonization capacity, Milicia excelsa (Moraceae).
Pub Year	2010
Mesh Headings	Africa [D000349] Bayes Theorem [D001499] Cluster Analysis [D016000] DNA, Chloroplast [D018742] genetics [Q000235] DNA, Plant [D018744] genetics [Q000235] Evolution, Molecular [D019143] Gene Flow [D051456] Gene Pool [D005788] Genetics, Population [D005828] Microsatellite Repeats [D018895] Models, Genetic [D008957] Moraceae [D029586] genetics [Q000235] Pollen [D011058]

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

Selected Topic: 6   [Previous Topic] [Next Topic] [Clear Topic]

Slide to adjust relevance metric:(2)

λ = 1   0.0   0.2   0.4   0.6   0.8   1.0

Intertopic Distance Map (via multidimensional scaling)

Marginal topic distribution

2%
5%
10%
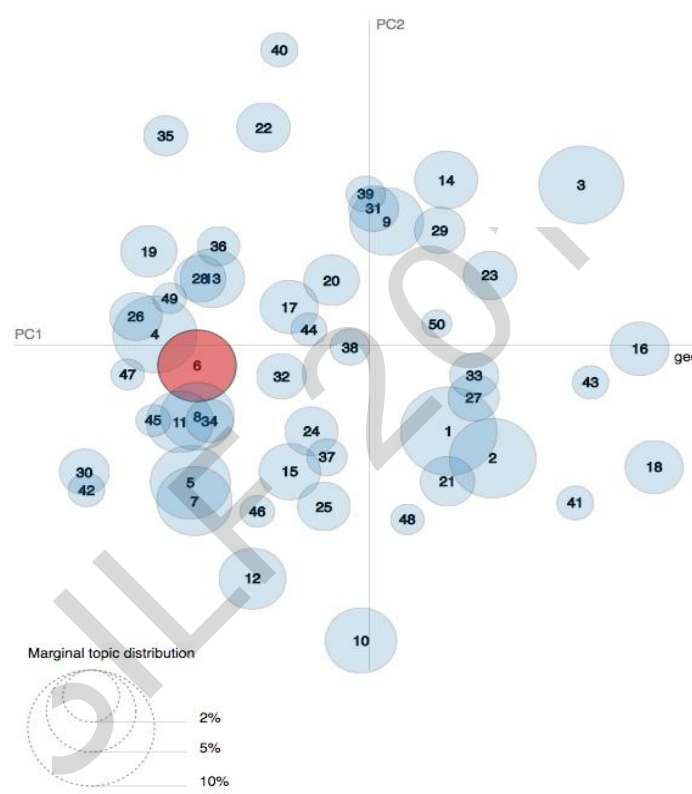
Top-30 Most Relevant Terms for Topic 6 (3.8% of tokens)

Overall term frequency
Estimated term frequency within the selected topic
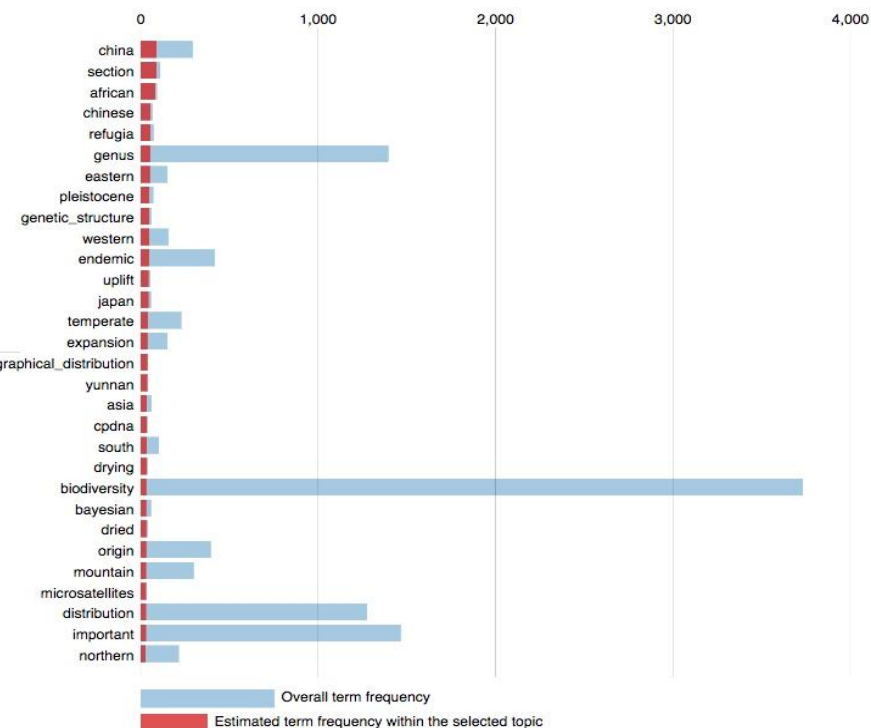
1. saliency(term w) = frequency(w) * [sum_t p(t | w) * log(p(t | w)/p(t))] for topics t; see Chuang et. al (2012)
2. relevance(term w | topic t) = λ * p(w | t) + (1 - λ) * p(w | t)/p(w); see Sievert & Shirley (2014)

Compare Topics

Pulls lists of paragraphs within topic. For larger models please allow time to load

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

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,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

river
amazon
mountain
peru
great
water
mouth
lake
pedro
town
bank
maragnon
quito
north
side
gog
rich
magog
indian
spaniard
south
brasil
popayan
channel
run
seat
conquest
fertil
granada
valley
gold
nation
rio
extent
rapid
vast
east
acogna
salvador
bogota
haven
guiana
kingdom
francisco
flood
negro
thi
renown
guyana
portugal
diego
fall
de
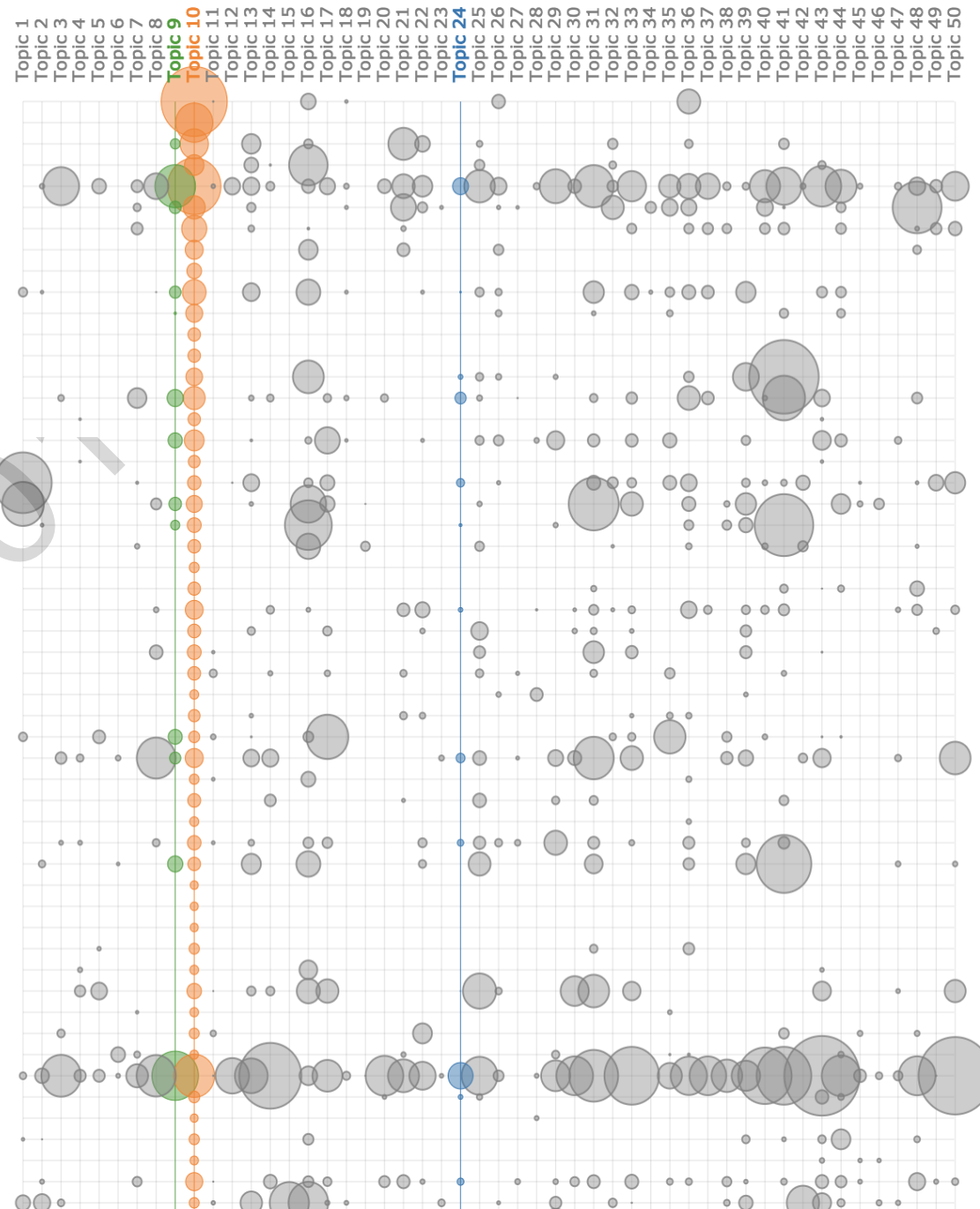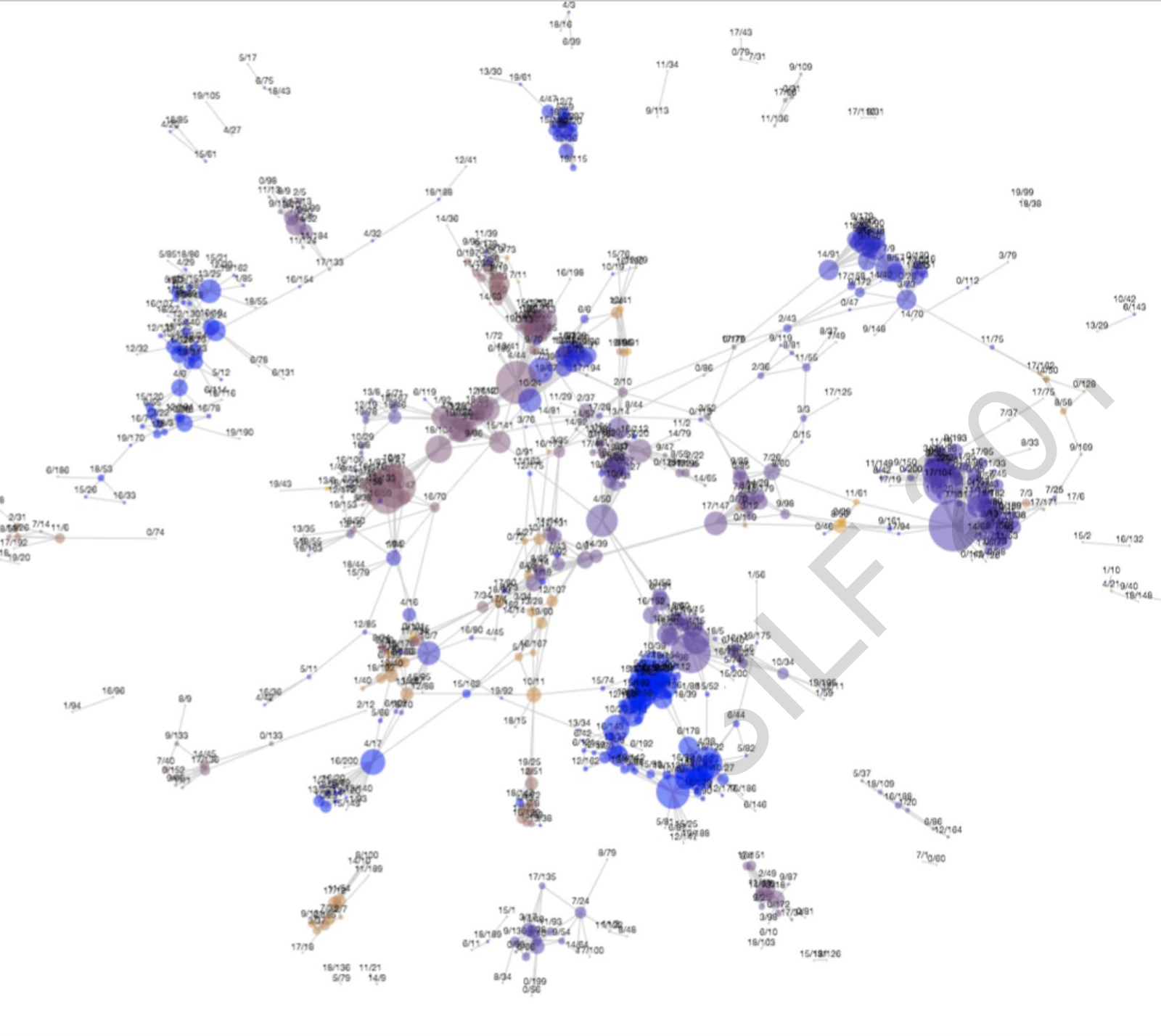
There are 69 labels, including -1.
Selected label: 2.0; # Edges: 43
Show By Cc / By Node.

CC	Model/Topic	Positive Terms
1.0	6/42	**expression 0.07**, **gene 0.04**, stress 0.03, tissue 0.02, response 0.02, promoter 0.02, regulate 0.02
1.0	13/48	evolution 0.03, specie 0.02
1.0	13/37	
1.0	1/62	**gene 0.11**, arabidopsis 0.02, **expression 0.02**
1.0	4/5	**expression 0.02**, mutant 0.02, **function 0.02**
1.0	18/178	**function 0.07**, mutant 0.06, control 0.03, **arabidopsis 0.03**, yeast 0.02, signal 0.02, cellular 0.02
1.0	12/166	**gene 0.06**, development 0.05, **function 0.03**, **expression 0.02**
1.0	12/189	**protein 0.13**, **domain 0.04**, family 0.02, **function 0.02**
1.0	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
1.0	19/122	**protein 0.25**, **domain 0.09**, sequence 0.03, conserve 0.03, terminal 0.03, motif 0.02
1.0	19/142	mutant 0.07, **arabidopsis 0.04**, mutation 0.03, **function 0.03**, phenotype 0.03
1.0	10/39	**gene 0.05**, specie 0.03, evolution 0.02
1.0	12/59	**expression 0.07**, promoter 0.04, **gene 0.04**, regulate 0.02
1.0	5/14	**gene 0.09**, **expression 0.04**, study 0.02, **identify 0.02**
1.0	12/147	pathway 0.05, signal 0.04, response 0.04, mechanism 0.03, mediate 0.03, stress 0.02
1.0	16/197	**gene 0.14**, intron 0.02
1.0	1/9	**protein 0.1**, **domain 0.03**
1.0	6/178	**protein 0.26**, **domain 0.07**, family 0.04, **identify 0.02**
1.0	6/71	**gene 0.19**, **identify 0.03**, analysis 0.03, **expression 0.02**, study 0.02, **arabidopsis 0.02**
1.0	19/188	enzyme 0.07, pathway 0.06, signal 0.04, bacterial 0.02
1.0	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**
1.0	1/73	mutant 0.05, **function 0.03**, **arabidopsis 0.03**, cell 0.03, **expression 0.02**
1.0	18/122	**protein 0.08**, **domain 0.05**, bind 0.03, structure 0.03
1.0	15/93	**protein 0.04**, yeast 0.03, **arabidopsis 0.03**, **function 0.03**, **show 0.02**, cell 0.02
1.0	4/22	**gene 0.08**
1.0	5/84	**protein 0.25**, **domain 0.06**
1.0	19/136	evolution 0.06, **arabidopsis 0.04**, **gene 0.04**, conserve 0.03, divergence 0.02, specie 0.02, **function 0.02**
1.0	15/182	**gene 0.13**, **expression 0.04**, **arabidopsis 0.04**, **function 0.03**
1.0	12/151	evolution 0.07, lineage 0.03, evolve 0.03, evolutionary 0.02, angiosperm 0.02, divergence 0.02, origin 0.02
1.0	6/90	yeast 0.04, complex 0.03, **protein 0.03**, subunit 0.02, mammalian 0.02
1.0	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
1.0	10/46	**protein 0.06**
1.0	4/38	**protein 0.08**, **domain 0.02**
1.0	6/64	evolution 0.06, **gene 0.04**, angiosperm 0.02, family 0.02
1.0	18/69	**gene 0.19**, **expression 0.06**, **show 0.03**, **function 0.03**, express 0.03, **arabidopsis 0.02**
1.0	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
1.0	5/100	**gene 0.09**
1.0	15/159	**protein 0.26**, **domain 0.08**
1.0	19/113	**protein 0.08**, yeast 0.03, **show 0.02**
1.0	10/27	**protein 0.04**, **domain 0.03**, family 0.02, sequence 0.02
1.0	10/26	**gene 0.06**, **expression 0.03**, arabidopsis 0.02
1.0	16/98	**protein 0.13**

Topic model: [+plant +biodiversity-bow [50t,1 ⬍] | Term: [_____]   [Check Models]

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

Select a topic to see the related documents.

Topic 6

[19723248] Phylogenetic origin of Phyllolobium with a further implicati	0.64
[23071663] Genetic diversity and population structure of cucumber (Cucu	0.54
[16622792] Biodiversity of Streptomyces of high-mountainous ecosystems	0.39
[26467618] Phylogeography of Phytophagous Weevils and Plant Species in	0.35
[23962409] Phylogeography sheds light on the central-marginal hypothesi	0.34
[24065181] Contemporary pollen-mediated gene immigration reflects the h	0.31
[17191876] Biologically active ibogan and vallesamine derivatives from	0.30
[18206283] Reduced nitrogen has a greater effect than oxidised nitrogen	0.28
[27886271] Speciation and genetic diversity in Centaurea subsect. Phalo	0.28
[22081412] Establishing the phylogenetic origin, history, and age of th	0.26
[22546007] Phylogeographic analysis reveals significant spatial genetic	0.26
[24498103] Genetic differentiation and genetic diversity of Castanopsis	0.26
[17638329] Topoisomerase-II-inhibitory principles from the stems of Spa	0.25
[20397228] Prenylated benzophenone peroxide derivatives from Hypericum	0.25
[16876446] Linking patterns and processes of species diversification in	0.24
[17509846] Diversity of viruses in Cryphonectria parasitica and C. nits	0.24
[18807258] Ectomycorrhizal characterization of an American chestnut (Ca	0.24
[20854478] Forest refugia revisited: nSSRs and cpDNA sequences support	0.24
[23469278] Effect of degradation intensity on grassland ecosystem servi	0.24
[23478944] Post-Boreotropical dispersals explain the pantropical disjun	0.24
[27974324] The evolutionary history of Eugenia sect. Phyllocalyx (Myrta	0.24
[25072783] Temperate pine barrens and tropical rain forests are both ri	0.23
[22182994] A phylogeny of Delphineae (Ranunculaceae) shows that Aconit	0.22
[23418542] Phylogeographic evidence for a link of species divergence of	0.22
[24028582] Large-scale pattern of genetic differentiation within Africa	0.22
[22730022] Range expansion of a selfing polyploid plant despite widespr	0.21
[23629053] Diversification of plant species in arid Northwest China: sp	0.21
[23560070] Tertiary origin and pleistocene diversification of dragon bl	0.20

PMID	20854478
Article Title	Forest refugia revisited: nSSRs and cpDNA sequences support historical isolation in a wide-spread African tree with high colonization capacity, Milicia excelsa (Moraceae).
Pub Year	2010
Mesh Headings	Africa [D000349] Bayes Theorem [D001499] Cluster Analysis [D016000] DNA, Chloroplast [D018742] genetics [Q000235] DNA, Plant [D018744] genetics [Q000235] Evolution, Molecular [D019143] Gene Flow [D051456] Gene Pool [D005788] Genetics, Population [D005828] Microsatellite Repeats [D018895] Models, Genetic [D008957] Moraceae [D029586] genetics [Q000235] Pollen [D011058]

enter a search term

table   cloud   timeline   json   [moors:china]   [moors:turks]   [america:china]   [america]   [othello]   [china]   [moors]   [moor]

1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680
turks 100%	turks 100%	moors 100%	turks 100%	turks 100%	moors 100%	turks 100%	saracens 64%, 68%	moors 100%, 69%	moors 100%, 75%	moors 100%, 69%	turks 71%, 100%
turkes 74%	turkes 80%	turks 100%	moors 100%	moors 100%	turks 100%	moors 100%	parthians 59%, 59%	turks 69%, 100%	turks 75%, 100%	turks 69%, 100%	moors 100%, 71%
saracens 70%	saracens 71%	turkes 78%	turkes 91%	turkes 81%	turkes 79%	turkes 79%	moors 100%	saracens 73%, 75%	tartars 69%, 74%	tartars 70%, 71%	spaniards 72%, 81%
assyrians 65%	persians 69%	tartars 68%	spaniards 69%	saracens 70%	saracens 71%	barbarians 72%	turks 100%	tartars 66%, 77%	spaniards 66%, 72%	saracens 67%, 71%	saracens 74%, 72%
hunnes 65%	pagans 68%	hungarians 67%	hungarians 67%	moores 66%	moores 66%	saracens 71%	turks 80%	spaniards 67%, 70%	saracens 66%, 68%	persians 66%, 69%	tartars 70%, 75%
persians 64%	barbarians 66%	tartarians 67%	romans 66%	pagans 67%	tartarians 65%	tartars 68%	pagans 75%	tartarians 68%, 67%	turkes 63%, 67%	indians 64%, 68%	indians 71%, 67%
vandales 64%	armenians 65%	saracens 66%	portugals 66%	mahumetans 66%	arabians 62%	moores 68%	vandals 70%	scythians 66%, 66%	sarazens 65%, 64%	sarazens 63%, 66%	barbarians 66%, 71%
saracenes 63%	assyrians 64%	spaniards 65%	barbarians 66%	tartars 64%	parthians 61%	scythians 67%	gothes 67%	turkes 83%	portugals 68%, 61%	arabians 63%, 64%	persians 65%, 72%
tartarians 61%	egyptians 62%	dalmatians 64%	tartars 65%	arabians 64%	vandales 59%	persians 64%	infidels 67%	moores 78%	muscovites 62%, 64%	tartareans 61%, 65%	germans 68%, 68%
arabians 61%	arabians 61%	nomades 64%	sarazins 65%	barbarians 64%	portugals 59%	romans 63%	tartars 65%	sarmatians 72%	hungarians 70%	armenians 67%	venetians 73%
spanyards 60%	infidels 61%	persians 64%	moores 65%	infidels 64%	visigothes 59%	tartarians 62%	persians 63%	pagans 67%	moores 67%	mahometans 67%	imperialists 68%
gothes 60%	gothes 61%	gaules 63%	sicilians 62%	armenians 63%	pagans 58%	danes 61%	moores 63%	huns 69%	carthaginians 66%	scythians 66%	hungarians 67%
medes 59%	scythians 60%	moores 61%	britans 62%	mahumetans 63%	spaniards 58%	indians 61%	arabians 63%	mahometans 69%	venetians 66%	mahumetans 66%	romans 67%
normans 59%	romans 59%	scythians 61%	sarasins 62%	persians 63%	persians 58%	venetians 61%	carthaginians 63%	infidels 69%	portuguez 65%	barbarians 65%	arabians 67%
moores 59%	sarasins 59%	lombardes 61%	persians 61%	grecians 61%	infidells 58%	hungarians 61%	danes 61%	vandals 68%	indians 65%	moscovites 65%	scythians 66%
		parthians 60%	carthaginians 61%	aethiopians 61%	indians 58%	polonians 61%	heathens 61%	mahumetans 68%	castilians 64%	infidels 64%	muscovites 66%
		gothes 60%	sirians 52%	pomerania 60%	alani 58%	getes 57%	grecians 61%	sarazens 68%	persians 64%	moores 63%	islanders 65%
		sacrata 60%	mahumetists 52%	epire 58%	tartars 58%	spartan 54%	tartarians 67%	goths 67%	germans 63%	goths 63%	cossacks 65%
		florentia 60%	perspicua 51%	benin 57%	goths 57%	patricians 54%	scythians 59%	persians 63%	pyrates 63%	portugals 63%	numidians 64%
		aider 60%	longi 50%	aria 57%	infidels 57%	scithians 53%	turkish 59%	turk 67%	mamalukes 63%	spaniards 61%	swedes 64%
		celtiberians 60%	bramas 50%	abassia 57%	herules 57%	libyan 53%	goths 59%	barbary 66%	arabians 63%	chineses 60%	gauls 64%

Topic model: `+plant +biodiversity-bow [50t,1 ⬍]` | Term: [   ] [Check Models]
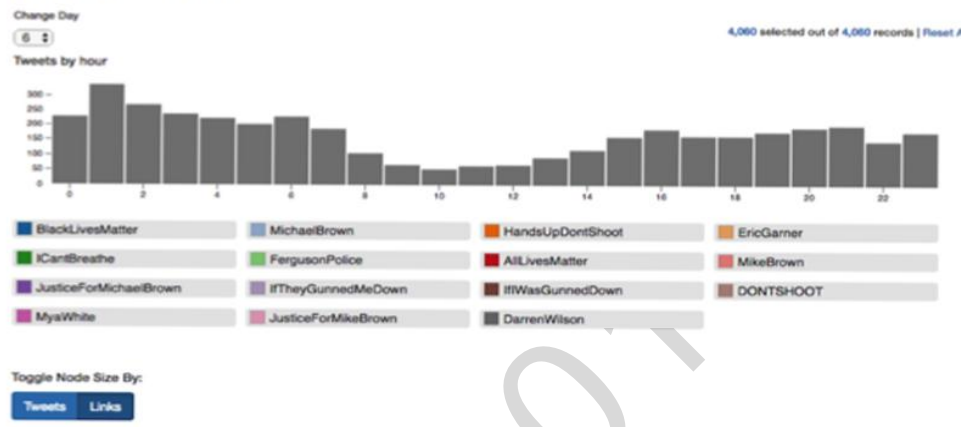
Topic models are trained on selected searches from the Pubmed corpus. Visualization based on the Python port of the LDAvis package.

Select a topic to see the related documents.

Topic 6

[19723248] Phylogenetic origin of Phyllolobium with a further implicati	0.64
[23071663] Genetic diversity and population structure of cucumber (Cucu	0.54
[16622792] Biodiversity of Streptomyces of high-mountainous ecosystems	0.39
[26467618] Phylogeography of Phytophagous Weevils and Plant Species in	0.35
[23962409] Phylogeography sheds light on the central-marginal hypothesi	0.34
[24065181] Contemporary pollen-mediated gene immigration reflects the h	0.31
[17191876] Biologically active ibogan and vallesamine derivatives from	0.30
[18206283] Reduced nitrogen has a greater effect than oxidised nitrogen	0.28
[27886271] Speciation and genetic diversity in Centaurea subsect. Phalo	0.28
[22081412] Establishing the phylogenetic origin, history, and age of th	0.26
[22546007] Phylogeographic analysis reveals significant spatial genetic	0.26
[24498103] Genetic differentiation and genetic diversity of Castanopsis	0.26
[17638329] Topoisomerase-II-inhibitory principles from the stems of Spa	0.25
[20397228] Prenylated benzophenone peroxide derivatives from Hypericum	0.25
[16876446] Linking patterns and processes of species diversification in	0.24
[17509846] Diversity of viruses in Cryphonectria parasitica and C. nits	0.24
[18807258] Ectomycorrhizal characterization of an American chestnut (Ca	0.24
[20854478] Forest refugia revisited: nSSRs and cpDNA sequences support	0.24
[23469278] Effect of degradation intensity on grassland ecosystem servi	0.24
[23478944] Post-Boreotropical dispersals explain the pantropical disjun	0.24
[27974324] The evolutionary history of Eugenia sect. Phyllocalyx (Myrta	0.24
[25072783] Temperate pine barrens and tropical rain forests are both ri	0.23
[22182994] A phylogeny of Delphinieae (Ranunculaceae) shows that Aconit	0.22
[23418542] Phylogeographic evidence for a link of species divergence of	0.22
[24028582] Large-scale pattern of genetic differentiation within Africa	0.22
[22730022] Range expansion of a selfing polyploid plant despite widespr	0.21
[23629053] Diversification of plant species in arid Northwest China: sp	0.21
[23560070] Tertiary origin and pleistocene diversification of dragon bl	0.20

PMID	20854478
Article Title	Forest refugia revisited: nSSRs and cpDNA sequences support historical isolation in a wide-spread African tree with high colonization capacity, Milicia excelsa (Moraceae).
Pub Year	2010
Mesh Headings	Africa [D000349]
	Bayes Theorem [D001499]
	Cluster Analysis [D016000]
	DNA, Chloroplast [D018742]
	genetics [Q000235]
	DNA, Plant [D018744]
	genetics [Q000235]
	Evolution, Molecular [D019143]
	Gene Flow [D051456]
	Gene Pool [D005788]
	Genetics, Population [D005828]
	Microsatellite Repeats [D018895]
	Models, Genetic [D008957]
	Moraceae [D029586]
	genetics [Q000235]
	Pollen [D011058]

Nov 24 to Dec 7 2014

Change Day
[6 ⬍]

4,060 selected out of 4,060 records | Reset All

Tweets by hour

- ■ BlackLivesMatter
- ■ MichaelBrown
- ■ HandsUpDontShoot
- ■ EricGarner
- ■ ICantBreathe
- ■ FergusonPolice
- ■ AllLivesMatter
- ■ MikeBrown
- ■ JusticeForMichaelBrown
- ■ IfTheyGunnedMeDown
- ■ IfIWasGunnedDown
- ■ DONTSHOOT
- ■ MyaWhite
- ■ JusticeForMikeBrown
- ■ DarrenWilson

Toggle Node Size By:
[Tweets] [Links]

Hashtag Frequency/Time chart range: [08/10/2014 -> 08/13/2014] reset

Hashtag Frequency

- AllLivesMatter
- BlackLivesMatter
- DONTSHOOT
- DarrenWilson
- EricGarner
- FergusonPolice
- HandsUpDontShoot
- ICantBreathe
- IfIWasGunnedDown
- IfTheyGunnedMeDown
- JusticeForMichaelBrown
- JusticeForMikeBrown
- MichaelBrown
- MikeBrown
- MyaWhite

Day of Week

- Sun
- Mon
- Tue
- Wed
- Thu
- Fri
- Sat

Retweeted vs Original Tweets

Original(18%)
Retweeted(81%)