Phylogenetic Network Workshop
27/07/2015 - Singapore

Exploring the community of phylogenetic networks

Philippe Gambette
Université Paris-Est Marne-la-Vallée

Parts of this work done with Tushar Agarwal, Maxime Morgado & David Morrison

Outline

- Who is who in phylogenetic networks?
- Exploring the research
- Discovering software
- Finding experts
- Following the community
- Analyzing the trends
- ISIPhyNC and subclasses of phylogenetic networks

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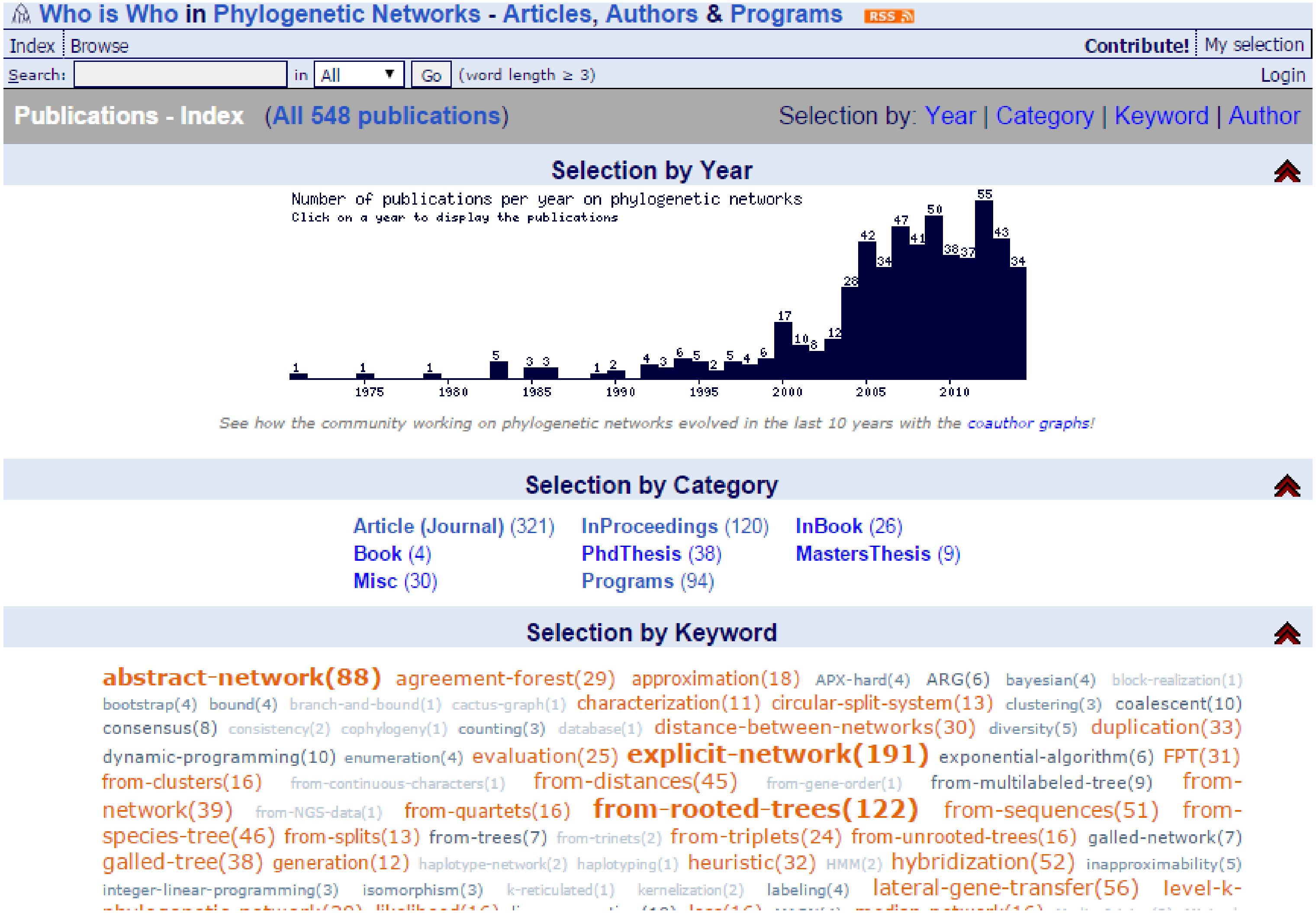
Who is who in Phylogenetic Networks?

An interactive bibliographic database started in 2007



Who is Who in Phylogenetic Networks - Articles, Authors & Programs

(word length ≥ 3)

Publications - Index (All 548 publications)

Selection by: Year | Category | Keyword | Author

Selection by Year

Number of publications per year on phylogenetic networks

Click on a year to display the publications

See how the community working on phylogenetic networks evolved in the last 10 years with the coauthor graphs!

Selection by Category

Article (Journal) (321)	InProceedings (120)	InBook (26)
Book (4)	PhdThesis (38)	MastersThesis (9)
Misc (30)	Programs (94)	

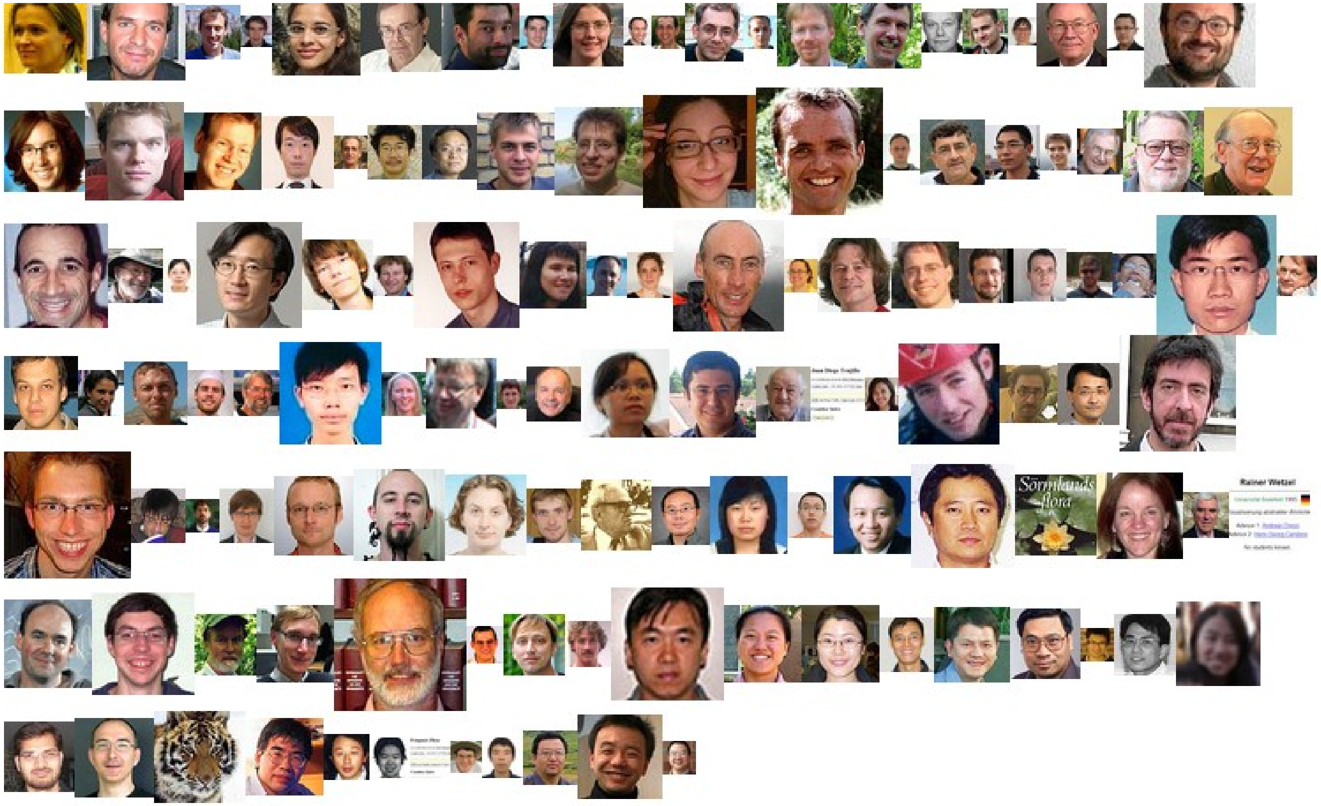
Selection by Keyword

abstract-network(88) agreement-forest(29) approximation(18) APX-hard(4) ARG(6) bayesian(4) block-realization(1) bootstrap(4) bound(4) branch-and-bound(1) cactus-graph(1) characterization(11) circular-split-system(13) clustering(3) coalescent(10) consensus(8) consistency(2) cophylogeny(1) counting(3) database(1) distance-between-networks(30) diversity(5) duplication(33) dynamic-programming(10) enumeration(4) evaluation(25) explicit-network(191) exponential-algorithm(6) FPT(31) from-clusters(16) from-continuous-characters(1) from-distances(45) from-gene-order(1) from-multilabeled-tree(9) from-network(39) from-NGS-data(1) from-quartets(16) from-rooted-trees(122) from-sequences(51) from-species-tree(46) from-splits(13) from-trees(7) from-trinets(2) from-triplets(24) from-unrooted-trees(16) galled-network(7) galled-tree(38) generation(12) haplotype-network(2) haplotyping(1) heuristic(32) HMM(2) hybridization(52) inapproximability(5) integer-linear-programming(3) isomorphism(3) k-reticulated(1) kernelization(2) labeling(4) lateral-gene-transfer(56) level-k-

http://www.lirmm.fr/~gambette/PhylogeneticNetworks/

Who is who in Phylogenetic Networks?

Based on the open source PHP+MySQL web application **BibAdmin** by Sergiu Chelcea (http://gforge.inria.fr/projects/bibadmin/), with a few changes.



Authors present in the database (size representing the number of publications, weighted by the number of coauthors on each publication)

Website maintained by Philippe Gambette.
Last modified: Tue August 03 2010 08:56:59
Please cite as: Philippe Gambette, *Who is Who in Phylogenetic Networks : Articles, Authors and Programs*, http://www.atgc-montpellier.fr/phylnet/.

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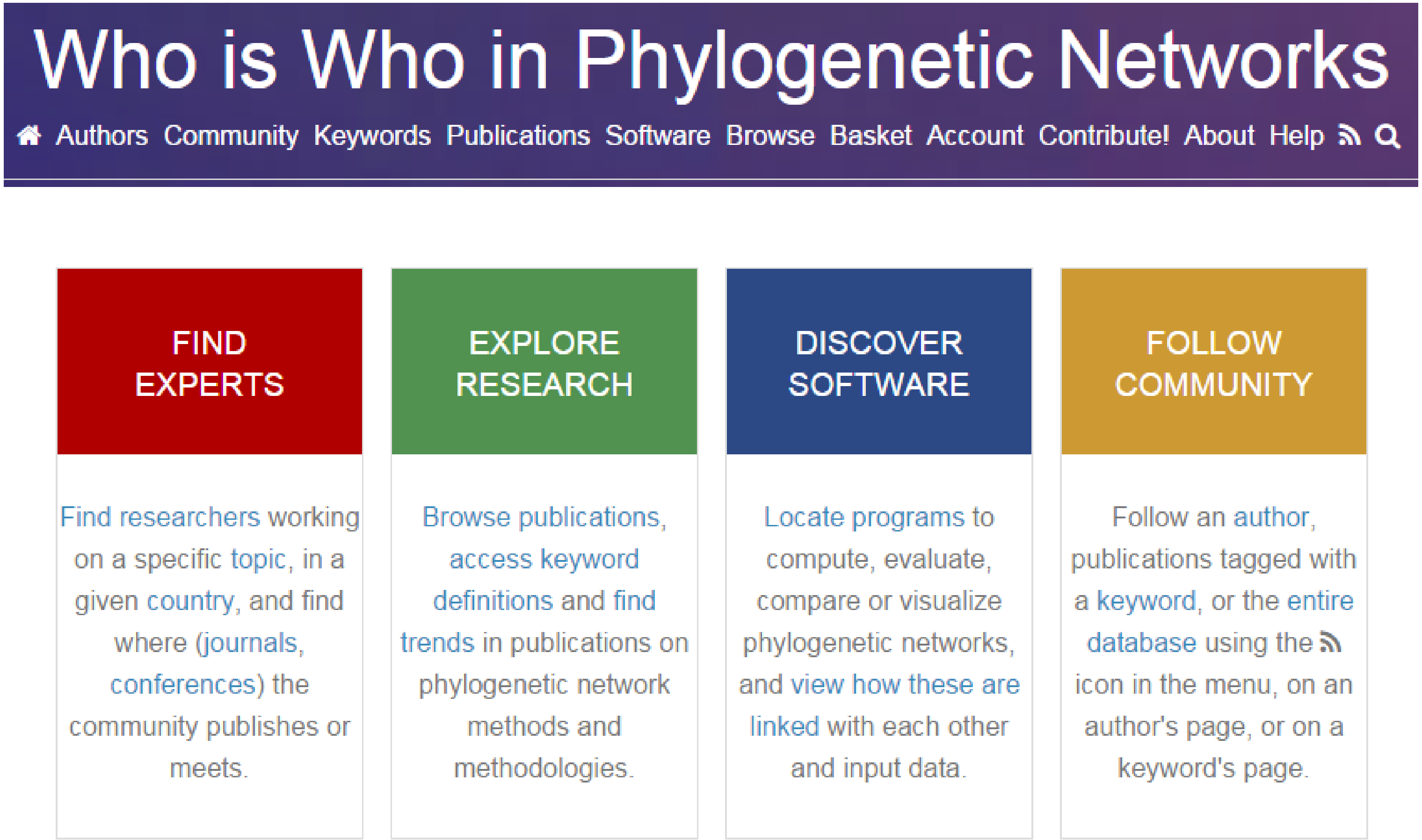
Who is who in Phylogenetic Networks?

A fresh look in 2015, with new functionalities:



Who is Who in Phylogenetic Networks

FIND EXPERTS

Find researchers working on a specific topic, in a given country, and find where (journals, conferences) the community publishes or meets.

EXPLORE RESEARCH

Browse publications, access keyword definitions and find trends in publications on phylogenetic network methods and methodologies.

DISCOVER SOFTWARE

Locate programs to compute, evaluate, compare or visualize phylogenetic networks, and view how these are linked with each other and input data.

FOLLOW COMMUNITY

Follow an author, publications tagged with a keyword, or the entire database using the icon in the menu, on an author's page, or on a keyword's page.

Google(phylnet) or http://phylnet.univ-mlv.fr/

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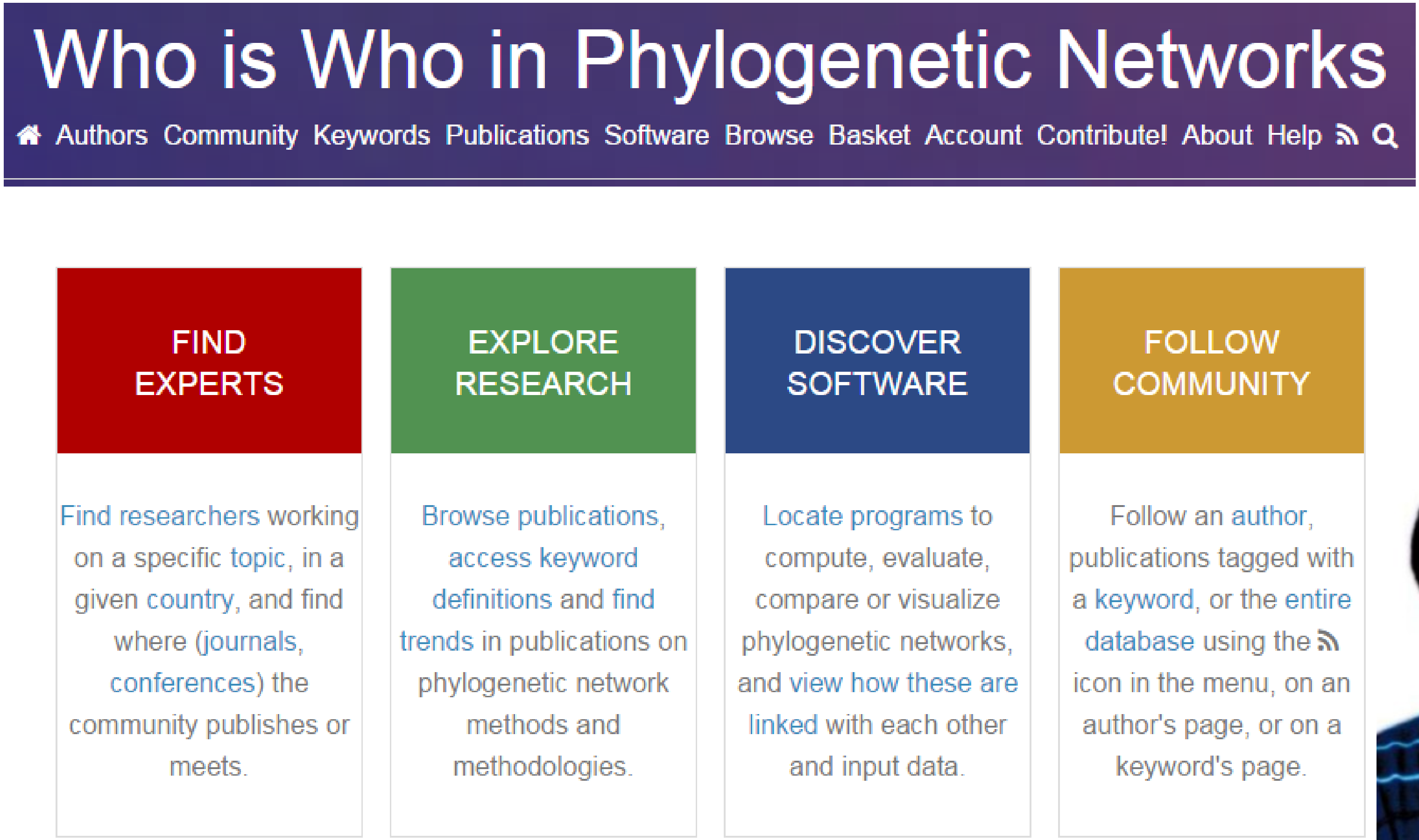

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Design & implementation by Tushar Agarwal (IIT Ropar),
advised by P. Gambette & D. Morrison

Google(phylnet) or http://phylnet.univ-mlv.fr/

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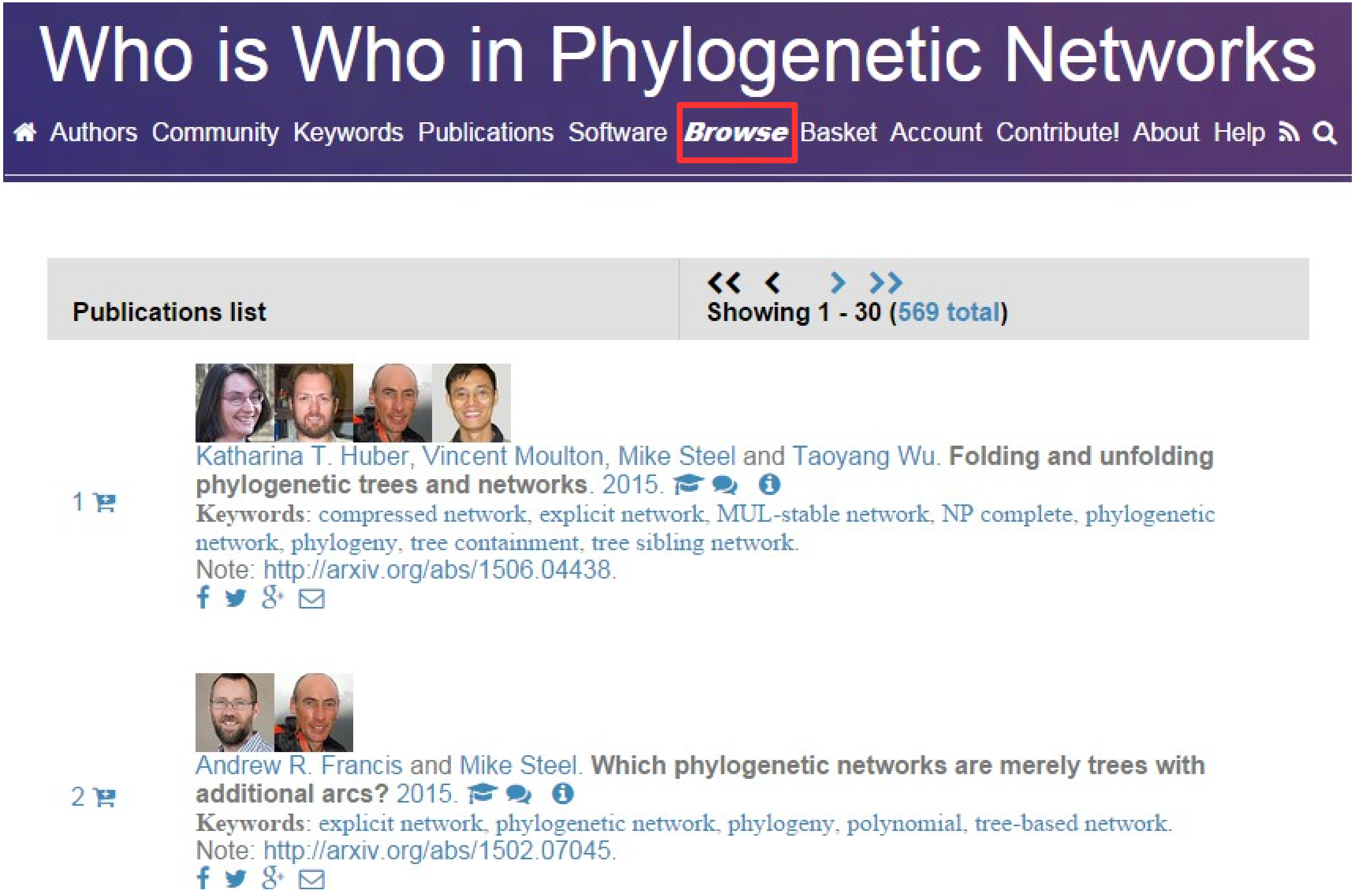
Exploring the research – getting the articles



Publications list

Showing 1 - 30 (569 total)

1 Katharina T. Huber, Vincent Moulton, Mike Steel and Taoyang Wu. **Folding and unfolding phylogenetic trees and networks**. 2015.
Keywords: compressed network, explicit network, MUL-stable network, NP complete, phylogenetic network, phylogeny, tree containment, tree sibling network.
Note: http://arxiv.org/abs/1506.04438.

2 Andrew R. Francis and Mike Steel. **Which phylogenetic networks are merely trees with additional arcs?** 2015.
Keywords: explicit network, phylogenetic network, phylogeny, polynomial, tree-based network.
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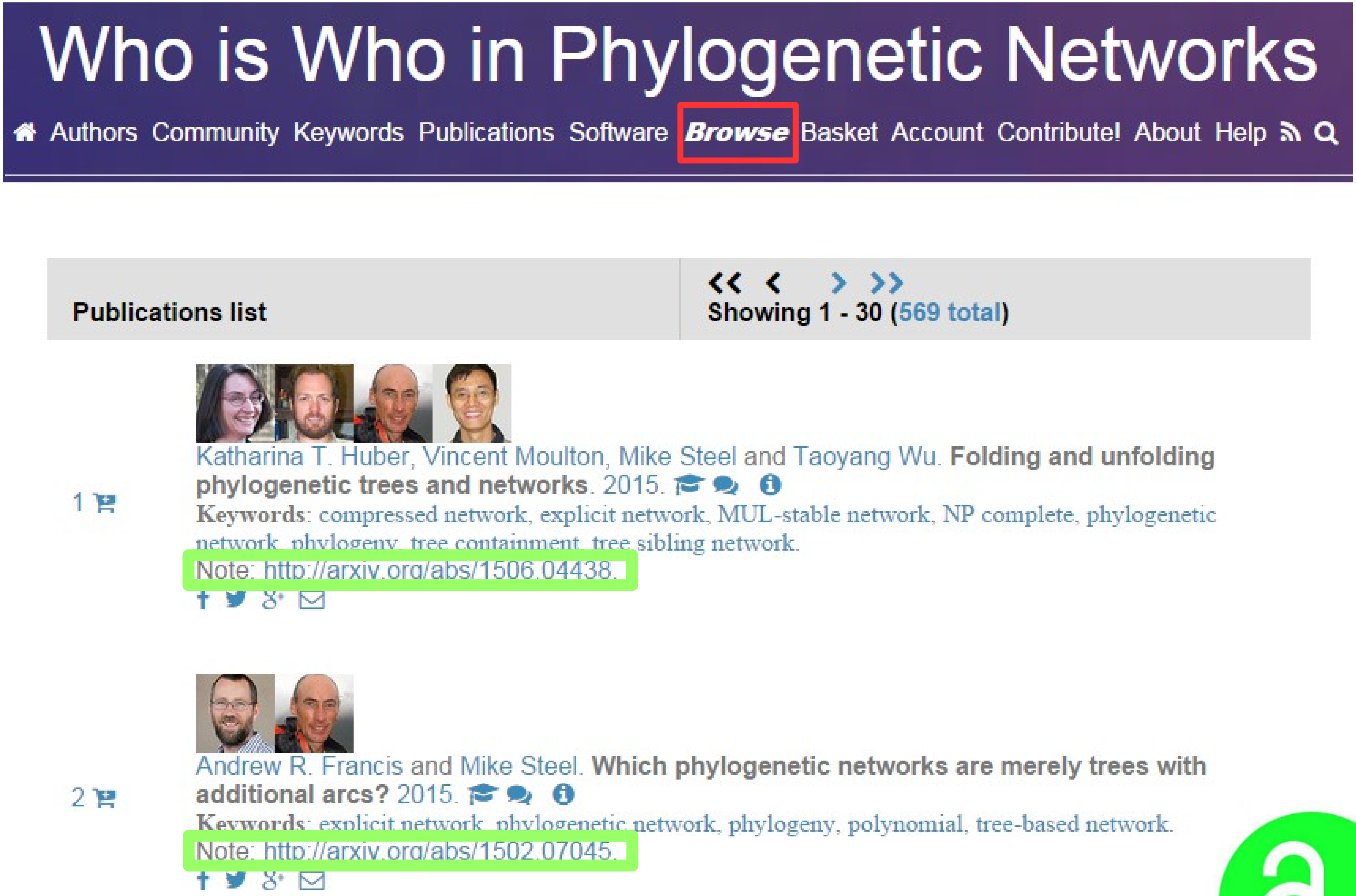

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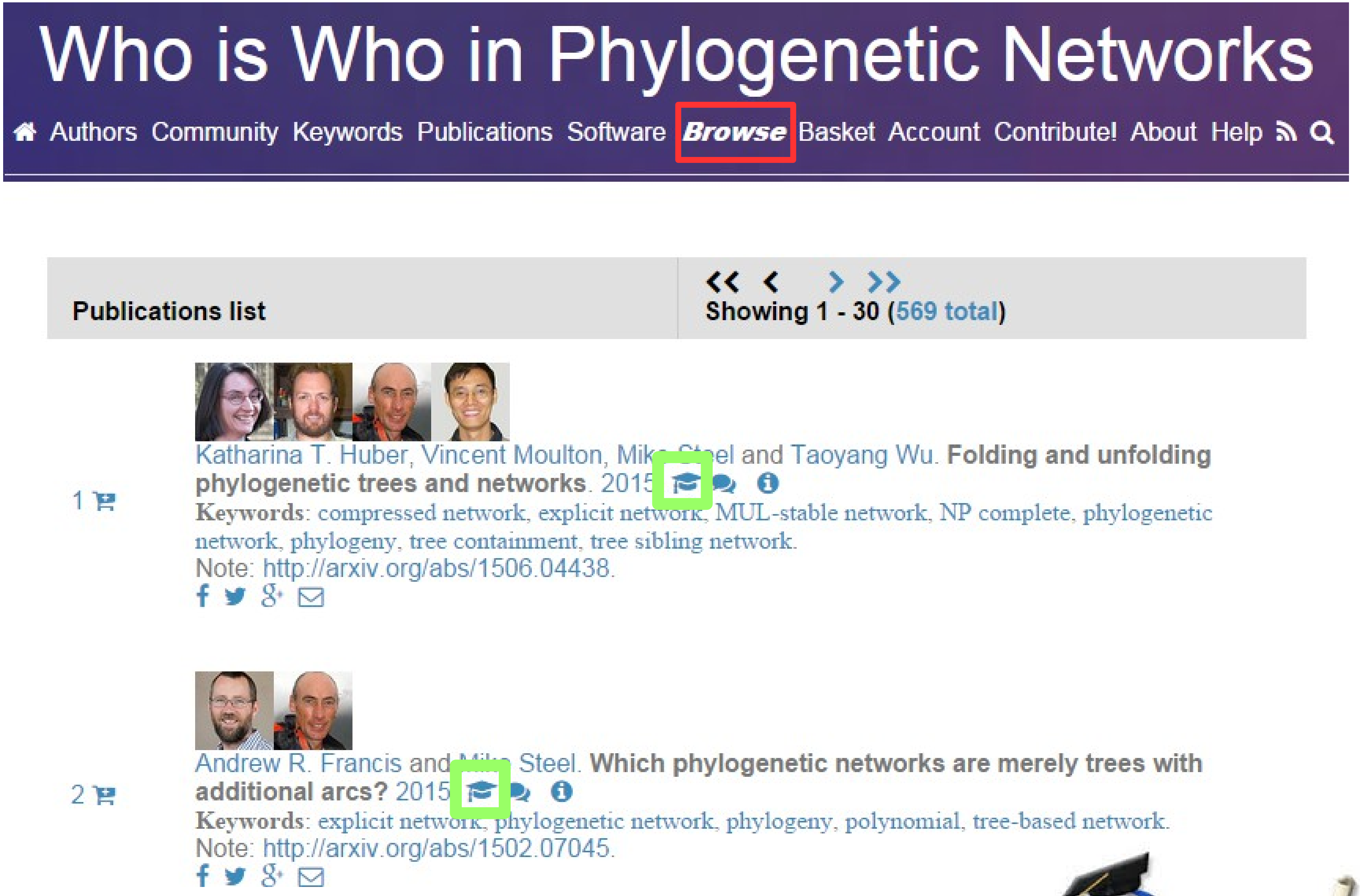

Who is Who in Phylogenetic Networks

Authors Community Keywords Publications Software **Browse** Basket Account Contribute! About Help

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Scholar

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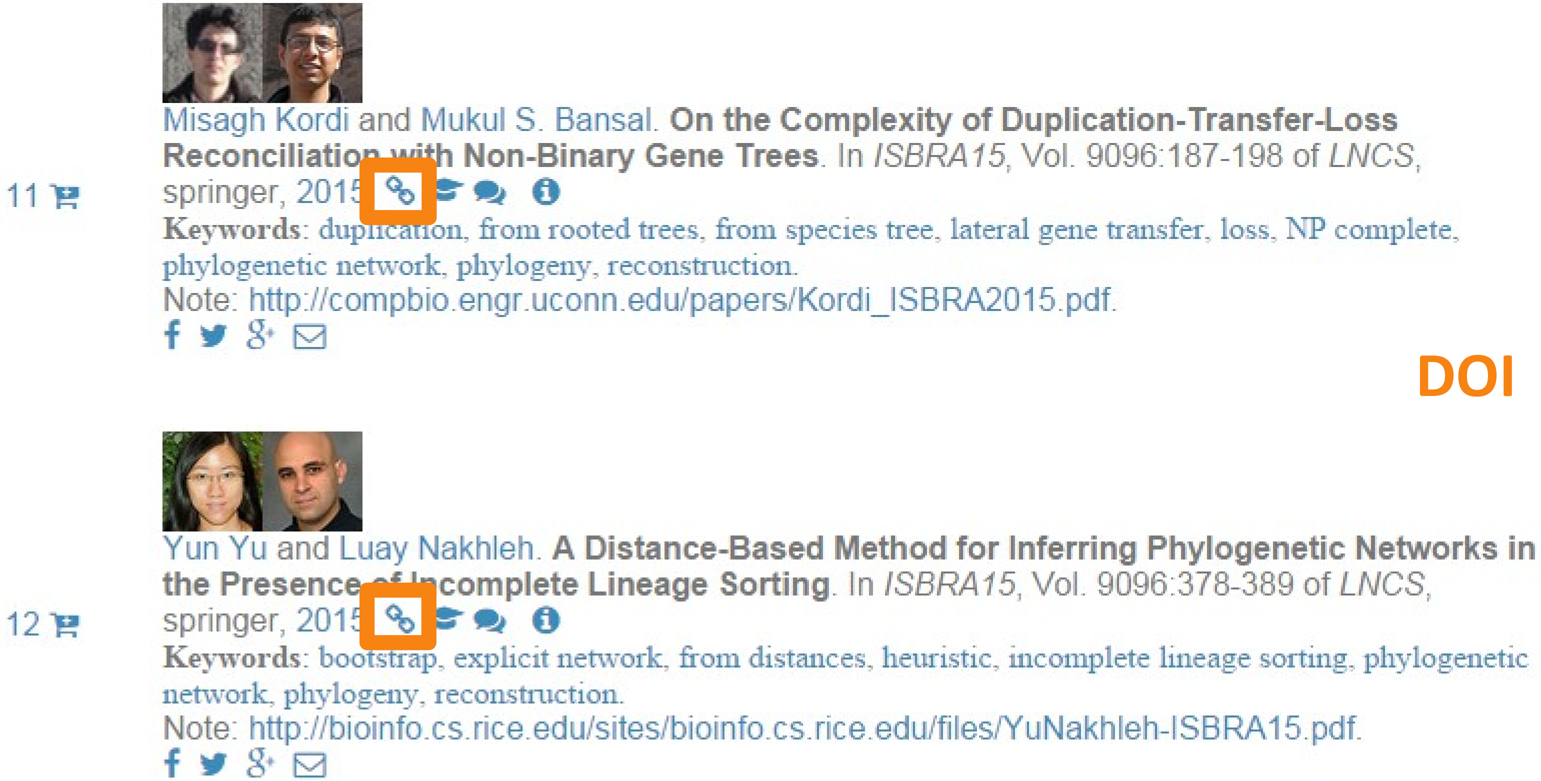

11

Misagh Kordi and Mukul S. Bansal. **On the Complexity of Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees**. In *ISBRA15*, Vol. 9096:187-198 of *LNCS*, springer, 2015.
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Yun Yu and Luay Nakhleh. **A Distance-Based Method for Inferring Phylogenetic Networks in the Presence of Incomplete Lineage Sorting**. In *ISBRA15*, Vol. 9096:378-389 of *LNCS*, springer, 2015.
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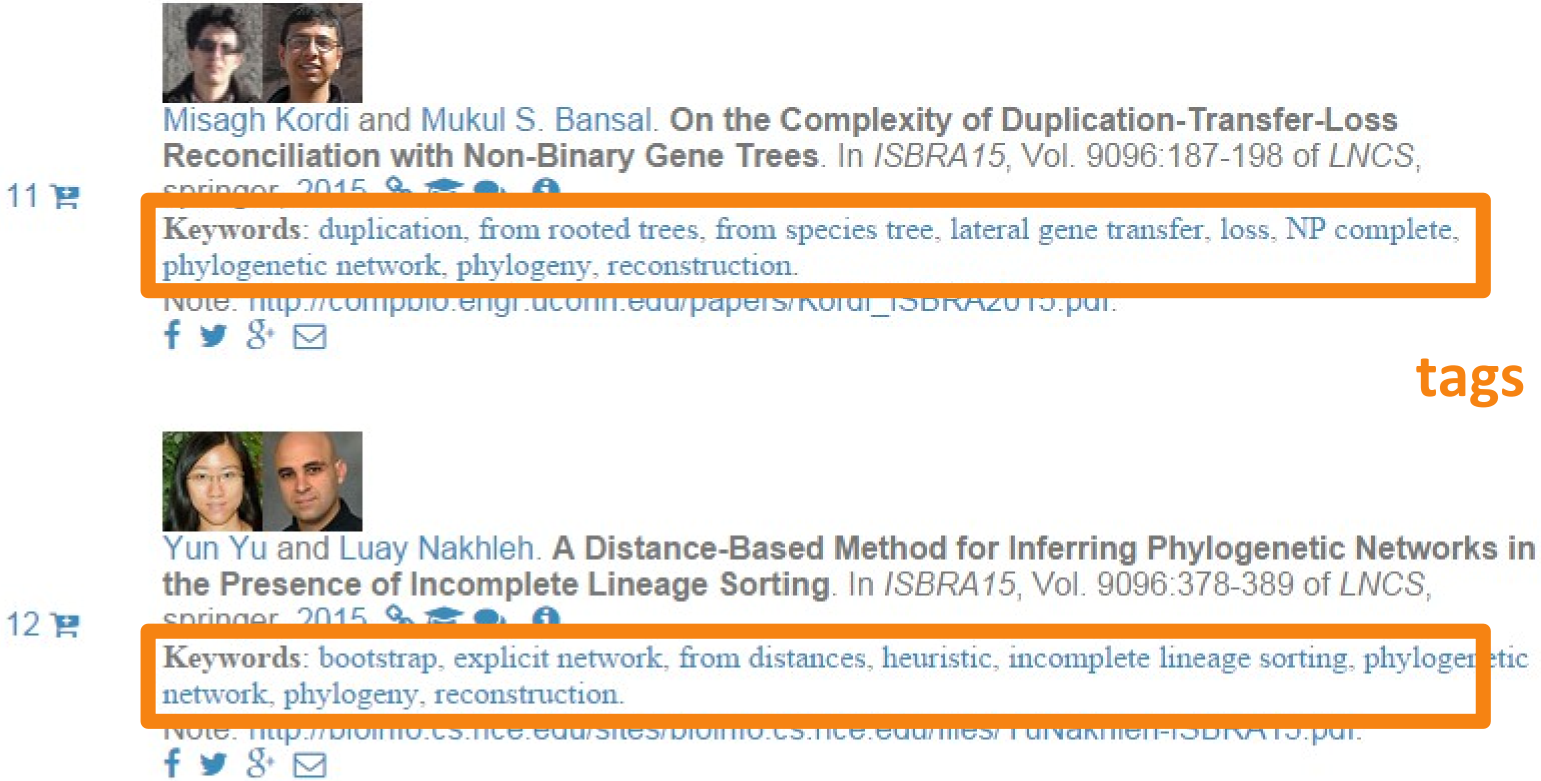
DOI

Exploring the research – understanding the topics



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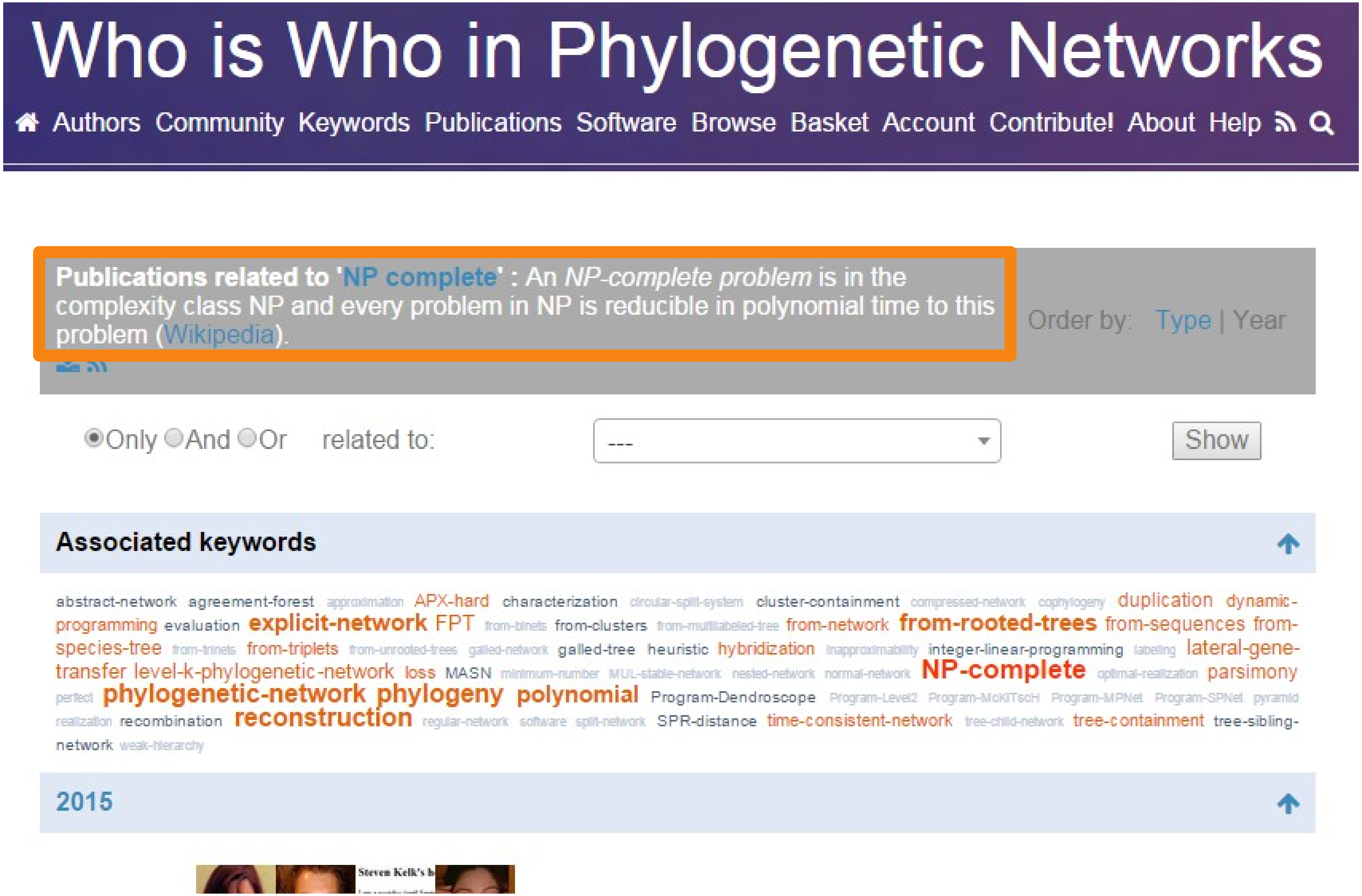
tags

Exploring the research – understanding the topics

A keyword page:



Publications related to 'NP complete' : An *NP-complete problem* is in the complexity class NP and every problem in NP is reducible in polynomial time to this problem (Wikipedia).

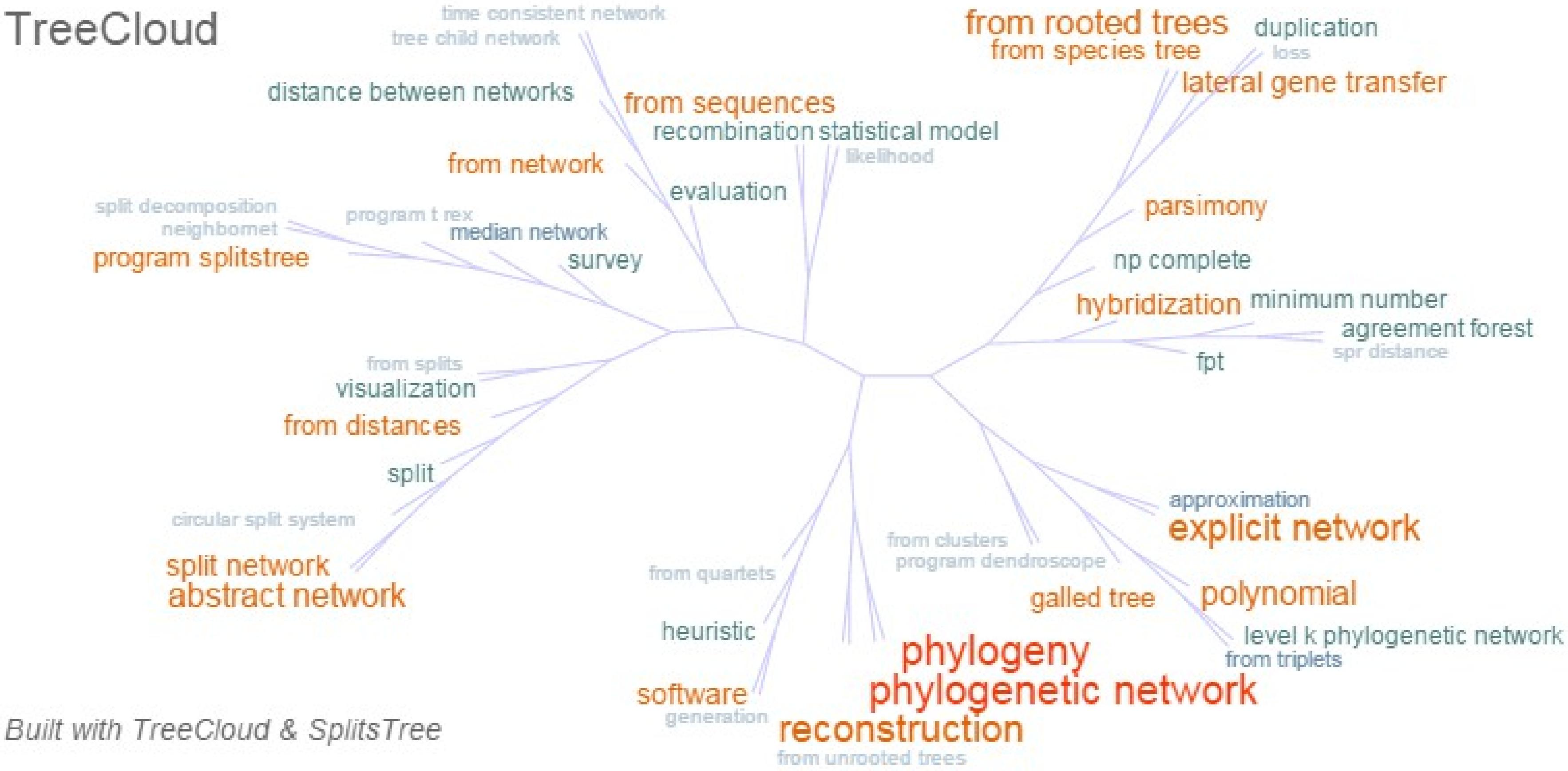
Associated keywords

abstract-network agreement-forest approximation APX-hard characterization circular-split-system cluster-containment compressed-network cophylogeny duplication dynamic-programming evaluation explicit-network FPT from-binets from-clusters from-multilabeled-tree from-network from-rooted-trees from-sequences from-species-tree from-trinets from-triplets from-unrooted-trees galled-network galled-tree heuristic hybridization inapproximability integer-linear-programming labeling lateral-gene-transfer level-k-phylogenetic-network loss MASN minimum-number MUL-stable-network nested-network normal-network NP-complete optimal-realization parsimony perfect phylogenetic-network phylogeny polynomial Program-Dendroscope Program-Level2 Program-McKITscH Program-MPNet Program-SPNet pyramid realization recombination reconstruction regular-network software split-network SPR-distance time-consistent-network tree-child-network tree-containment tree-sibling-network weak-hierarchy

2015

Exploring the research – understanding the topics

Main keywords in June 2015: the tree cloud

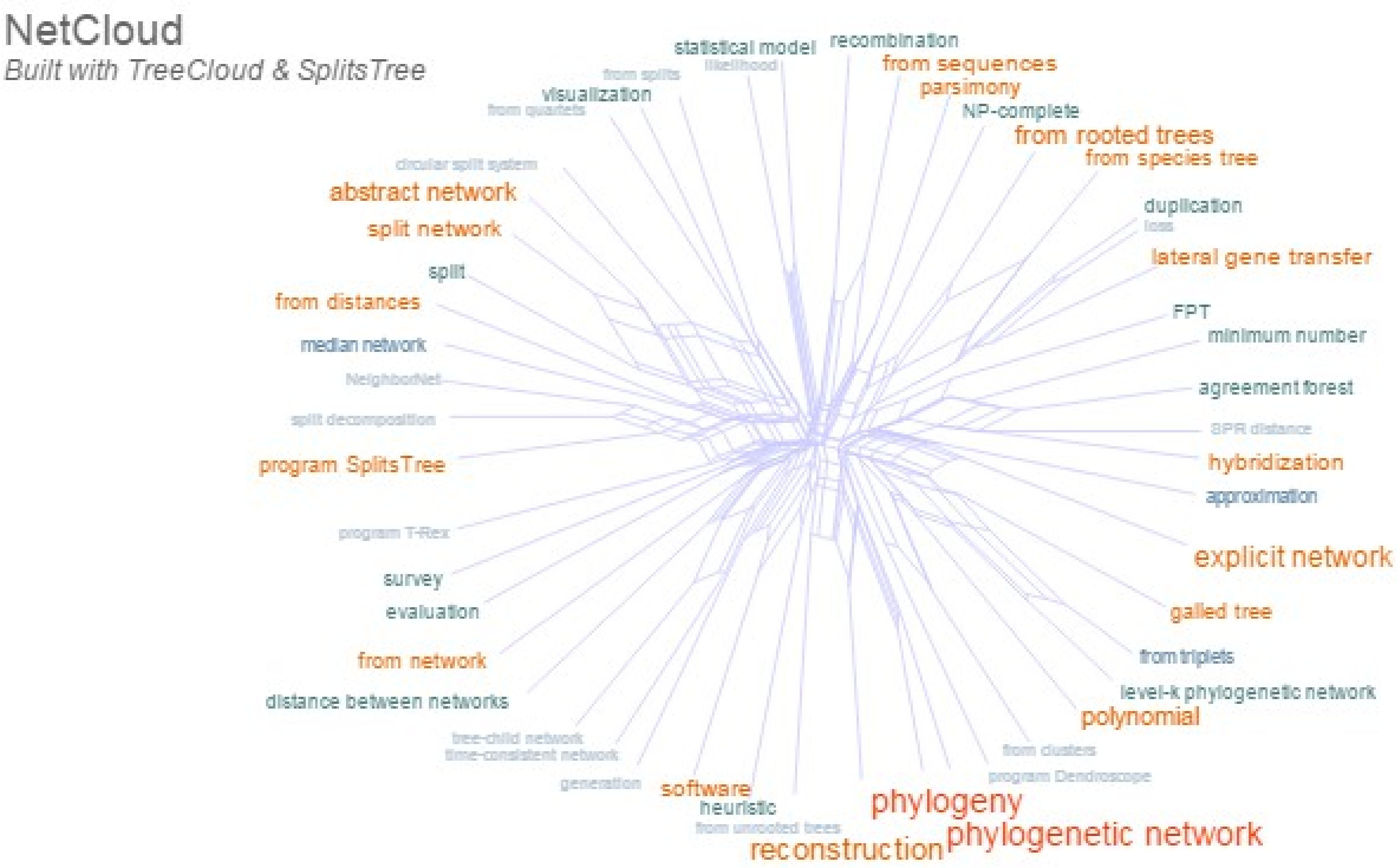


Gambette & Véronis, 2009 - http://www.treecloud.org

See also PhyloPlot (https://github.com/adamzy/PhyloPlot/) by Zheng Yu

Exploring the research – understanding the topics

Main keywords in June 2015: the network cloud



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Exploring the research – understanding the topics

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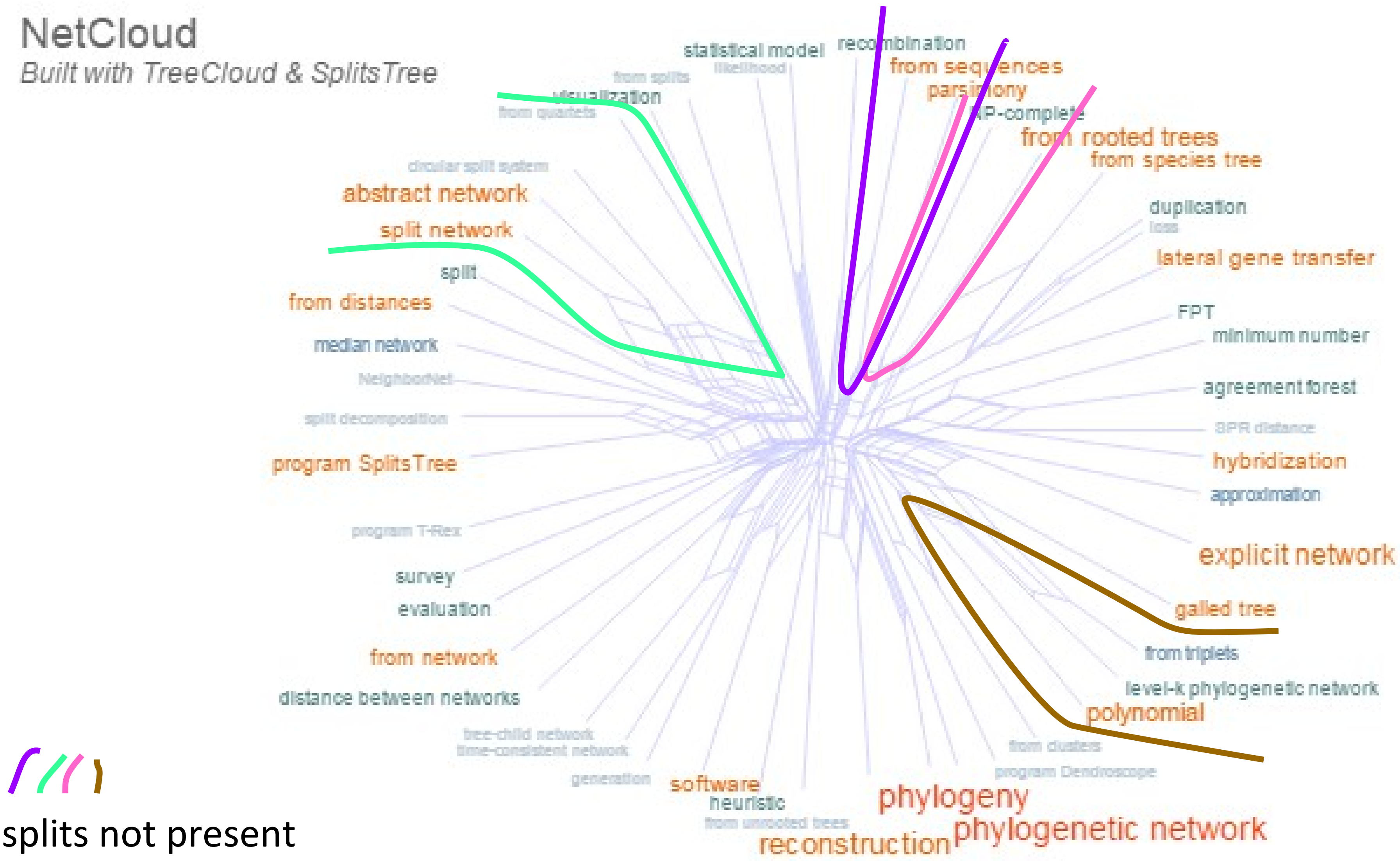
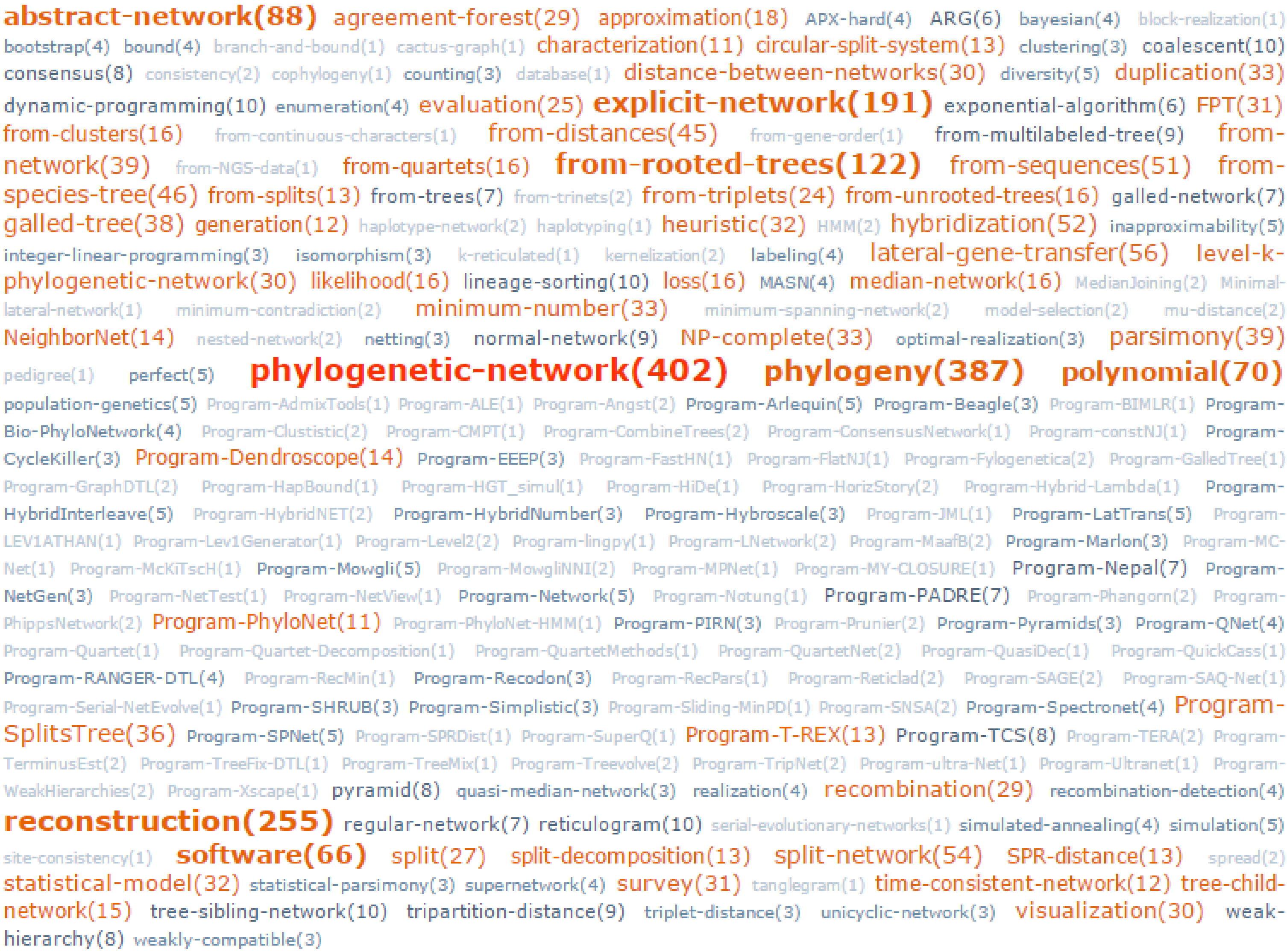


splits not present
in the tree cloud

Gambette & Véronis, 2009 - http://www.treecloud.org

Exploring the research – understanding the topics

All keywords:



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Exploring the research – understanding the topics

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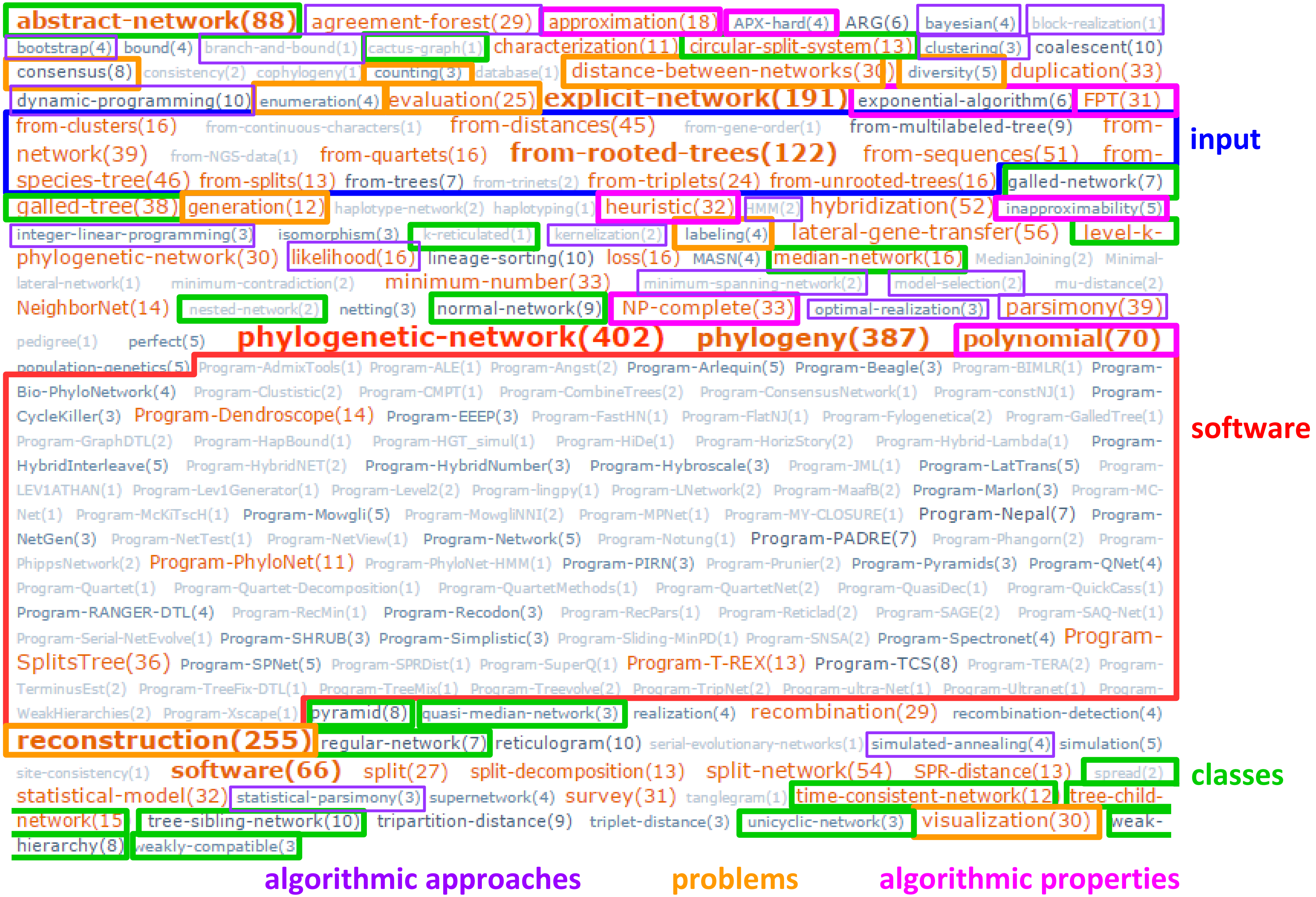
input

software

Exploring the research – understanding the topics



abstract-network(88) agreement-forest(29) approximation(18) APX-hard(4) ARG(6) bayesian(4) block-realization(1) bootstrap(4) bound(4) branch-and-bound(1) cactus-graph(1) characterization(11) circular-split-system(13) clustering(3) coalescent(10) consensus(8) consistency(2) cophylogeny(1) counting(3) database(1) distance-between-networks(30) diversity(5) duplication(33) dynamic-programming(10) enumeration(4) evaluation(25) explicit-network(191) exponential-algorithm(6) FPT(31) from-clusters(16) from-continuous-characters(1) from-distances(45) from-gene-order(1) from-multilabeled-tree(9) from-network(39) from-NGS-data(1) from-quartets(16) from-rooted-trees(122) from-sequences(51) from-species-tree(46) from-splits(13) from-trees(7) from-trinets(2) from-triplets(24) from-unrooted-trees(16) galled-network(7) galled-tree(38) generation(12) haplotype-network(2) haplotyping(1) heuristic(32) HMM(2) hybridization(52) inapproximability(5) integer-linear-programming(3) isomorphism(3) k-reticulated(1) kernelization(2) labeling(4) lateral-gene-transfer(56) level-k-phylogenetic-network(30) likelihood(16) lineage-sorting(10) loss(16) MASN(4) median-network(16) MedianJoining(2) Minimal-lateral-network(1) minimum-contradiction(2) minimum-number(33) minimum-spanning-network(2) model-selection(2) mu-distance(2) NeighborNet(14) nested-network(2) netting(3) normal-network(9) NP-complete(33) optimal-realization(3) parsimony(39) pedigree(1) perfect(5) phylogenetic-network(402) phylogeny(387) polynomial(70) population-genetics(5) Program-AdmixTools(1) Program-ALE(1) Program-Angst(2) Program-Arlequin(5) Program-Beagle(3) Program-BIMLR(1) Program-Bio-PhyloNetwork(4) Program-Clustistic(2) Program-CMPT(1) Program-CombineTrees(2) Program-ConsensusNetwork(1) Program-constNJ(1) Program-CycleKiller(3) Program-Dendroscope(14) Program-EEEP(3) Program-FastHN(1) Program-FlatNJ(1) Program-Fylogenetica(2) Program-GalledTree(1) Program-GraphDTL(2) Program-HapBound(1) Program-HGT_simul(1) Program-HiDe(1) Program-HorizStory(2) Program-Hybrid-Lambda(1) Program-HybridInterleave(5) Program-HybridNET(2) Program-HybridNumber(3) Program-Hybroscale(3) Program-JML(1) Program-LatTrans(5) Program-LEV1ATHAN(1) Program-Lev1Generator(1) Program-Level2(2) Program-lingpy(1) Program-LNetwork(2) Program-MaafB(2) Program-Marlon(3) Program-MC-Net(1) Program-McKiTscH(1) Program-Mowgli(5) Program-MowgliNNI(2) Program-MPNet(1) Program-MY-CLOSURE(1) Program-Nepal(7) Program-NetGen(3) Program-NetTest(1) Program-NetView(1) Program-Network(5) Program-Notung(1) Program-PADRE(7) Program-Phangorn(2) Program-PhippsNetwork(2) Program-PhyloNet(11) Program-PhyloNet-HMM(1) Program-PIRN(3) Program-Prunier(2) Program-Pyramids(3) Program-QNet(4) Program-Quartet(1) Program-Quartet-Decomposition(1) Program-QuartetMethods(1) Program-QuartetNet(2) Program-QuasiDec(1) Program-QuickCass(1) Program-RANGER-DTL(4) Program-RecMin(1) Program-Recodon(3) Program-RecPars(1) Program-Reticlad(2) Program-SAGE(2) Program-SAQ-Net(1) Program-Serial-NetEvolve(1) Program-SHRUB(3) Program-Simplistic(3) Program-Sliding-MinPD(1) Program-SNSA(2) Program-Spectronet(4) Program-SplitsTree(36) Program-SPNet(5) Program-SPRDist(1) Program-SuperQ(1) Program-T-REX(13) Program-TCS(8) Program-TERA(2) Program-TerminusEst(2) Program-TreeFix-DTL(1) Program-TreeMix(1) Program-Treevolve(2) Program-TripNet(2) Program-ultra-Net(1) Program-Ultranet(1) Program-WeakHierarchies(2) Program-Xscape(1) pyramid(8) quasi-median-network(3) realization(4) recombination(29) recombination-detection(4) reconstruction(255) regular-network(7) reticulogram(10) serial-evolutionary-networks(1) simulated-annealing(4) simulation(5) site-consistency(1) software(66) split(27) split-decomposition(13) split-network(54) SPR-distance(13) spread(2) statistical-model(32) statistical-parsimony(3) supernetwork(4) survey(31) tanglegram(1) time-consistent-network(12) tree-child-network(15) tree-sibling-network(10) tripartition-distance(9) triplet-distance(3) unicyclic-network(3) visualization(30) weak-hierarchy(8) weakly-compatible(3)

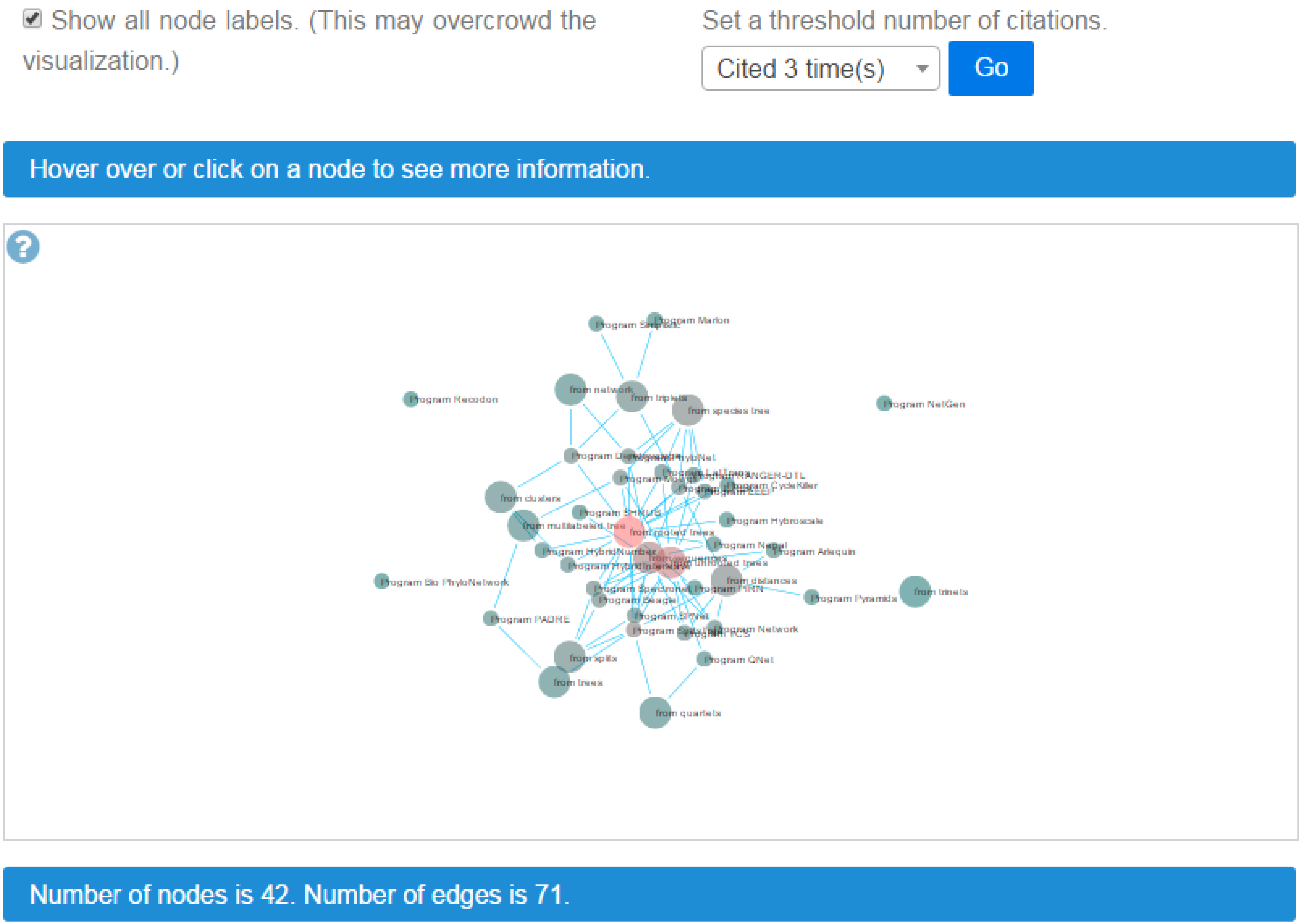
→ missing references: ARG, pedigrees, haplotyping, etc...

Outline

- Who is who in phylogenetic networks?
- Exploring the research
- Discovering software
- Finding experts
- Following the community
- Analyzing the trends
- ISIPhyNC and subclasses of phylogenetic networks

Exploring the research – discovering software

Software and input data:



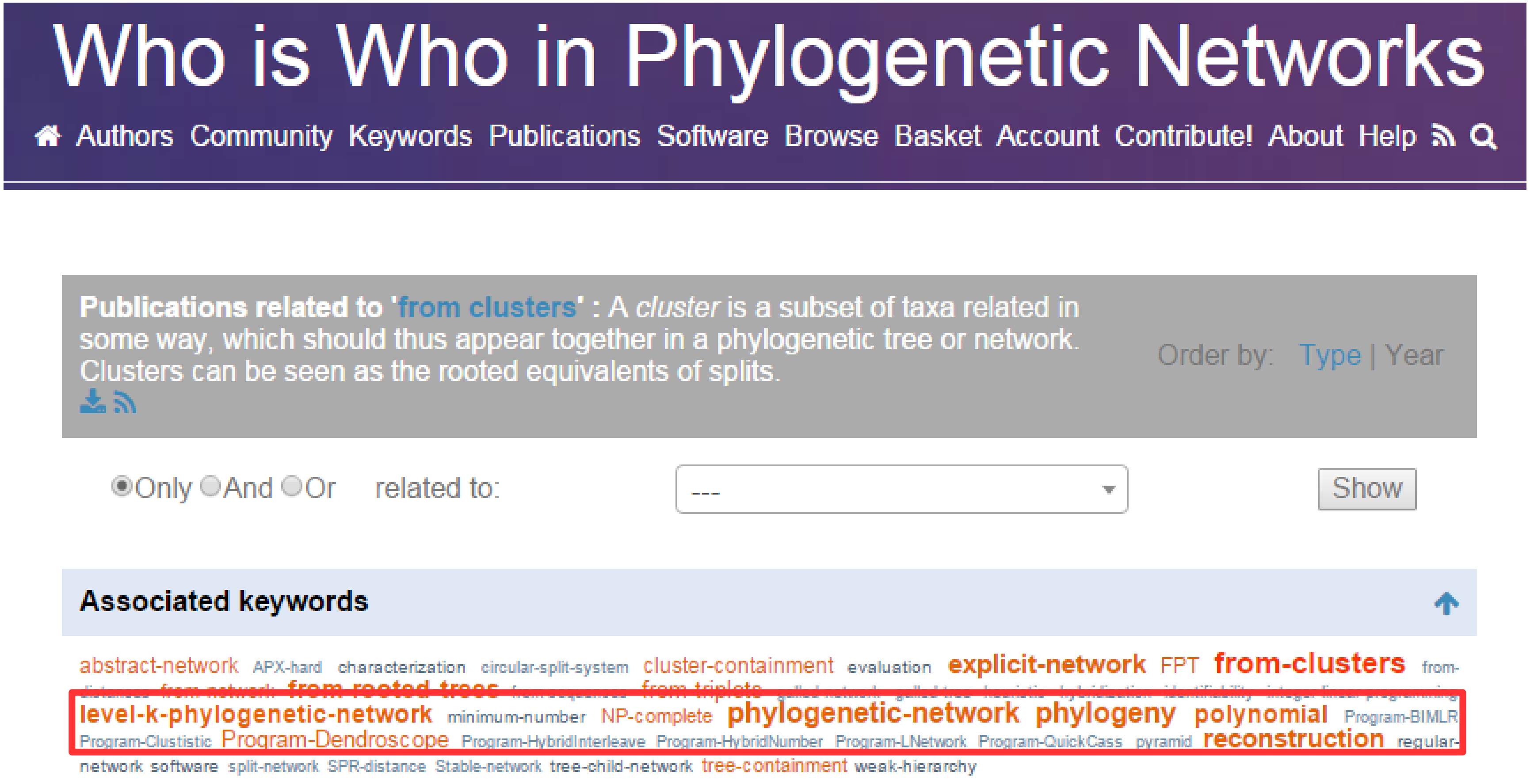
☑ Show all node labels. (This may overcrowd the visualization.)

Set a threshold number of citations.

Hover over or click on a node to see more information.

Number of nodes is 42. Number of edges is 71.

Exploring the research – discovering software

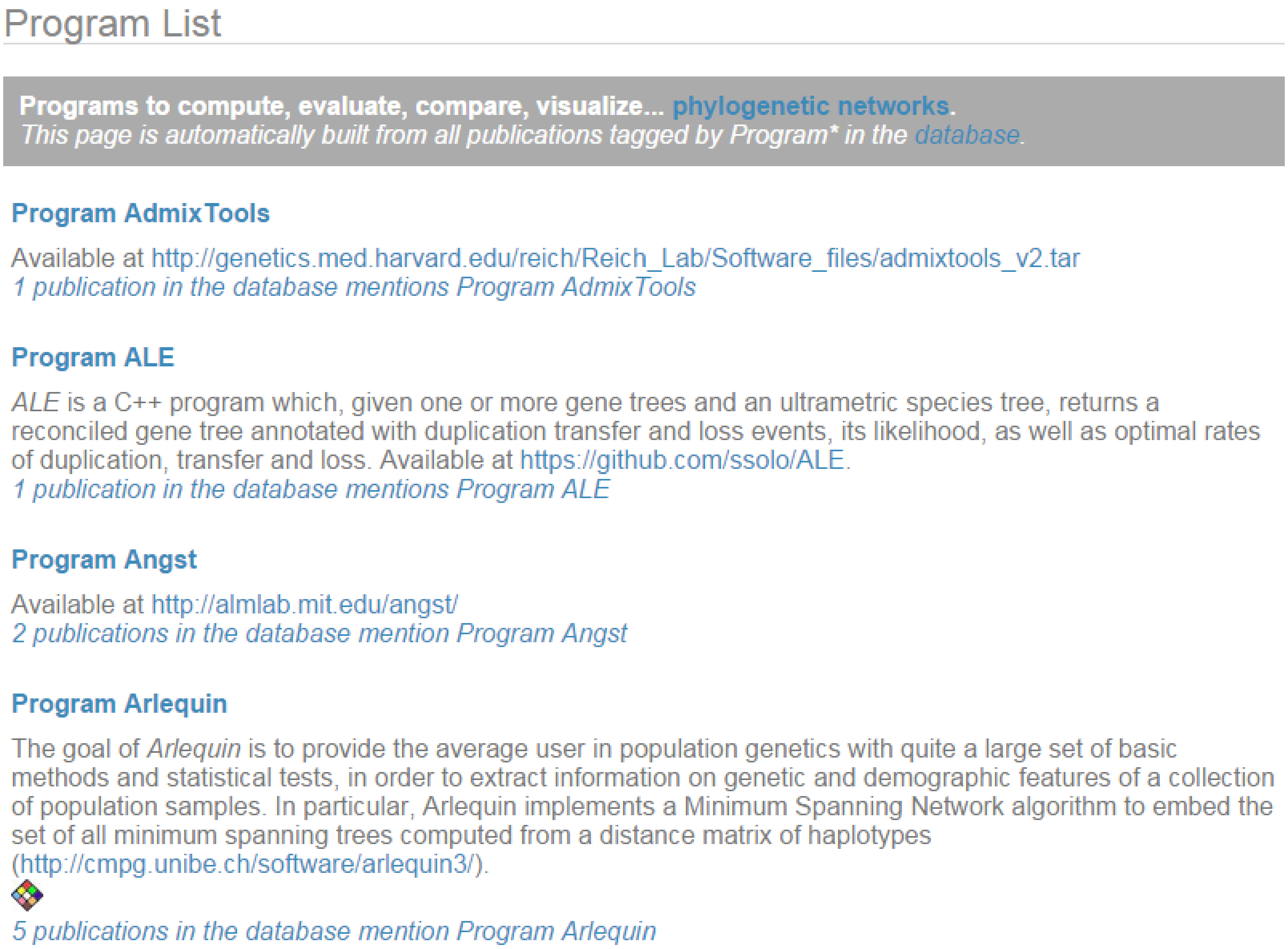


Publications related to 'from clusters' : A *cluster* is a subset of taxa related in some way, which should thus appear together in a phylogenetic tree or network. Clusters can be seen as the rooted equivalents of splits.

Associated keywords

abstract-network APX-hard characterization circular-split-system cluster-containment evaluation explicit-network FPT from-clusters from-distances from-network from-rooted-trees from-sequences from-triplets galled-network galled-tree heuristic hybridization identifiability integer-linear-programming level-k-phylogenetic-network minimum-number NP-complete phylogenetic-network phylogeny polynomial Program-BIMLR Program-Clustistic Program-Dendroscope Program-HybridInterleave Program-HybridNumber Program-LNetwork Program-QuickCass pyramid reconstruction regular-network software split-network SPR-distance Stable-network tree-child-network tree-containment weak-hierarchy

Exploring the research – discovering software



Program List

Programs to compute, evaluate, compare, visualize... phylogenetic networks.
This page is automatically built from all publications tagged by Program in the database.*

Program AdmixTools

Available at http://genetics.med.harvard.edu/reich/Reich_Lab/Software_files/admixtools_v2.tar
1 publication in the database mentions Program AdmixTools

Program ALE

ALE is a C++ program which, given one or more gene trees and an ultrametric species tree, returns a reconciled gene tree annotated with duplication transfer and loss events, its likelihood, as well as optimal rates of duplication, transfer and loss. Available at https://github.com/ssolo/ALE.
1 publication in the database mentions Program ALE

Program Angst

Available at http://almlab.mit.edu/angst/
2 publications in the database mention Program Angst

Program Arlequin

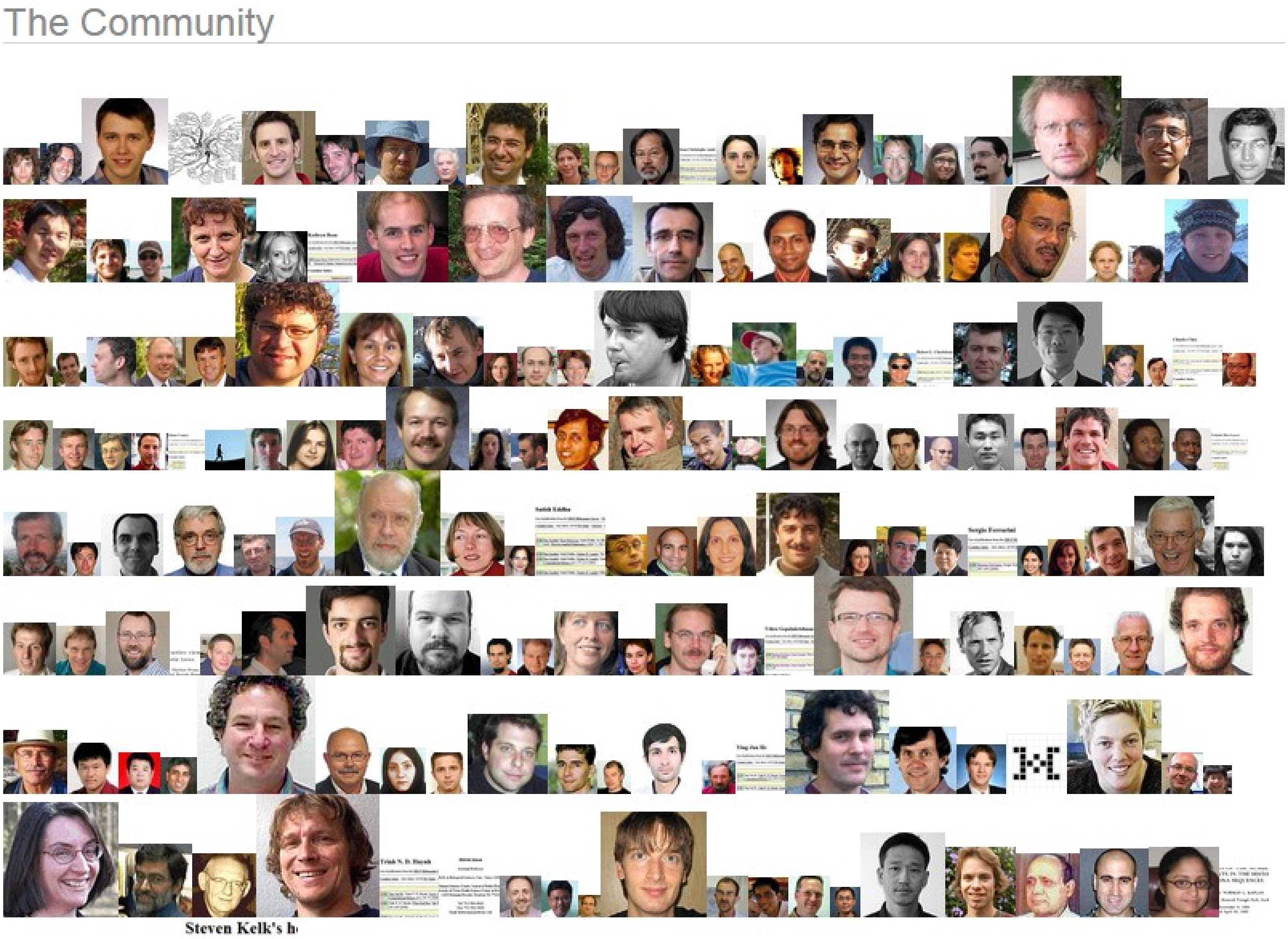
The goal of *Arlequin* is to provide the average user in population genetics with quite a large set of basic methods and statistical tests, in order to extract information on genetic and demographic features of a collection of population samples. In particular, Arlequin implements a Minimum Spanning Network algorithm to embed the set of all minimum spanning trees computed from a distance matrix of haplotypes (http://cmpg.unibe.ch/software/arlequin3/).

5 publications in the database mention Program Arlequin

Outline

- Who is who in phylogenetic networks?
- Exploring the research
- Discovering software
- Finding experts
- Following the community
- Analyzing the trends
- ISIPhyNC and subclasses of phylogenetic networks

Finding experts – In pictures!

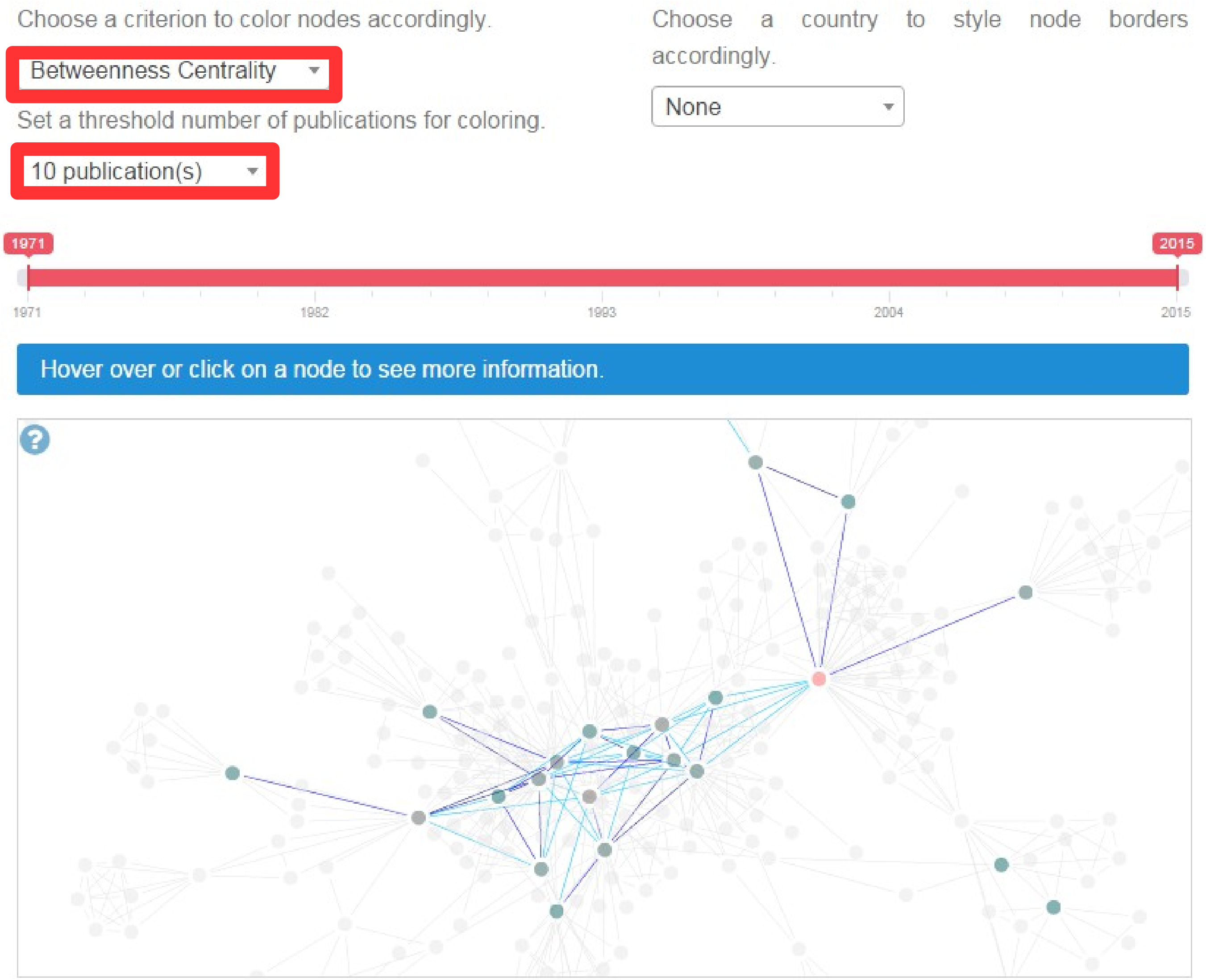


The Community

Steven Kelk's h

Finding experts – Who works with whom?

Exploring the co-author graph and social network measures:



Choose a criterion to color nodes accordingly.

Betweenness Centrality

Set a threshold number of publications for coloring.

10 publication(s)

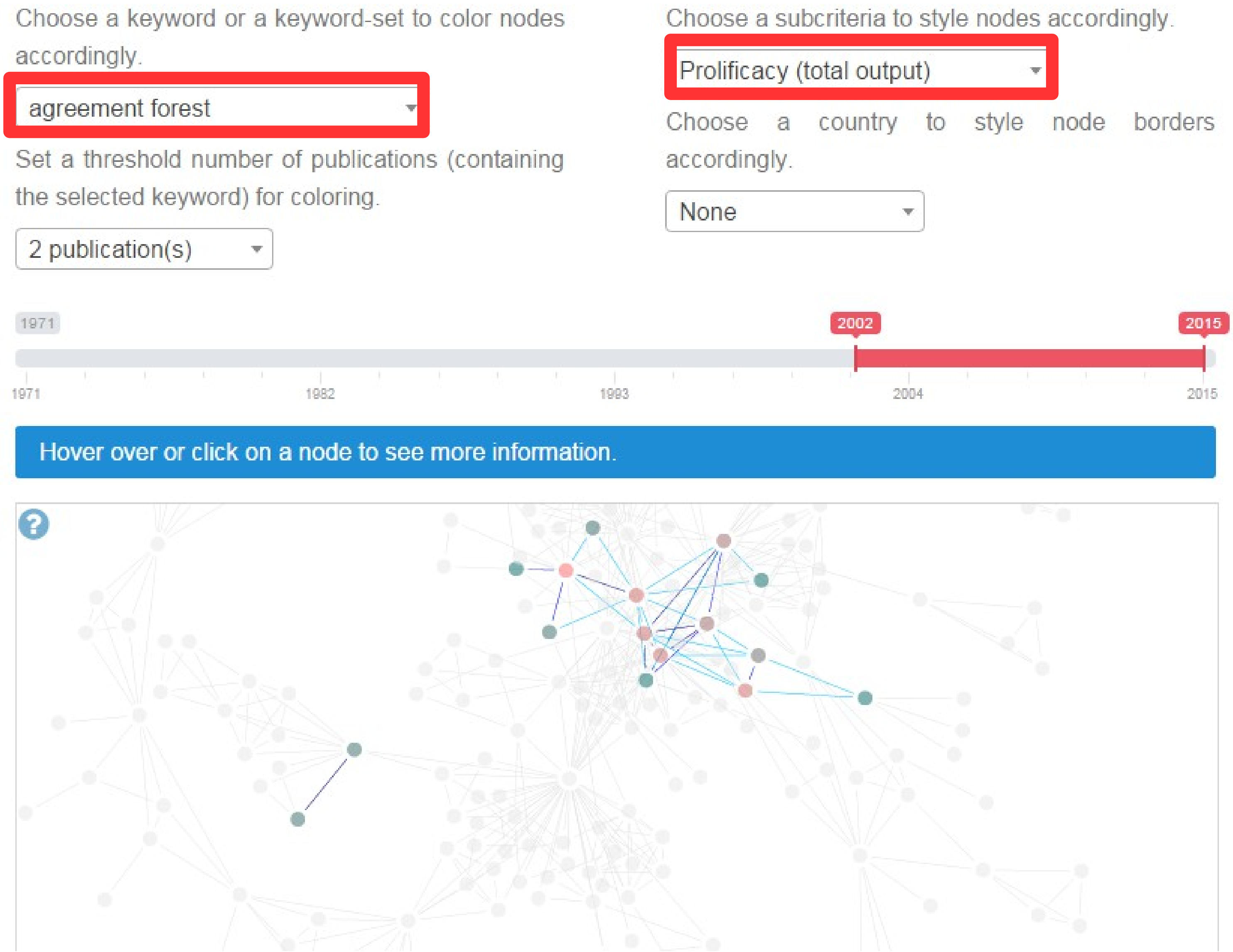
Choose a country to style node borders accordingly.

None

Hover over or click on a node to see more information.

Finding experts – Who works on that keyword?

Coloring the co-author graph with respect to a keyword:



Choose a keyword or a keyword-set to color nodes accordingly.

agreement forest

Set a threshold number of publications (containing the selected keyword) for coloring.

2 publication(s)

Choose a subcriteria to style nodes accordingly.

Prolificacy (total output)

Choose a country to style node borders accordingly.

None

Hover over or click on a node to see more information.

Finding experts – Who works on that keyword?

Coloring the co-author graph with respect to a keyword:

Choose a keyword or a keyword-set to color nodes accordingly.

agreement forest

Set a threshold number of publications (containing the selected keyword) for coloring.

2 publication(s)

Choose a subcriteria to style nodes accordingly.

Focus (fraction of total output)

Choose a country to style node borders accordingly.

None

Hover over or click on a node to see more information.

Finding experts – Where to meet/read them?

Where the community publishes:

Conferences

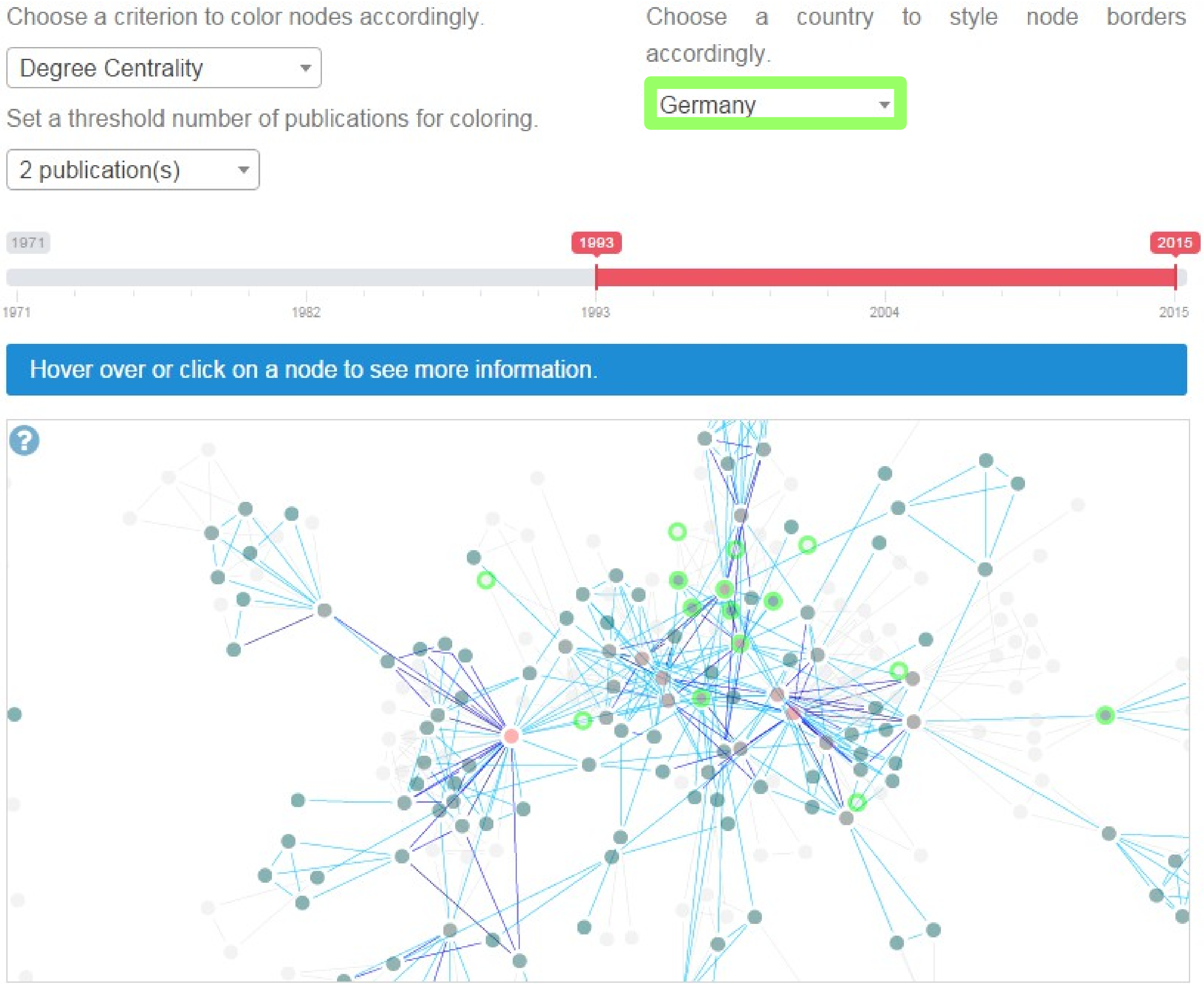
HENNIG-II(4) ALCOB2015(2) ALENEX12(1) APBC05(1) APBC08(1) BIBE05(2) BIOT'09(1) CIBCB13(1) COCOA07(1) COCOA08(1) COCOON04(1) COCOON05(1) COCOON06(1) COCOON07(1) CPM07(1) CPM09(2) CPM10(1) CPM12(1) CPM98(1) CSB03(1) CSB05(1) CSB06(1) CSB10(1) ECCB03(1) ECCB05(1) ECCB06(1) ECCB12(1) ICCABS11(1) IFCS00(1) IFCS02(1) IFCS04(1) IFCS06(1) GFKL93(1) ISAAC04(1) ISAAC05(1) ISAAC08(1) ISBRA07(2) ISBRA09(1) ISBRA10(1) ISBRA12(1) ISBRA13(1) ISBRA15(2) ISMB05(1) ISMB10(2) ISMB11(1) ISMB12(1) ISMB14(1) ISMBECCB09(1) ISPAN'12(1) IWBRA05(1) JOBIM04(1) Logic-and-Program-Semantics(1) MCCMB11(1) MFCS05(1) NCS05(1) PACBB'12(1) PADL03(1) PReMI'07(1) CATS'04(1) SPIE-BBS-II(1) RECOMB-CG'10(2) Alcoma'99(1) RECOMB-CG'06(1) PPSN'IX(1) SEA'10(1) ICTCS'05(1) ICDCIT'05(1) WEA'08(1) RECOMB-CG'08(1) SMBE'05(1) SYRCoDIS'08(1) ICTCS'07(1) JCSSE'15(1) PSB03(2) PSB04(1) RECOMB-CG'12(1) RECOMB-CG'13(1) RECOMB01(1) RECOMB02(1) RECOMB04(3) **RECOMB05(4)** RECOMB07(1) RECOMB08(2) RECOMB13(2) RECOMB15(1) RECOMB99(1) SAC01(1) SFC05(1) SODA05(1) SODA94(1) TAMC12(1) TCSB2(1) Verhandlungen-des-Naturwissenschaftlichen-Vereins-Hamburg(1) JMDA'08(1) WABI02(1) WABI03(3) WABI05(1) WABI06(1) WABI07(1) WABI08(3) WABI09(1) WABI12(2) WG14(1)

Journals

ABIO(1) ACM-Transactions-on-Algorithms(1) **ACOM(7)** Advances-in-Applied-Mathematics(2) Advances-In-Intelligent-and-Soft-Computing(1) Advances-In-Mathematics(1) Advances-In-Research(1) African-Journal-of-Biotechnology (1) ALG(3) Algorithmica(1) Algorithms-for-Molecular-Biology(1) ALMOB(3) AMB(1) American-Journal-of-Botany(1) Annals-of-Combinatorics(1) Annals-of-the-Missouri-Botanical-Garden(1) Annual-Research-&-Review-In-Biology(1) Applied-Mathematics-Letters(2) ARG(1) Australian-&-New-Zealand-Journal-of-Statistics(1) **BIO(13)** BioEssays(1) BioInformatics(1) BioInformatics-India(1) Biology-and-Philosophy(2) Biology-Direct(2) BioMed-Research-International(1) **BMB(13)** BMC-Systems-Biology(1) **BMCB(12)** **BMCEB(9)** Briefings-In-BioInformatics(1) CC(1) Cladistics(2) Computers-and-the-Humanities(1) CSQ(1) Current-Protocols-In-BioInformatics(1) **DAM(9)** Discrete-and-Computational-Geometry(1) DM(1) EBIO(1) EJC(1) EMBnet.journal(1) Evolution(1) Evolutionary-BioInformatics(1) Frontiers-In-Genetics(1) Fundamenta-Informaticae(1) **GEN(7)** Gene(1) Genetics(1) Genetics-and-Molecular-Research(1) Genome-Biology-and-Evolution(1) Genome-Informatics(1) GR(1) IJBRA(1) IJP(1) In-Silico-Biology(1) INCOMP(1) Information-Sciences(2) International-Journal-of-Emerging-Technology-and-Advanced-Engineering(1) IPL(4) **JBCB(13)** **JCB(21)** JCLA(5) JCO(2) JMAB(6) JMB(2) JME(4) Journal-of-Applied-Mathematics-and-Computing(1) Journal-of-Classification(1) Journal-of-Discrete-Algorithms(2) Journal-of-Theoretical-Biology(2) Language,-Journal-of-the-Linguistic-Society-of-America(1) **MBE(16)** MBIO(5) Methods-In-Molecular-Biology(1) MOLE(1) Molecular-Ecology-Ressources(1) MPE(6) NAR(2) Natural-Computing(1) Nature(1) Pattern-Recognition(1) PLoS-Computational-Biology(2) PLoS-Genetics(2) PLoS-ONE(3) PNAS(3) PONE(1) PSE(1) Revue-de-Statistique-Appliquée(1) Rose-Hulman-Undergraduate-Math-Journal(1) **SB(24)** Science(1) SIAM-Journal-on-Discrete-Mathematics(3) SICOMP(3) Systematic-Botany(1) Systematic-Zoology(2) Taxon(1) **TCBB(34)** TCS(3) TEE(2) The-American-Naturalist(1) The-Scientific-World-Journal(1) Theoretical-Population-Biology(1) Theory-and-Practice-of-Logic-Programming(1) TPP(1) Trends-In-Ecology-and-Evolution(1) Trends-In-Genetics(1) Trends-In-Plant-Science(1) Zoologica-Scripta(1)

Finding experts – Where do they live?

Automatic extraction of country from webpage URL:



Choose a criterion to color nodes accordingly.

Degree Centrality

Set a threshold number of publications for coloring.

2 publication(s)

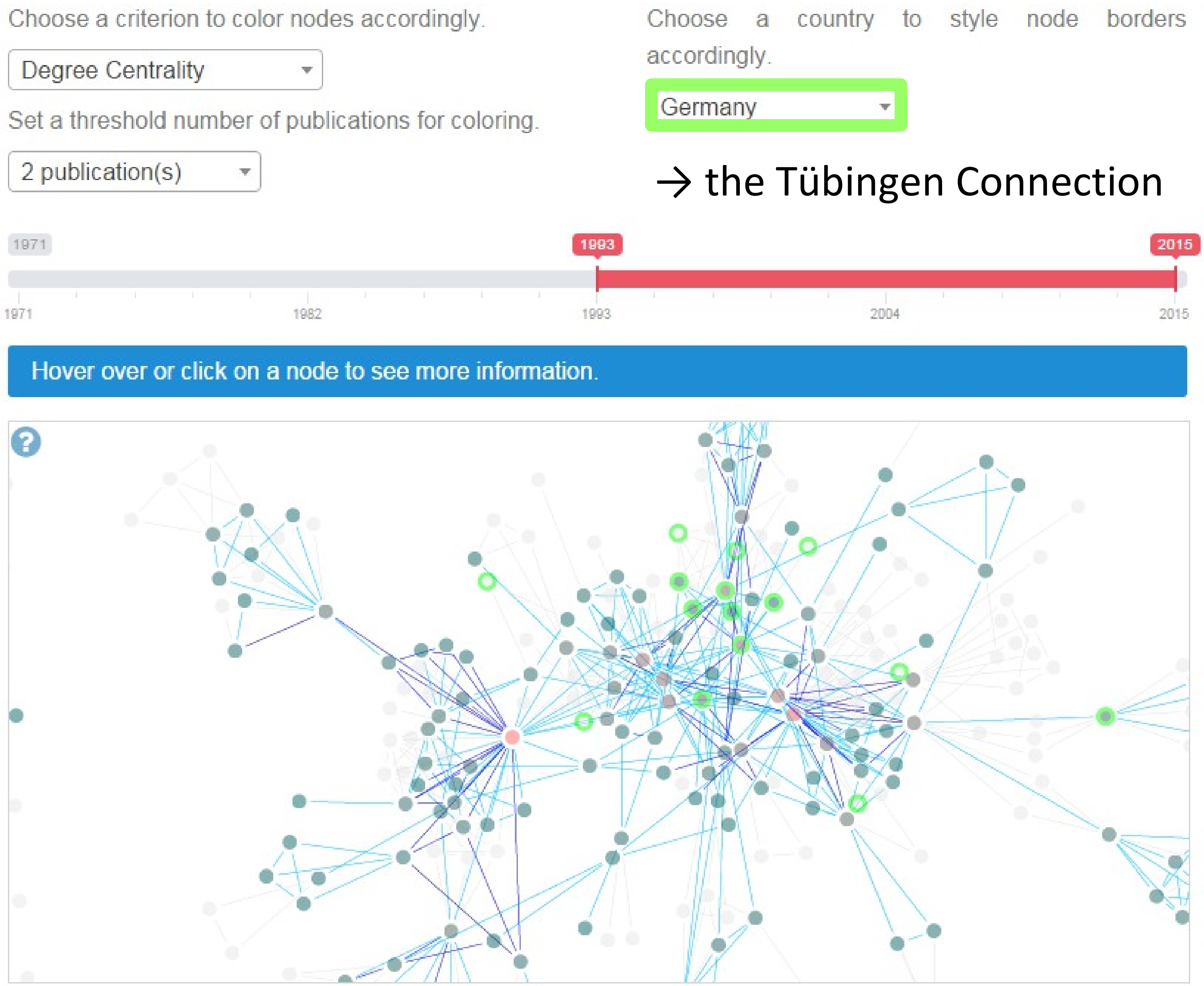
Choose a country to style node borders accordingly.

Germany

Hover over or click on a node to see more information.

Finding experts – Where do they live?

Automatic extraction of country from webpage URL:



Choose a criterion to color nodes accordingly.

Degree Centrality

Set a threshold number of publications for coloring.

2 publication(s)

Choose a country to style node borders accordingly.

Germany

→ the Tübingen Connection

Hover over or click on a node to see more information.

Outline

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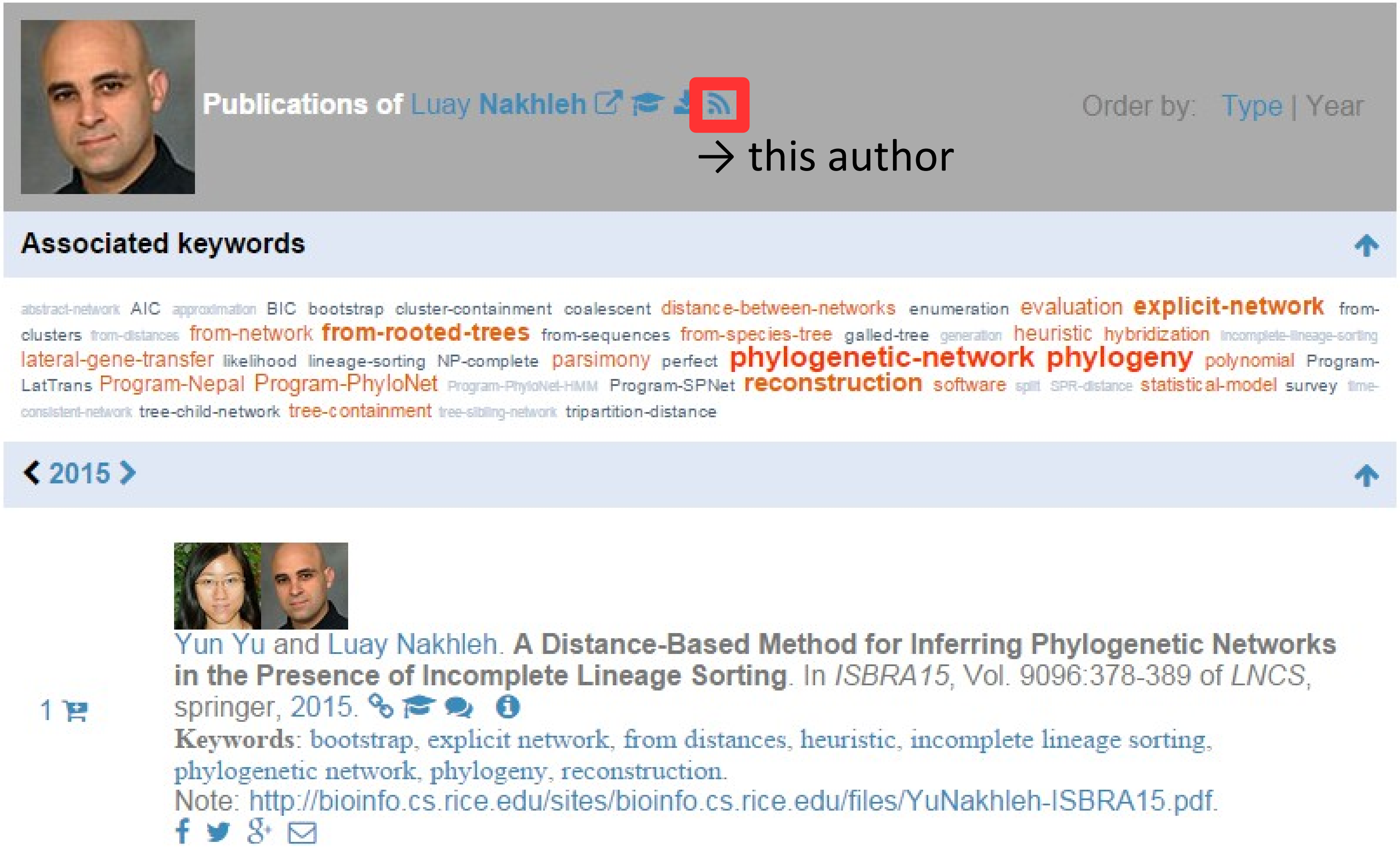
Following the community – RSS feeds

Who is Who in Phylogenetic Networks

→ whole website



Publications of Luay Nakhleh

Order by: Type | Year

→ this author

Associated keywords

abstract-network AIC approximation BIC bootstrap cluster-containment coalescent distance-between-networks enumeration evaluation explicit-network from-clusters from-distances from-network from-rooted-trees from-sequences from-species-tree galled-tree generation heuristic hybridization incomplete-lineage-sorting lateral-gene-transfer likelihood lineage-sorting NP-complete parsimony perfect phylogenetic-network phylogeny polynomial Program-LatTrans Program-Nepal Program-PhyloNet Program-PhyloNet-HMM Program-SPNet reconstruction software split SPR-distance statistical-model survey time-consistent-network tree-child-network tree-containment tree-sibling-network tripartition-distance

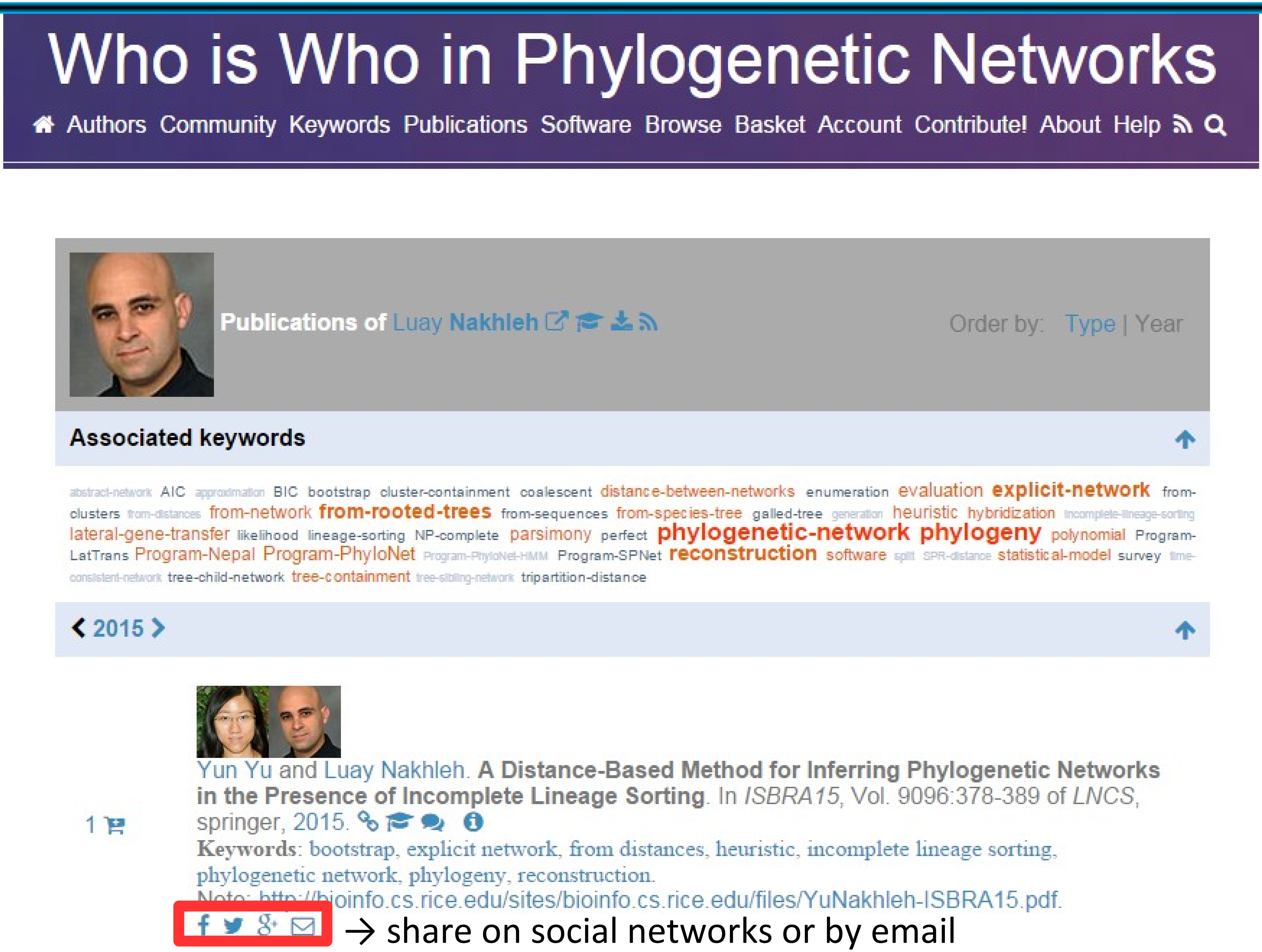
2015

1 Yun Yu and Luay Nakhleh. **A Distance-Based Method for Inferring Phylogenetic Networks in the Presence of Incomplete Lineage Sorting**. In *ISBRA15*, Vol. 9096:378-389 of *LNCS*, springer, 2015.

Keywords: bootstrap, explicit network, from distances, heuristic, incomplete lineage sorting, phylogenetic network, phylogeny, reconstruction.

Note: http://bioinfo.cs.rice.edu/sites/bioinfo.cs.rice.edu/files/YuNakhleh-ISBRA15.pdf.

Following the community – Social networks



Who is Who in Phylogenetic Networks

Authors Community Keywords Publications Software Browse Basket Account Contribute! About Help

Publications of Luay **Nakhleh**

Order by: Type | Year

Associated keywords

abstract-network AIC approximation BIC bootstrap cluster-containment coalescent distance-between-networks enumeration evaluation **explicit-network** from-clusters from-distances from-network **from-rooted-trees** from-sequences from-species-tree galled-tree generation heuristic hybridization incomplete-lineage-sorting lateral-gene-transfer likelihood lineage-sorting NP-complete parsimony perfect **phylogenetic-network phylogeny** polynomial Program-LatTrans Program-Nepal Program-PhyloNet Program-PhyloNet-HMM Program-SPNet **reconstruction** software split SPR-distance statistical-model survey time-consistent-network tree-child-network tree-containment tree-sibling-network tripartition-distance

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Note: http://bioinfo.cs.rice.edu/sites/bioinfo.cs.rice.edu/files/YuNakhleh-ISBRA15.pdf.

→ share on social networks or by email

Following the community – Professional networks

Who is Who in Phylogenetic Networks

→ on Google Scholar

Publications of Luay Nakhleh

Order by: Type | Year

→ download BibTeX basket including Scopus query about the DOIs

Associated keywords

abstract-network AIC approximation BIC bootstrap cluster-containment coalescent distance-between-networks enumeration evaluation explicit-network from-clusters from-distances from-network from-rooted-trees from-sequences from-species-tree galled-tree generation heuristic hybridization incomplete-lineage-sorting lateral-gene-transfer likelihood lineage-sorting NP-complete parsimony perfect phylogenetic-network phylogeny polynomial Program-LatTrans Program-Nepal Program-PhyloNet Program-PhyloNet-HMM Program-SPNet reconstruction software split SPR-distance statistical-model survey time-consistent-network tree-child-network tree-containment tree-sibling-network tripartition-distance

‹ 2015 ›

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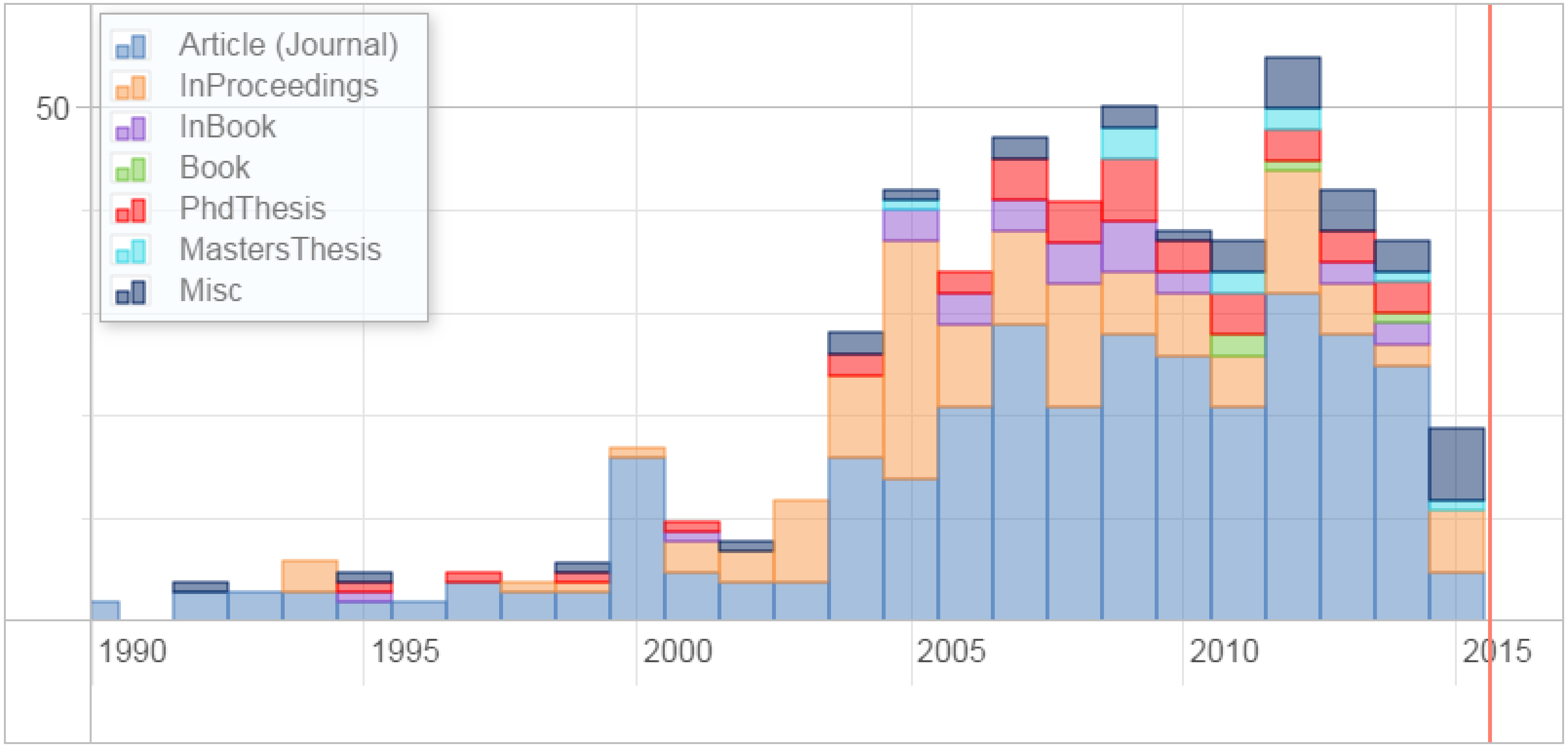
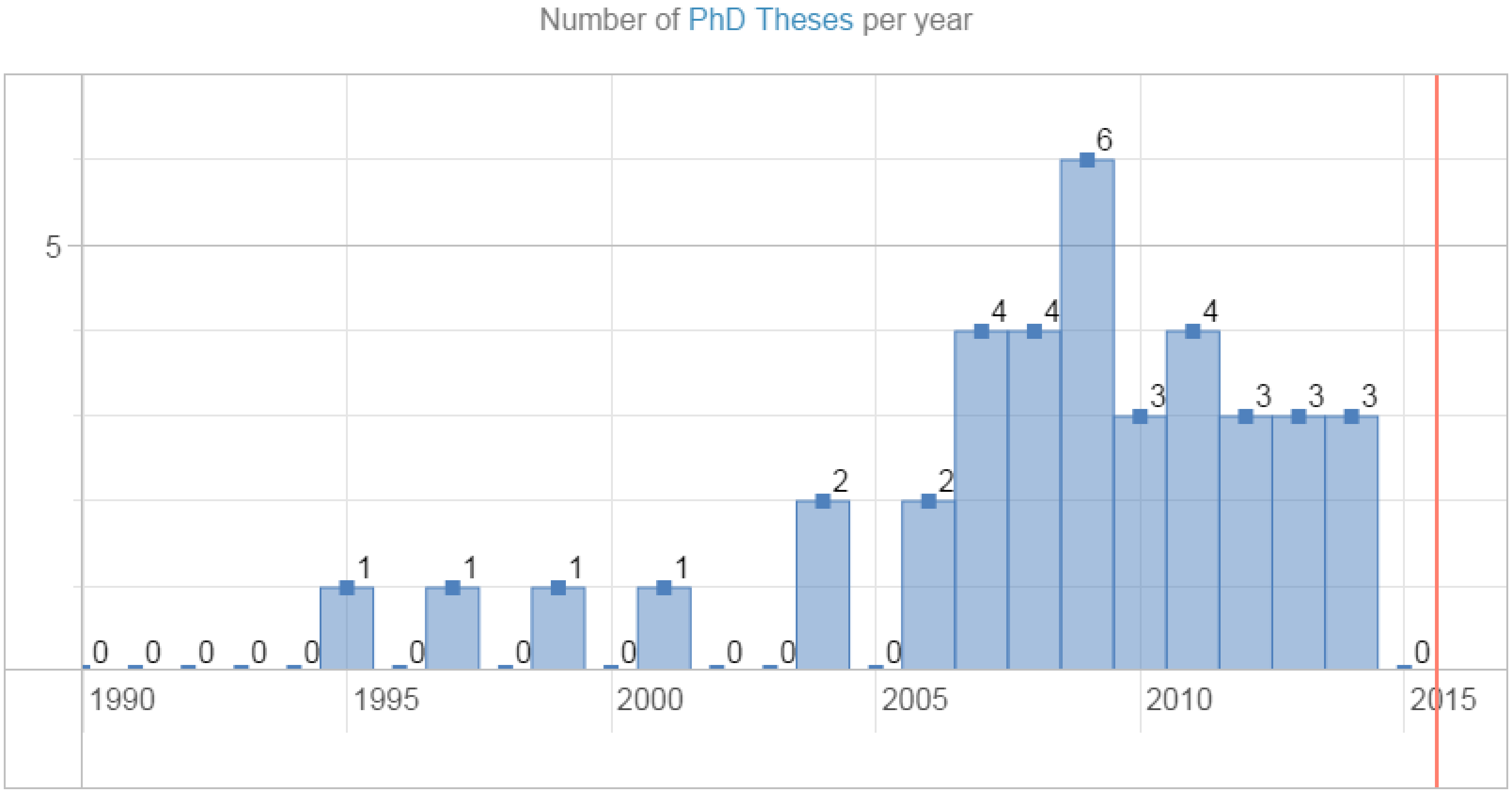
Analyzing the trends – general trends of the field

About 40 publications a year:

Browse publications: Article (Journal), InProceedings, InBook, Book, PhdThesis, MastersThesis, Misc



Analyzing the trends – general trends of the field

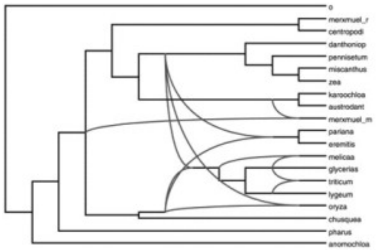


Analyzing the trends – general trends of the field

Explicit networks versus abstract networks?

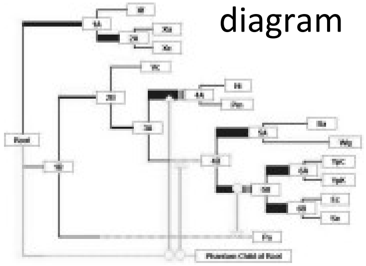
- **explicit** phylogenetic networks

model evolution



galled network

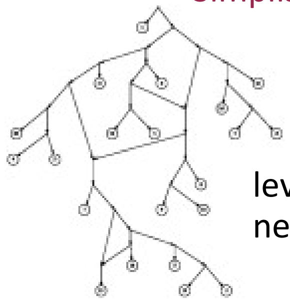
Dendroscope



synthesis diagram

HorizStory

Simplistic

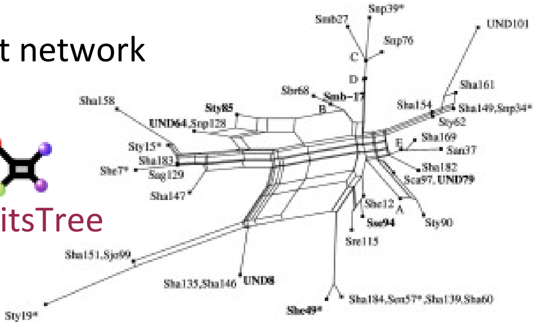


level-2 network

- **abstract** phylogenetic networks

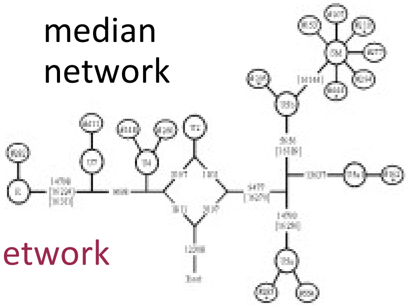
classify, **visualize** data

split network



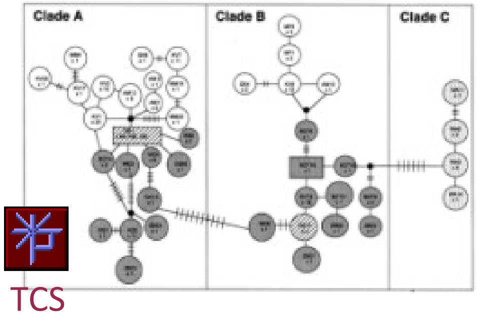
SplitsTree

median network



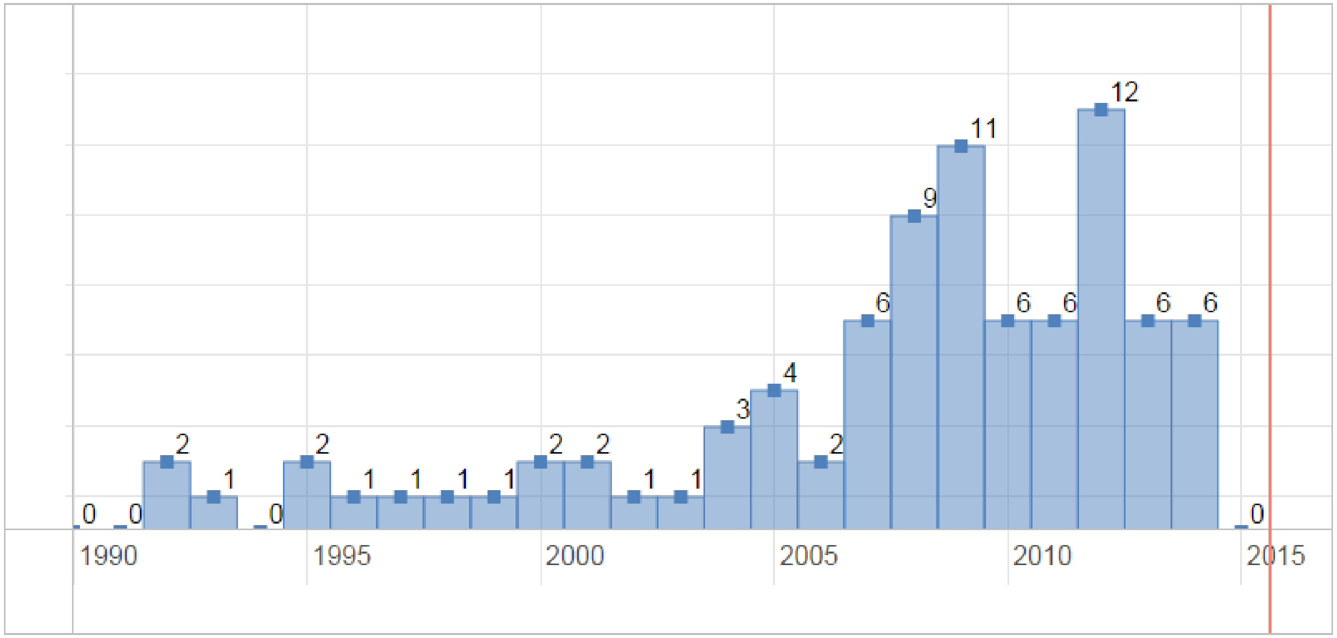
Network

minimum spanning network



TCS

Analyzing the trends – general trends of the field



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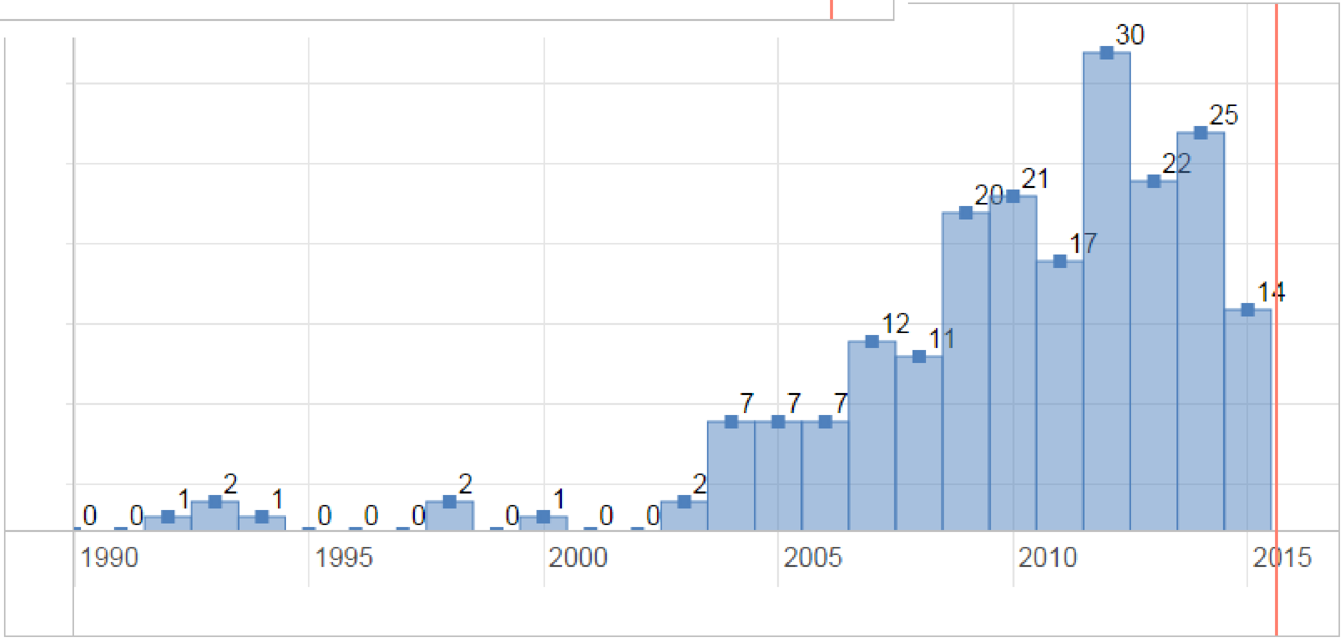
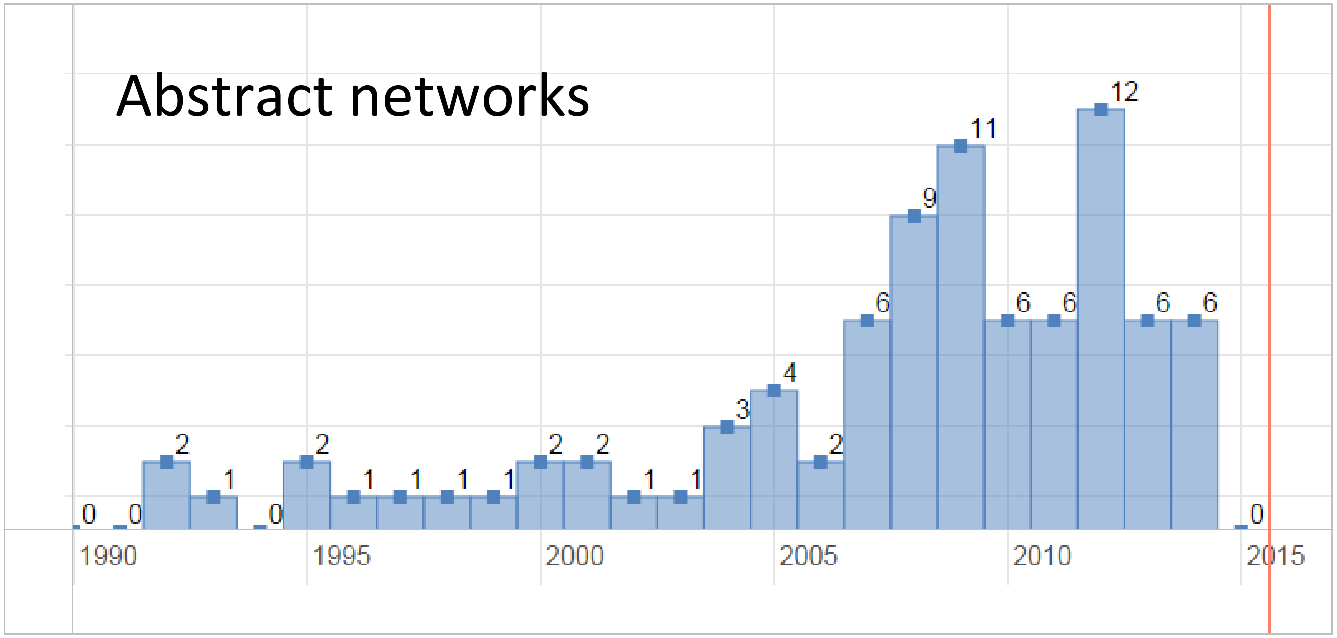
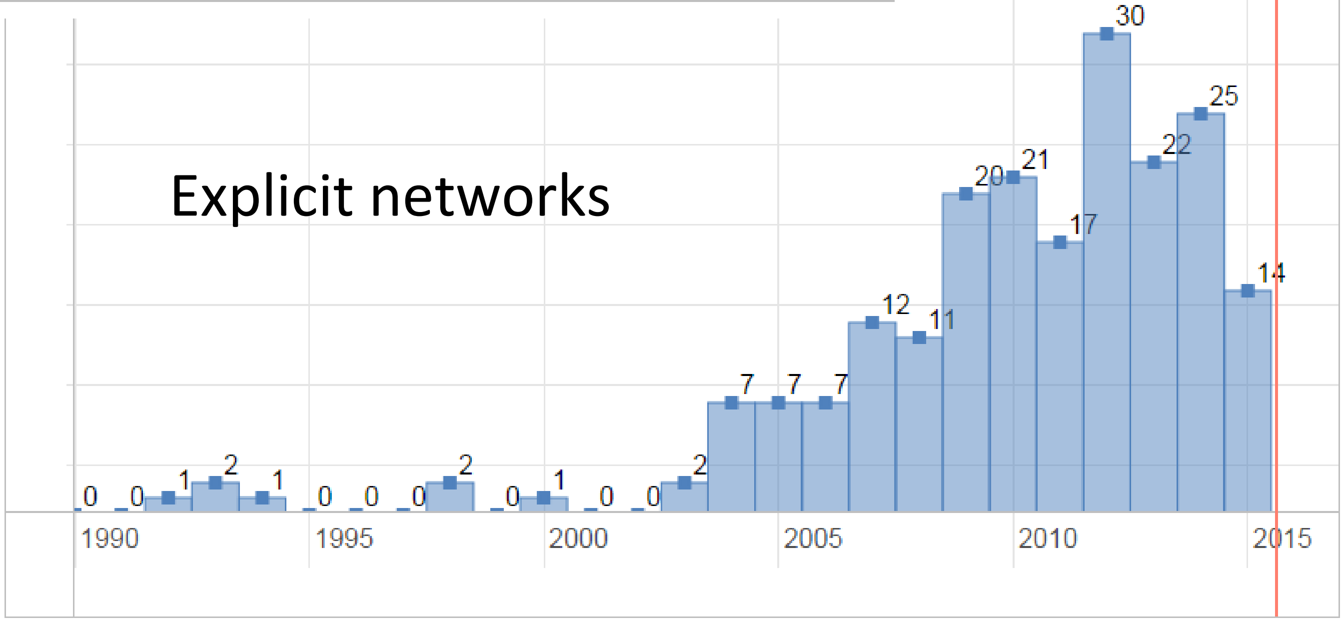
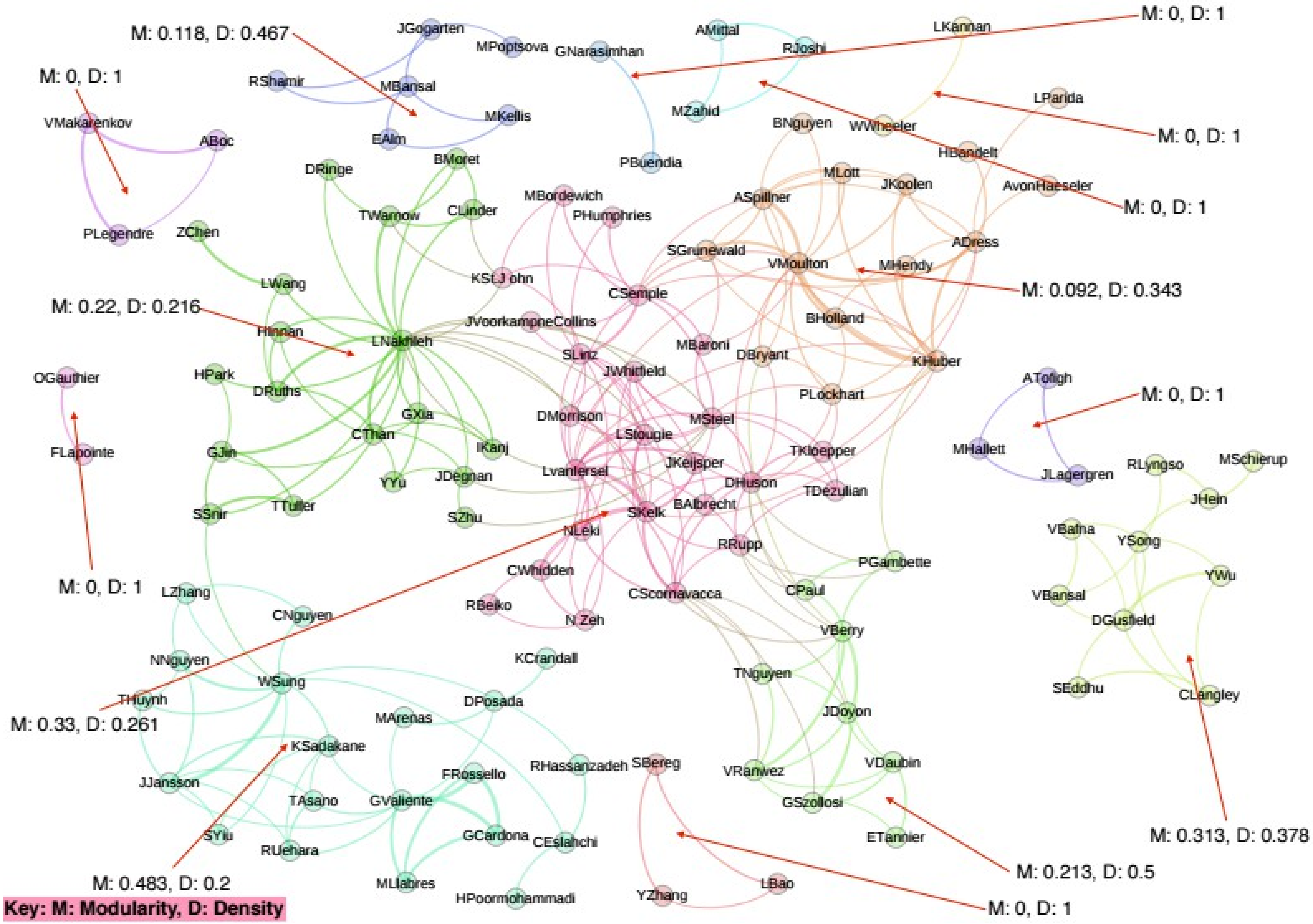


Analyzing the trends – general trends of the field


Abstract networks


Explicit networks

Analyzing the trends – A less clusterized field?



M: 0.118, D: 0.467

M: 0, D: 1

M: 0, D: 1

M: 0, D: 1

M: 0, D: 1

M: 0.092, D: 0.343

M: 0.22, D: 0.216

M: 0, D: 1

M: 0, D: 1

M: 0.33, D: 0.261

M: 0.313, D: 0.378

M: 0.213, D: 0.5

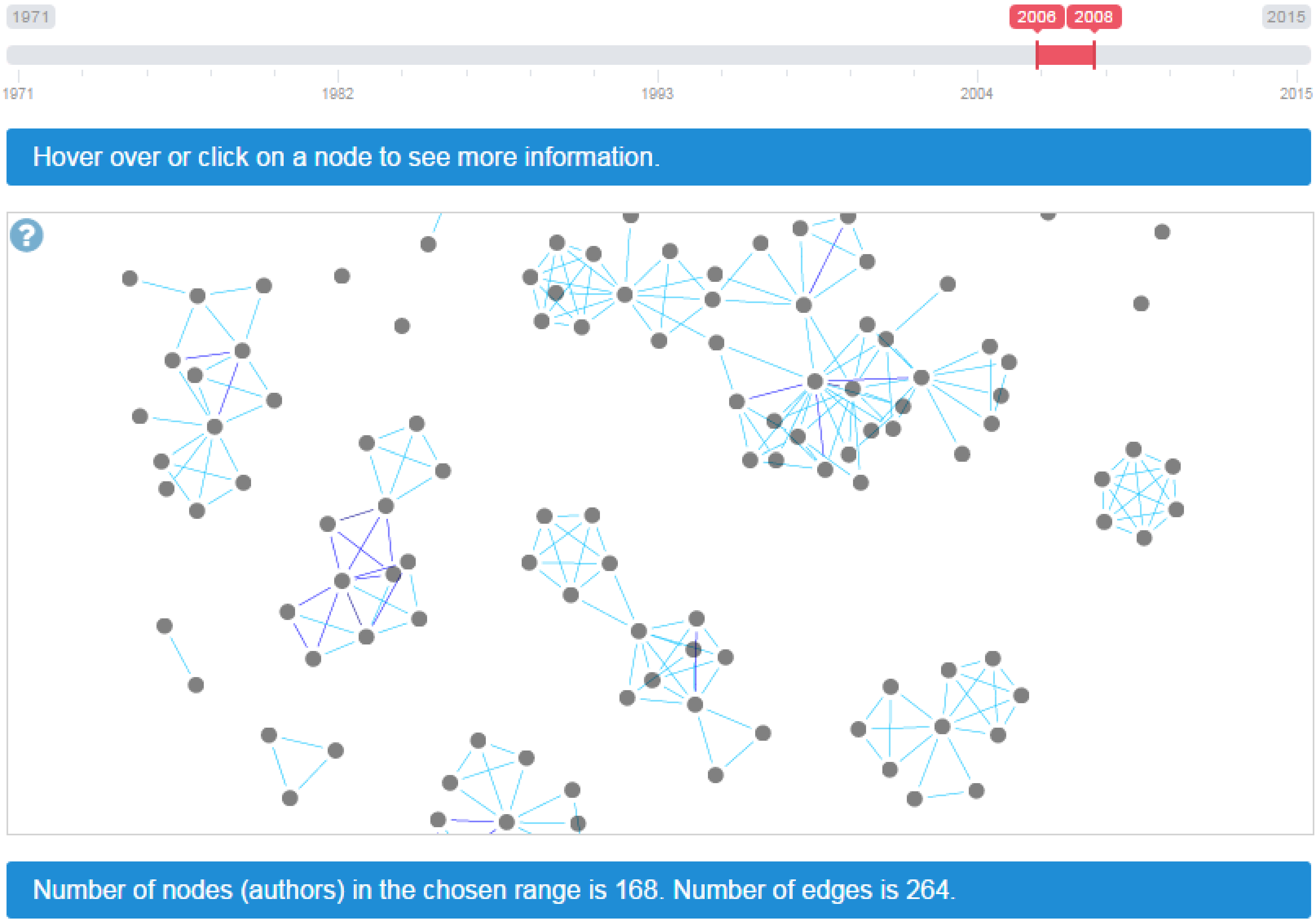
M: 0.483, D: 0.2

M: 0, D: 1

Key: M: Modularity, D: Density

Gephi visualization of the coauthor network clustering → reflects the history

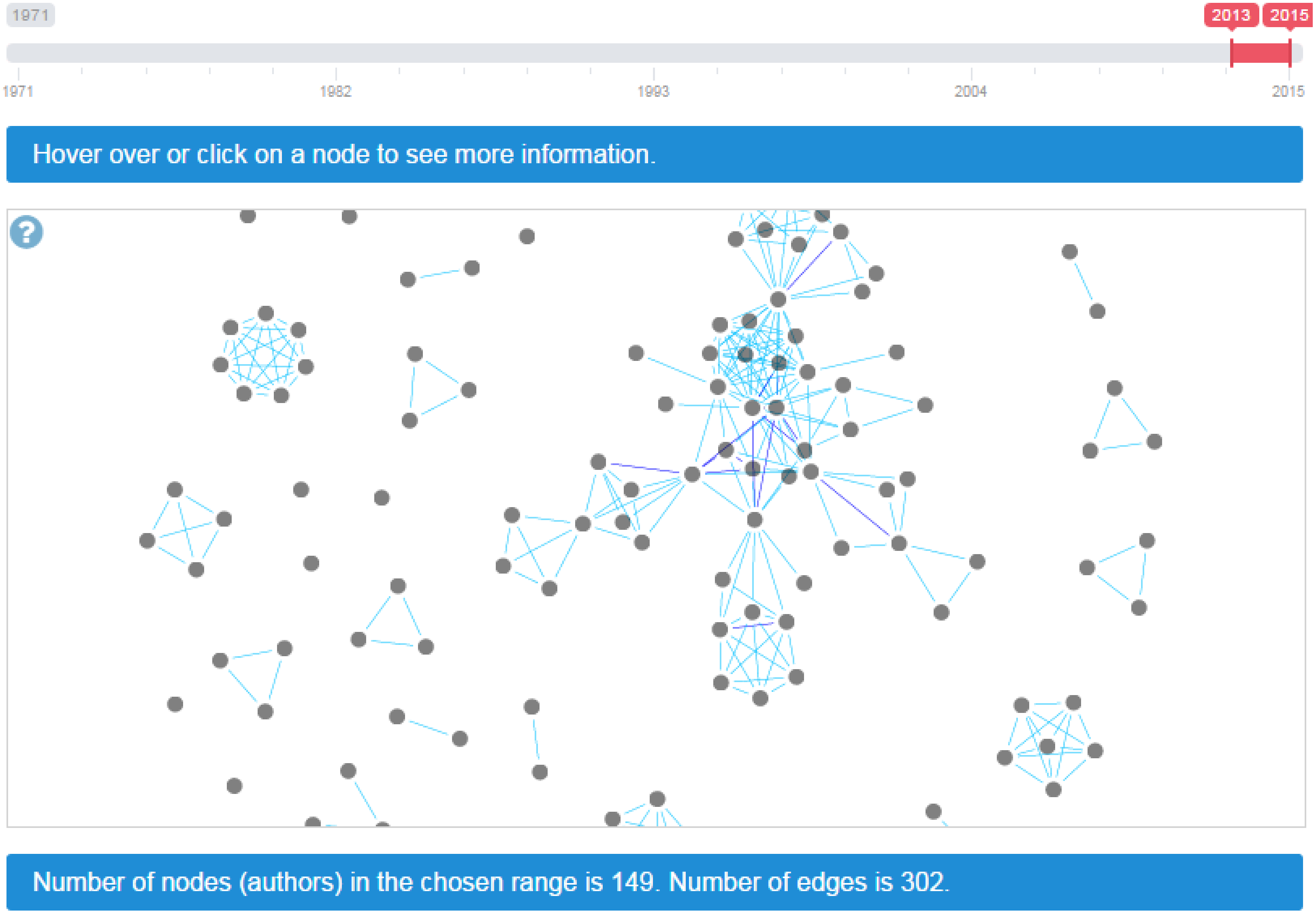
Analyzing the trends – A less clusterized field?



Hover over or click on a node to see more information.

Number of nodes (authors) in the chosen range is 168. Number of edges is 264.

Analyzing the trends – A less clusterized field?

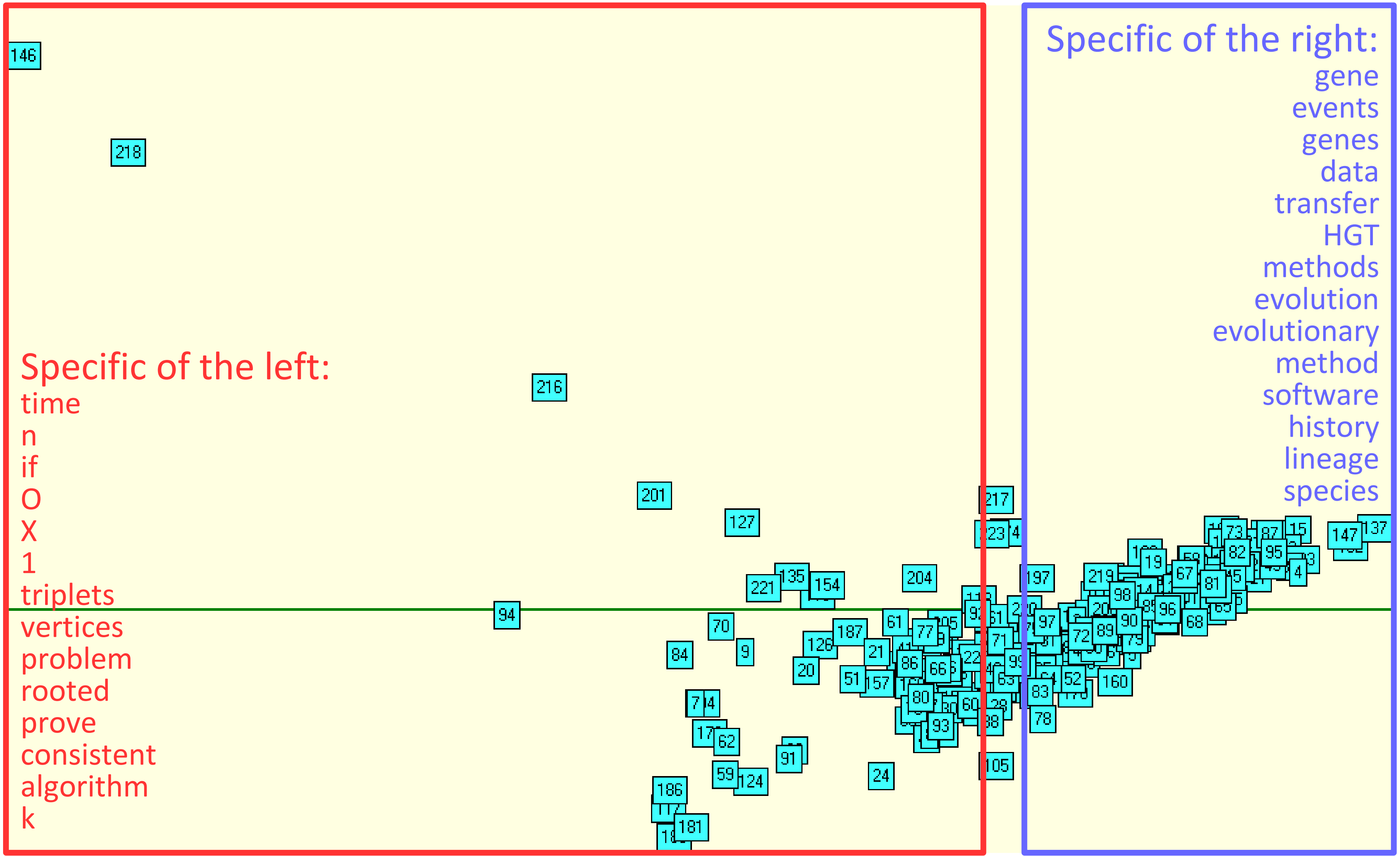


Hover over or click on a node to see more information.

Number of nodes (authors) in the chosen range is 149. Number of edges is 302.

Analyzing the trends – Classifying abstracts

Factor analysis (with Lexico) of the abstracts of the journal articles with DOI in the database available on Scopus:

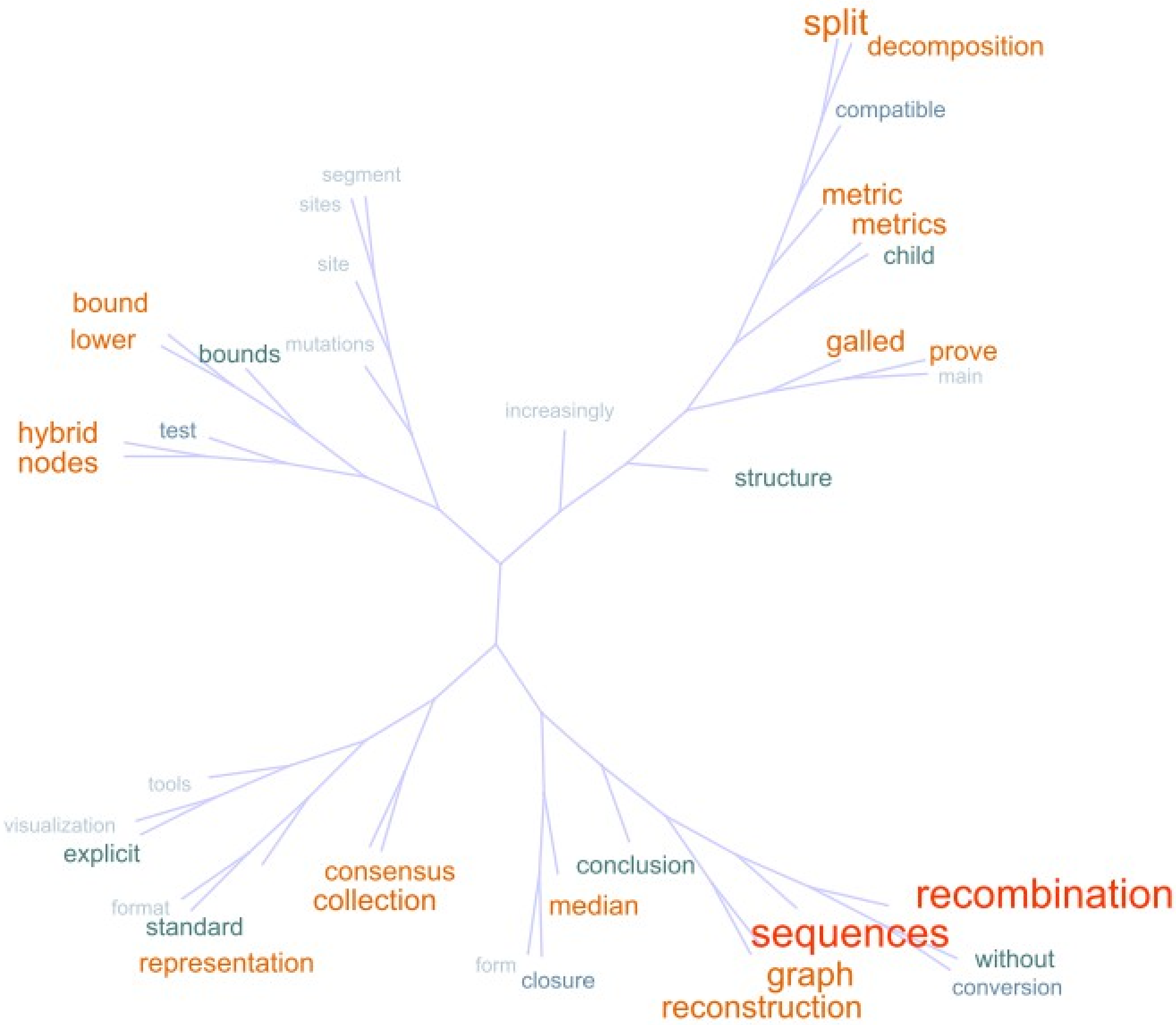


Specific of the left:
time
n
if
O
X
1
triplets
vertices
problem
rooted
prove
consistent
algorithm
k

Specific of the right:
gene
events
genes
data
transfer
HGT
methods
evolution
evolutionary
method
software
history
lineage
species

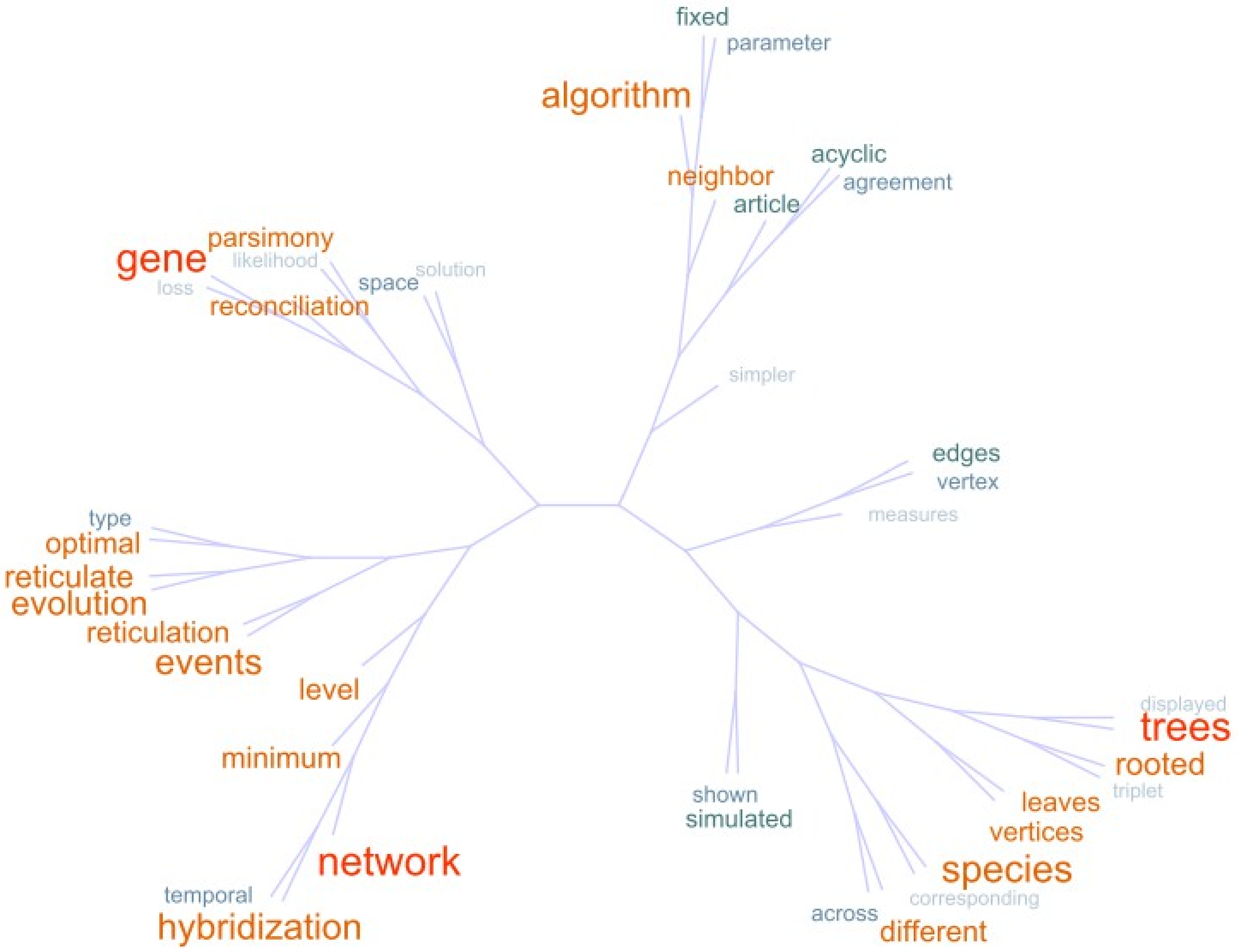
Analyzing the trends – Temporal evolutions

TreeCloud of the vocabulary specific to abstracts before 2010



Analyzing the trends – Temporal evolutions

TreeCloud of the vocabulary specific to abstracts of 2010-2015

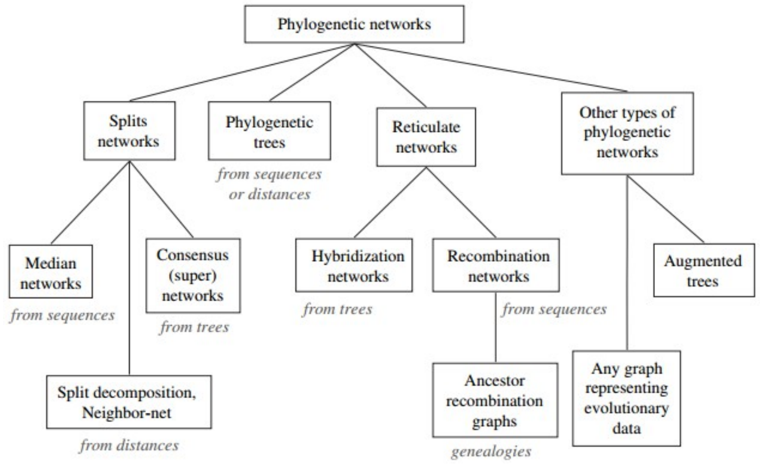


Outline

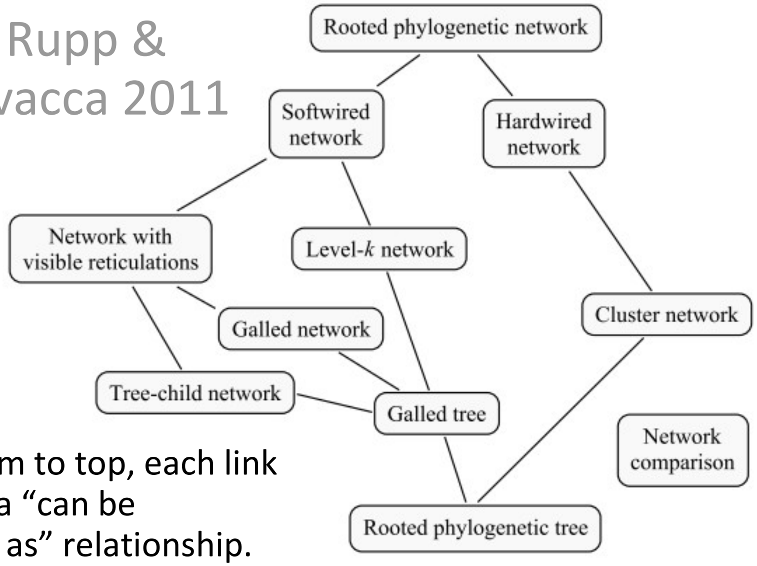
- Who is who in phylogenetic networks?
- Exploring the research
- Discovering software
- Finding experts
- Following the community
- Analyzing the trends
- ISIPhyNC and subclasses of phylogenetic networks

Subclasses of phylogenetic networks

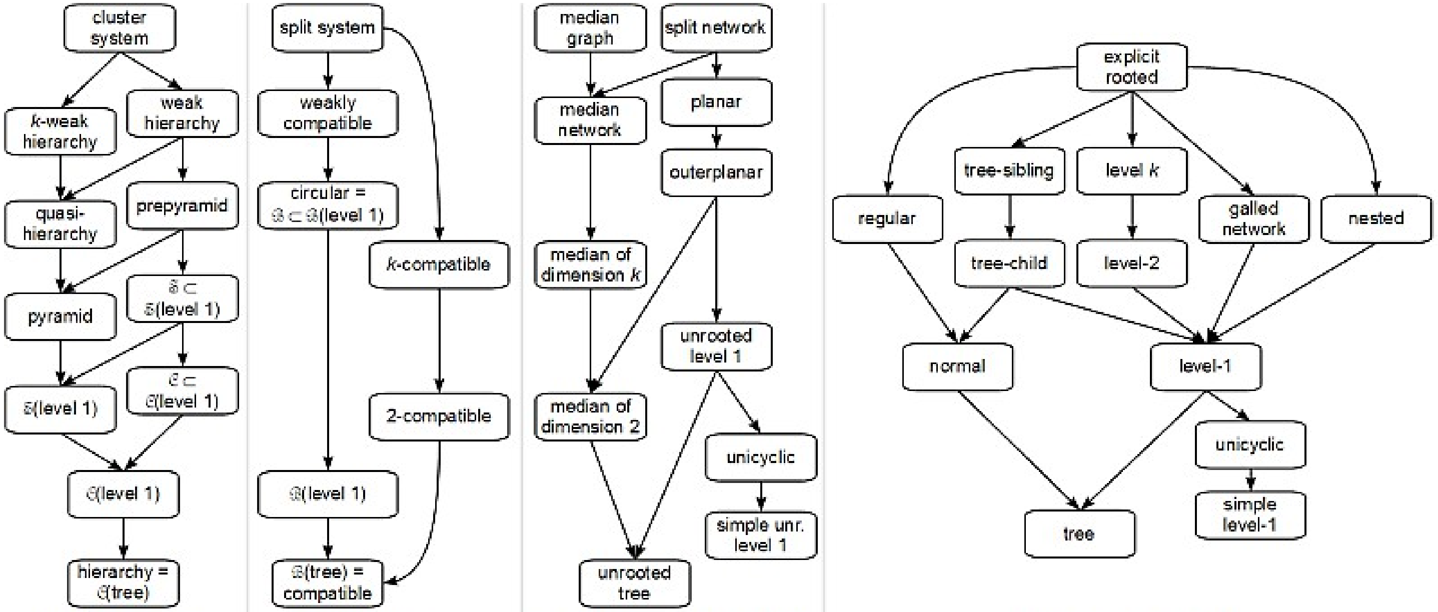
Huson & Bryant 2006



Huson, Rupp & Scornavacca 2011



From bottom to top, each link represents a “can be interpreted as” relationship.



Gambette 2010

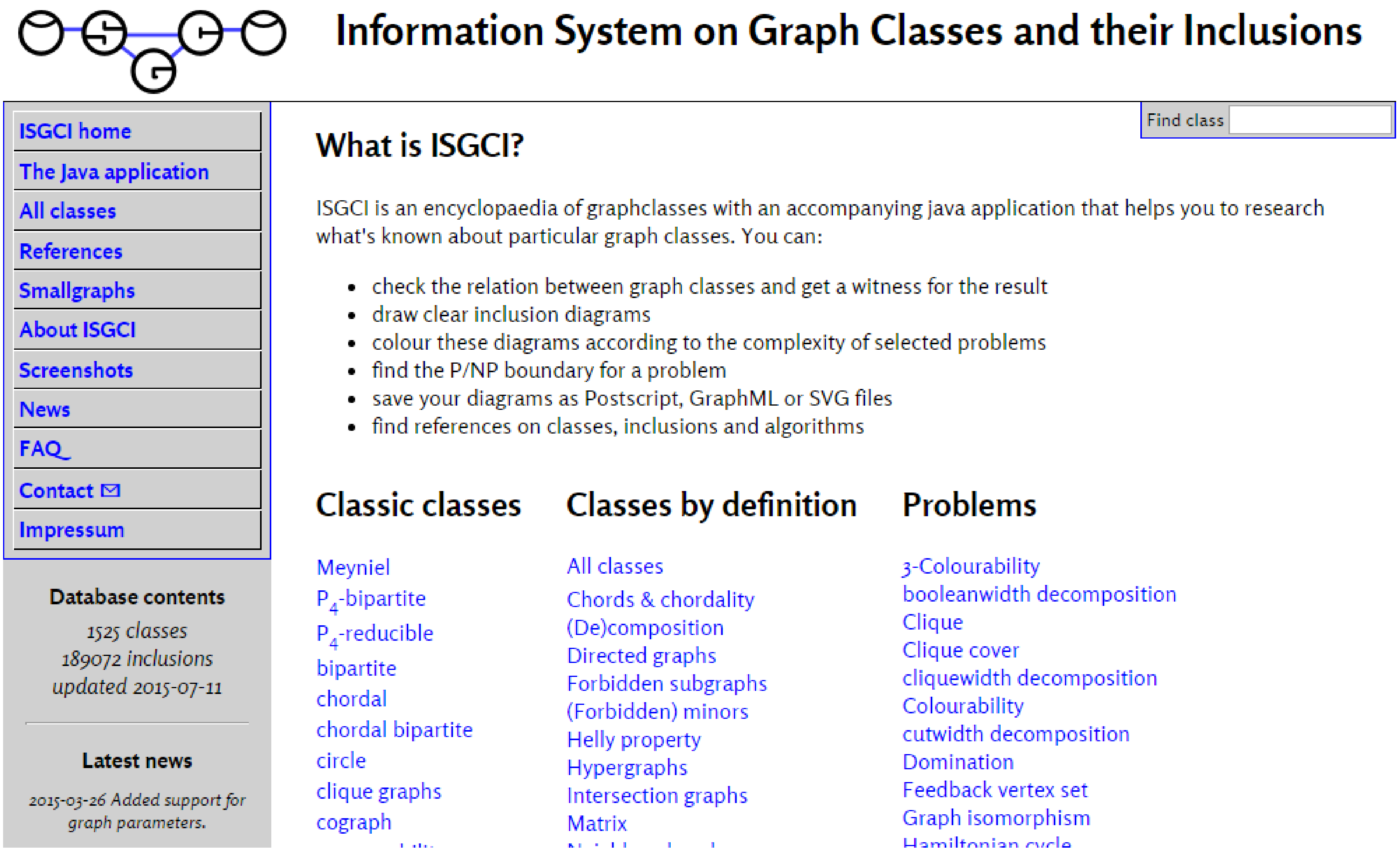
Cluster systems

Split systems

Abstract unrooted networks

Explicit rooted networks

Information System on Graph Classes and their Inclusions



Information System on Graph Classes and their Inclusions

What is ISGCI?

ISGCI is an encyclopaedia of graphclasses with an accompanying java application that helps you to research what's known about particular graph classes. You can:

- check the relation between graph classes and get a witness for the result
- draw clear inclusion diagrams
- colour these diagrams according to the complexity of selected problems
- find the P/NP boundary for a problem
- save your diagrams as Postscript, GraphML or SVG files
- find references on classes, inclusions and algorithms

Database contents

1525 classes
189072 inclusions
updated 2015-07-11

Latest news

2015-03-26 Added support for graph parameters.

Classic classes

Meyniel
P_4-bipartite
P_4-reducible
bipartite
chordal
chordal bipartite
circle
clique graphs
cograph

Classes by definition

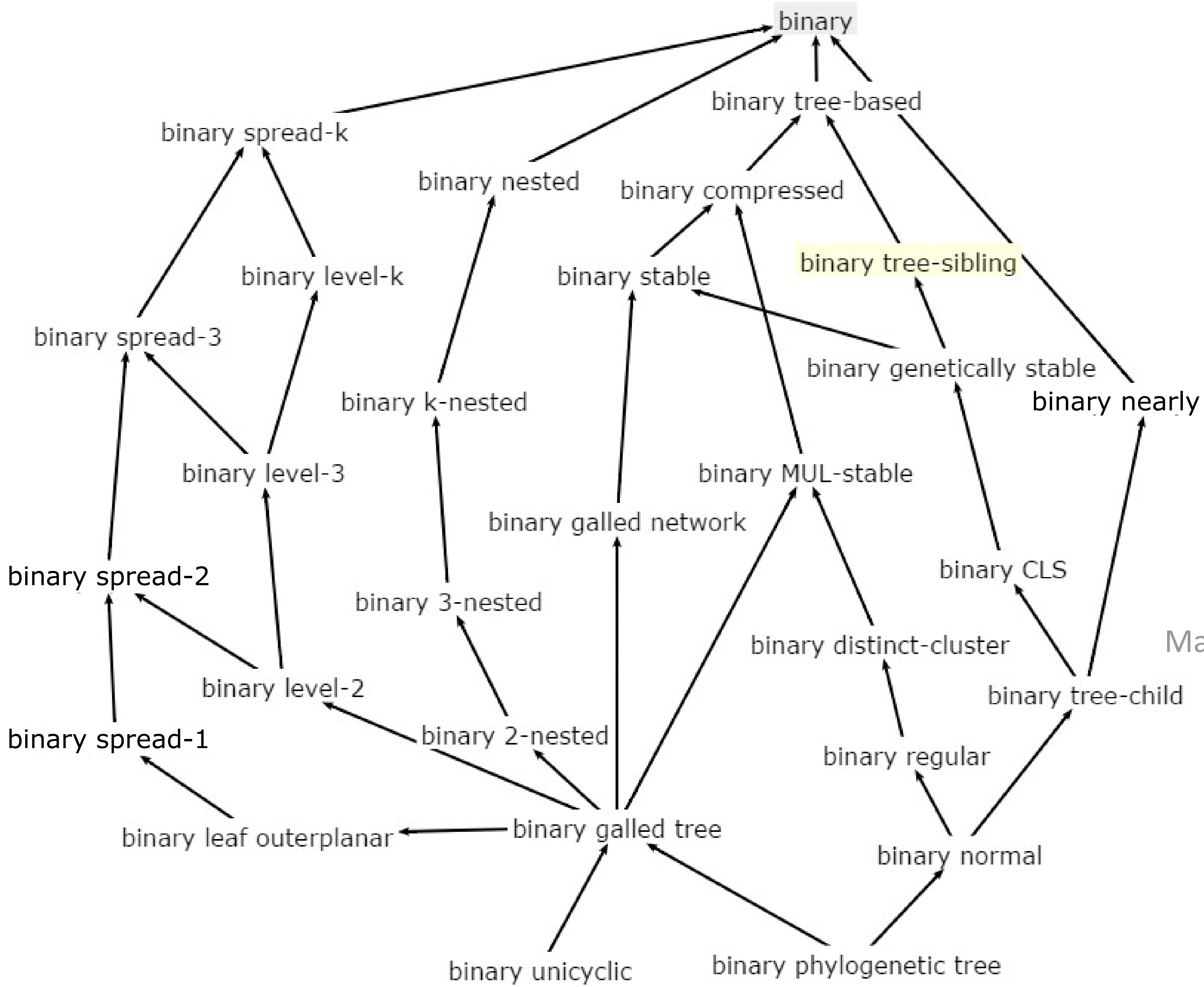
All classes
Chords & chordality
(De)composition
Directed graphs
Forbidden subgraphs
(Forbidden) minors
Helly property
Hypergraphs
Intersection graphs
Matrix

Problems

3-Colourability
booleanwidth decomposition
Clique
Clique cover
cliquewidth decomposition
Colourability
cutwidth decomposition
Domination
Feedback vertex set
Graph isomorphism

H.N. de Ridder et al. The Information System on Graph Classes and their Inclusions ISGCI
http://www.graphclasses.org (1999–2015)

ISIPhyNC and subclasses of phylogenetic networks



binary

binary tree-based

binary spread-k

binary nested

binary compressed

binary tree-sibling

binary level-k

binary stable

binary spread-3

binary genetically stable

binary k-nested

binary nearly stable

binary level-3

binary MUL-stable

binary galled network

binary spread-2

binary CLS

binary 3-nested

binary distinct-cluster

binary level-2

binary tree-child

binary spread-1

binary 2-nested

binary regular

binary leaf outerplanar

binary galled tree

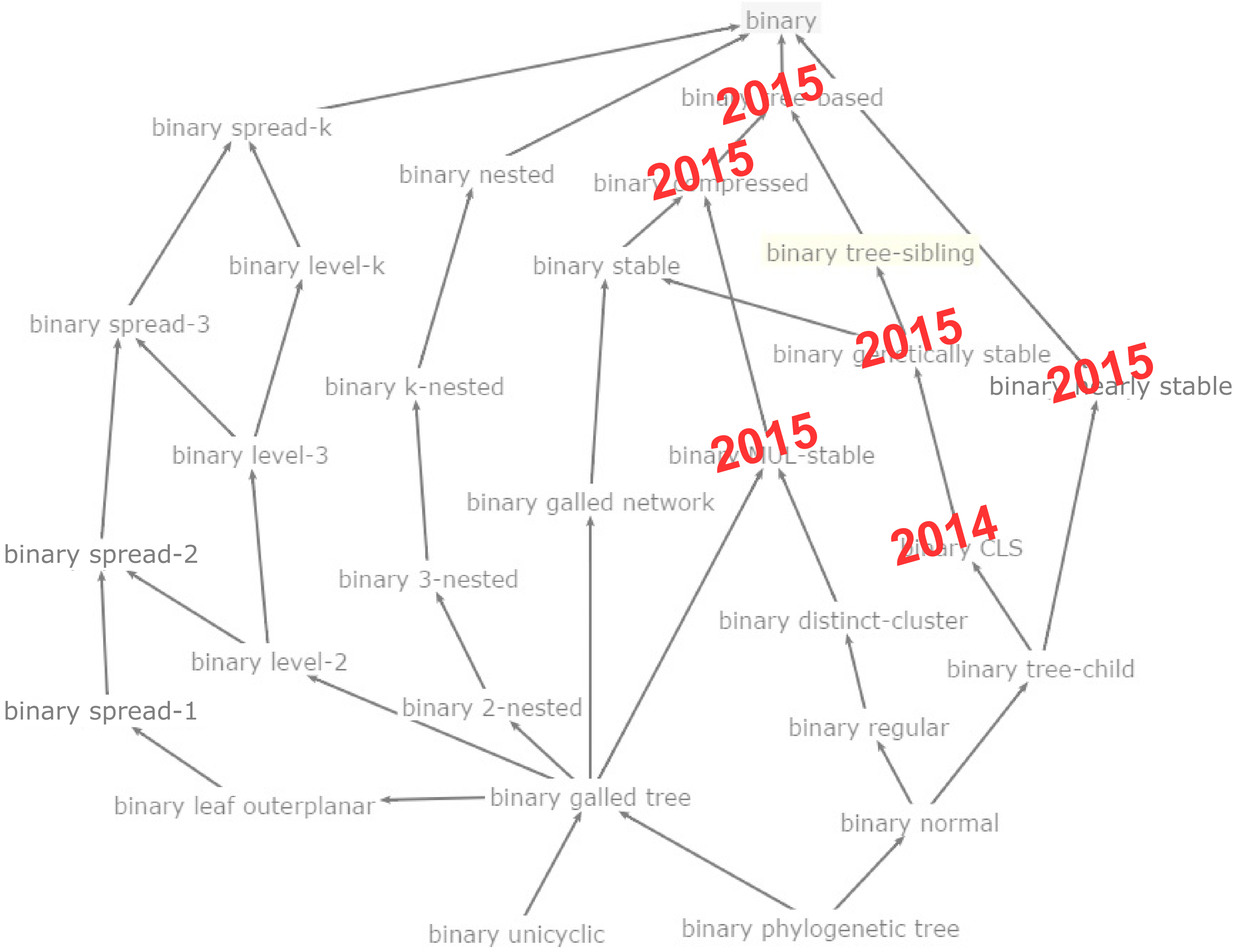
binary normal

binary unicyclic

binary phylogenetic tree

Internship of
Maxime Morgado,
2015

ISIPhyNC and subclasses of phylogenetic networks



binary

binary tree-based

2015

binary spread-k

binary nested

binary compressed

2015

binary level-k

binary stable

binary tree-sibling

binary spread-3

binary genetically stable

2015

binary nearly stable

2015

binary k-nested

binary level-3

binary MUL-stable

2015

binary galled network

binary spread-2

binary CLS

2014

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binary distinct-cluster

binary level-2

binary tree-child

binary 2-nested

binary spread-1

binary regular

binary galled tree

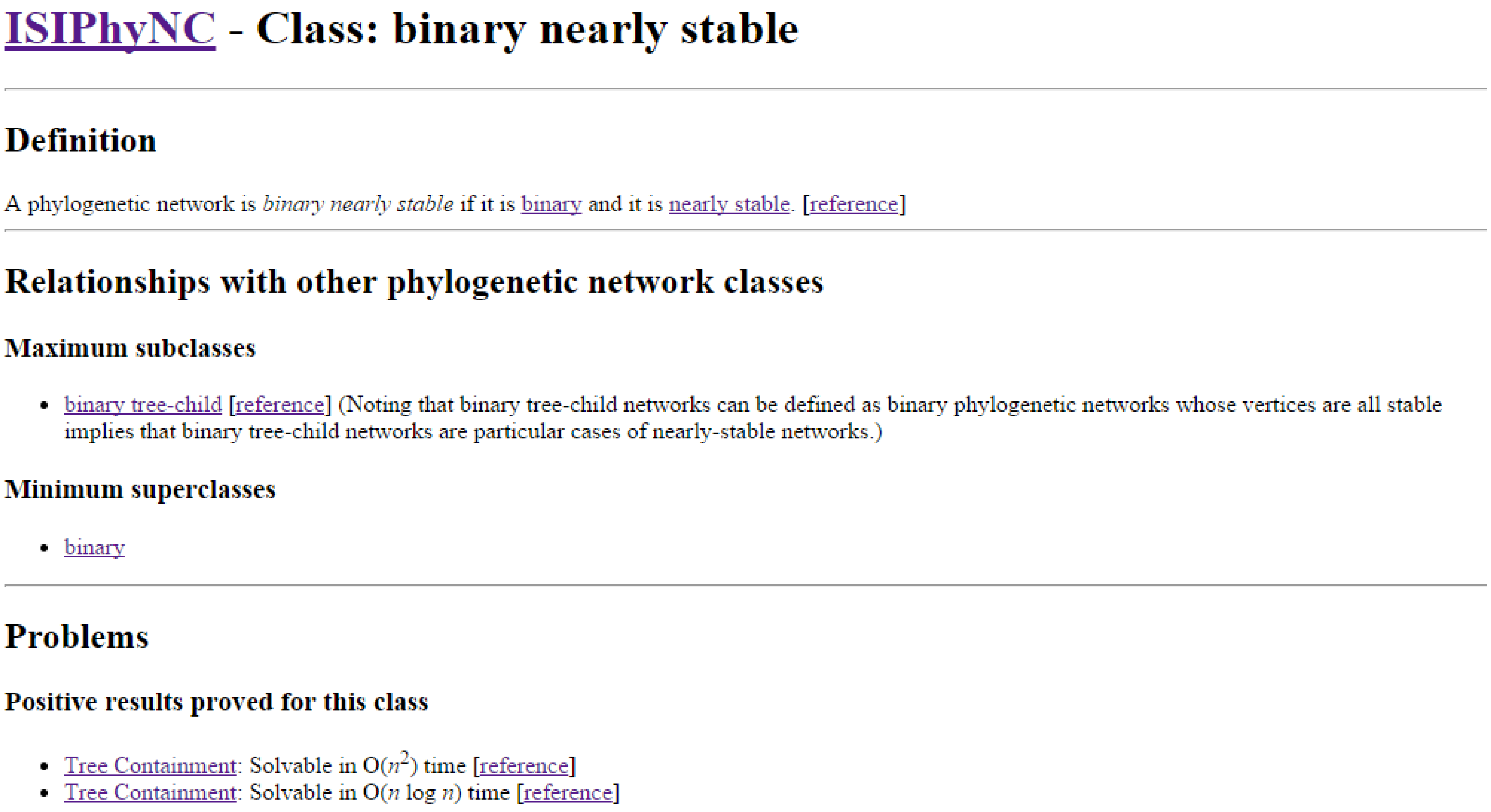
binary leaf outerplanar

binary normal

binary unicyclic

binary phylogenetic tree

ISIPhyNC – The classes



ISIPhyNC - Class: binary nearly stable

Definition

A phylogenetic network is *binary nearly stable* if it is binary and it is nearly stable. [reference]

Relationships with other phylogenetic network classes

Maximum subclasses

- binary tree-child [reference] (Noting that binary tree-child networks can be defined as binary phylogenetic networks whose vertices are all stable implies that binary tree-child networks are particular cases of nearly-stable networks.)

Minimum superclasses

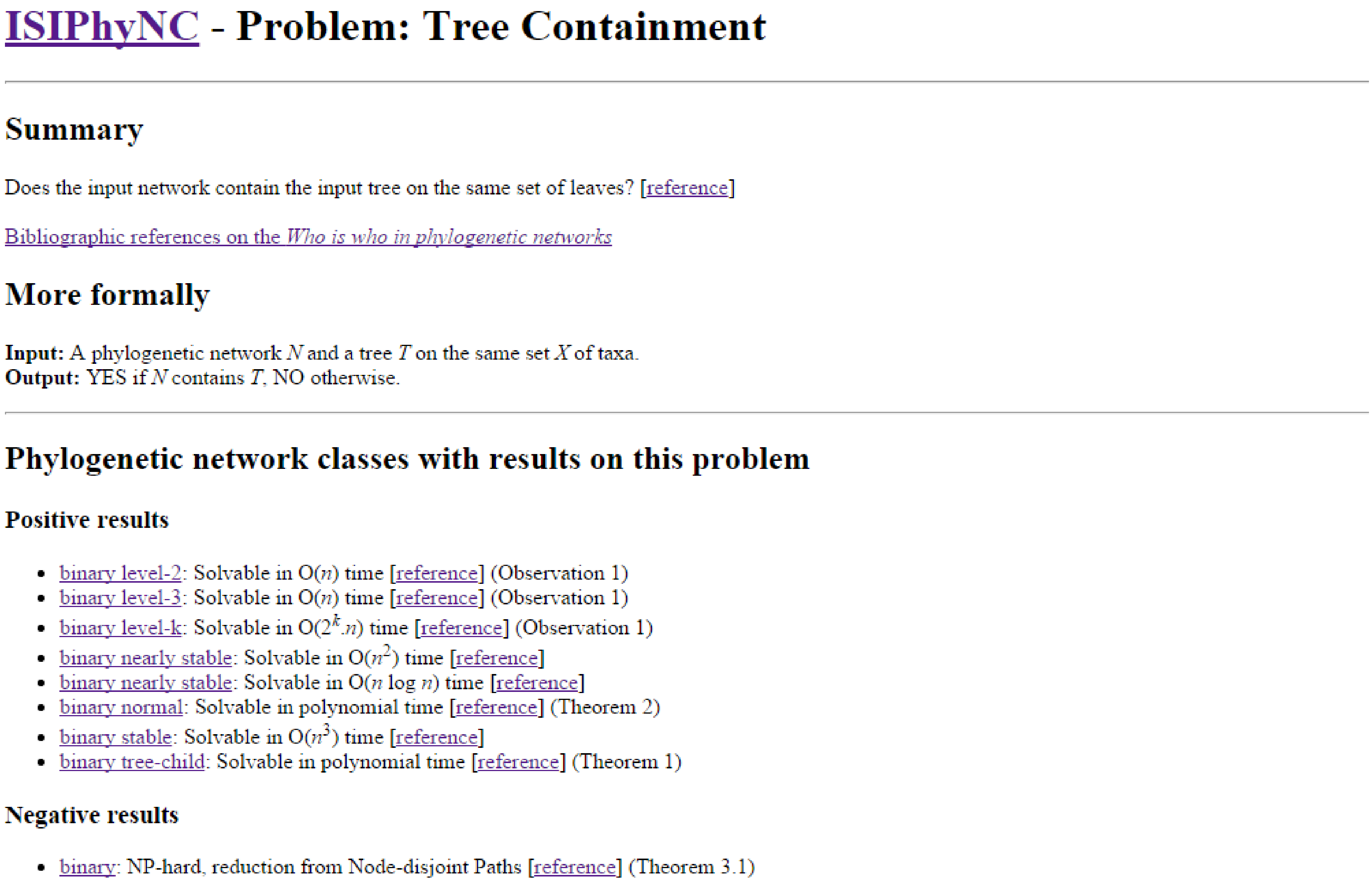
- binary

Problems

Positive results proved for this class

- Tree Containment: Solvable in O(n^2) time [reference]
- Tree Containment: Solvable in O(n log n) time [reference]

ISIPhyNC – The problems



ISIPhyNC - Problem: Tree Containment

Summary

Does the input network contain the input tree on the same set of leaves? [reference]

Bibliographic references on the *Who is who in phylogenetic networks*

More formally

Input: A phylogenetic network N and a tree T on the same set X of taxa.
Output: YES if N contains T, NO otherwise.

Phylogenetic network classes with results on this problem

Positive results

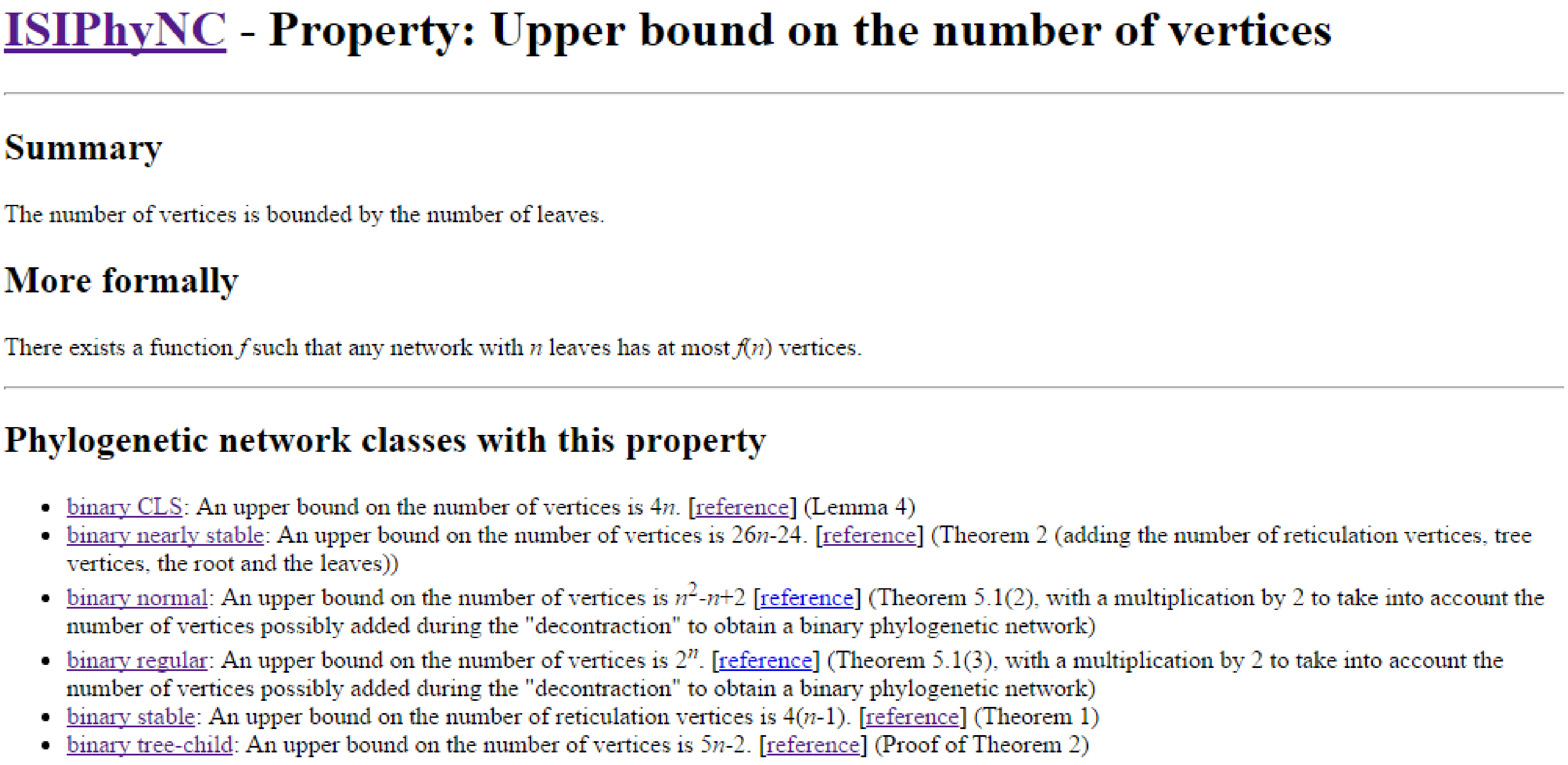
- binary level-2: Solvable in O(n) time [reference] (Observation 1)
- binary level-3: Solvable in O(n) time [reference] (Observation 1)
- binary level-k: Solvable in O($2^k.n$) time [reference] (Observation 1)
- binary nearly stable: Solvable in O(n^2) time [reference]
- binary nearly stable: Solvable in O(n log n) time [reference]
- binary normal: Solvable in polynomial time [reference] (Theorem 2)
- binary stable: Solvable in O(n^3) time [reference]
- binary tree-child: Solvable in polynomial time [reference] (Theorem 1)

Negative results

- binary: NP-hard, reduction from Node-disjoint Paths [reference] (Theorem 3.1)

Other problems: Cluster Containment, recognition, etc.

ISIPhyNC – The properties



ISIPhyNC - Property: Upper bound on the number of vertices

Summary

The number of vertices is bounded by the number of leaves.

More formally

There exists a function *f* such that any network with n leaves has at most $f(n)$ vertices.

Phylogenetic network classes with this property

- binary CLS: An upper bound on the number of vertices is $4n$. [reference] (Lemma 4)
- binary nearly stable: An upper bound on the number of vertices is $26n$-24. [reference] (Theorem 2 (adding the number of reticulation vertices, tree vertices, the root and the leaves))
- binary normal: An upper bound on the number of vertices is n^2-n+2 [reference] (Theorem 5.1(2), with a multiplication by 2 to take into account the number of vertices possibly added during the "decontraction" to obtain a binary phylogenetic network)
- binary regular: An upper bound on the number of vertices is 2^n. [reference] (Theorem 5.1(3), with a multiplication by 2 to take into account the number of vertices possibly added during the "decontraction" to obtain a binary phylogenetic network)
- binary stable: An upper bound on the number of reticulation vertices is 4(n-1). [reference] (Theorem 1)
- binary tree-child: An upper bound on the number of vertices is $5n$-2. [reference] (Proof of Theorem 2)

Other properties: unbounded number of vertices,
formula … is / is not a distance metric on this class.

Annoying issues

Binarity:

→ makes the network of subclasses more complex as every class is doubled (or more...)

→ some results need to be extended/adapted to the non-binary case

Annoying issues

Binarity:

→ makes the network of subclasses more complex as every class is doubled (or more...)

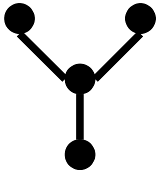
→ some results need to be extended/adapted to the non-binary case

Example:

«level» = maximum over all blobs of the minimum number of arcs to remove to obtain a tree from the blob

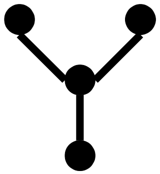
Annoying issues

Cluster-distinct property:

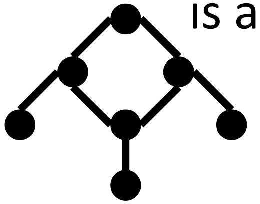
→ forbidden pattern: 

Annoying issues

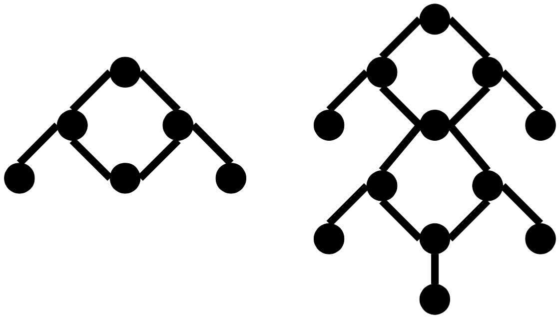
Cluster-distinct property:

→ forbidden pattern: 

Possibility 1: direct integration

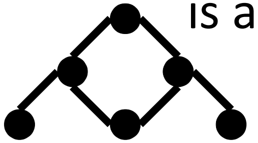


is a binary regular network,
i.e. a «decontracted» regular network which is binary

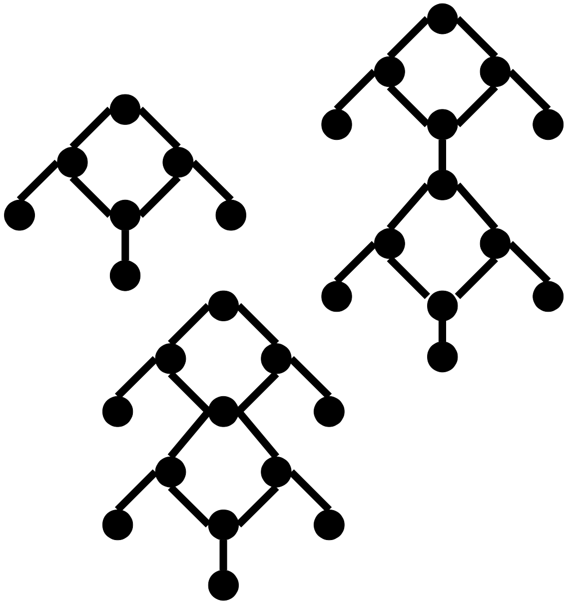


ARE not

Possibility 2: stick with definition

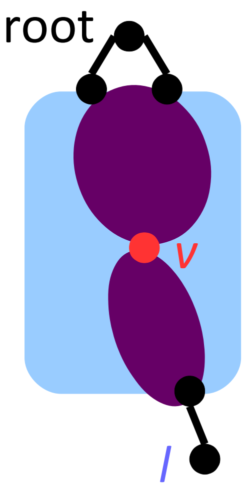


is a binary regular network



are not

Annoying issues



Agreeing on names:

«Stable 1»

→ visible vertex *v* (Huson, Rupp & Scornavacca 2011):
there exists a leaf *l* such that every path from the root to *l* contains *v*
(*v* is a stable ancestor of *l*)

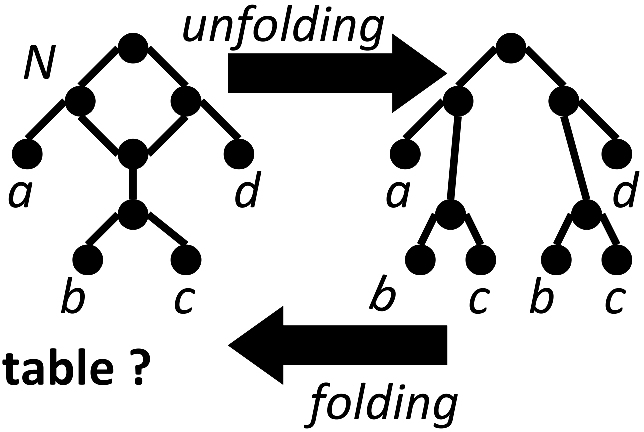
→ network «with the visibility property»: every reticulation vertex is visible

?

→ called «stable» in Gunawan, DasGupta & Zhang 2015

«Stable 2»

→ the «folding» of the multilabeled tree obtained by «unfolding» *N* is equal to *N* (Huber, Moulton, Steel & Wu 2015)



reticulation-stable and **MUL-stable ?**

Thank you for your attention!

Looking forward to getting your feedback about:

→ « Who is Who in Phylogenetic Networks »

http://phylnet.univ-mlv.fr

→ « ISIPhyNC »

http://phylnet.univ-mlv.fr/isiphync/