LRI-LIX BioInfo Seminar
19/01/2017 - Palaiseau

Finding a gene tree in a phylogenetic network

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Outline

- Phylogenetic networks
- Classes of phylogenetic networks
- The Tree Containment Problem

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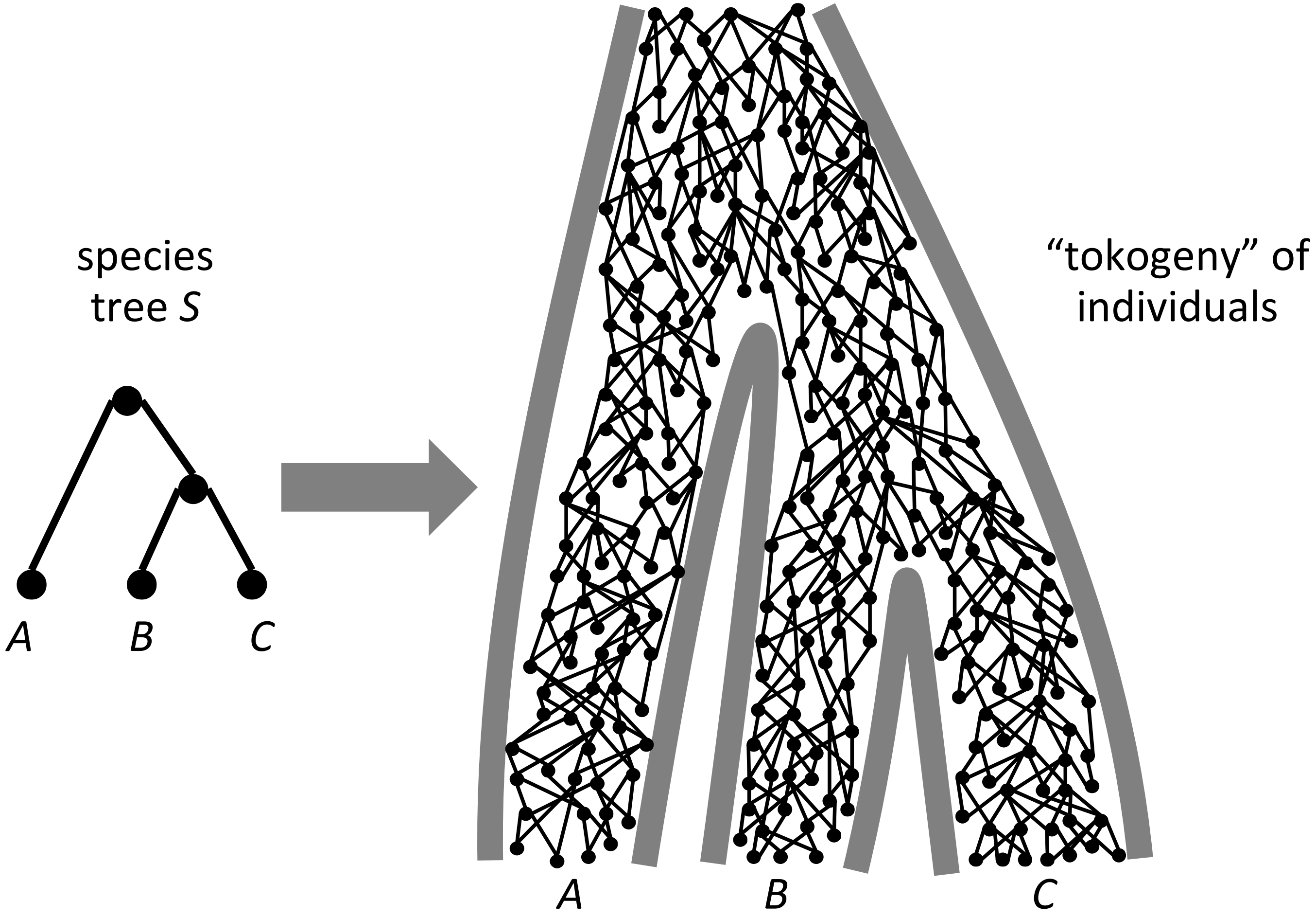
- Classes of phylogenetic networks
- The Tree Containment Problem

Phylogenetic trees

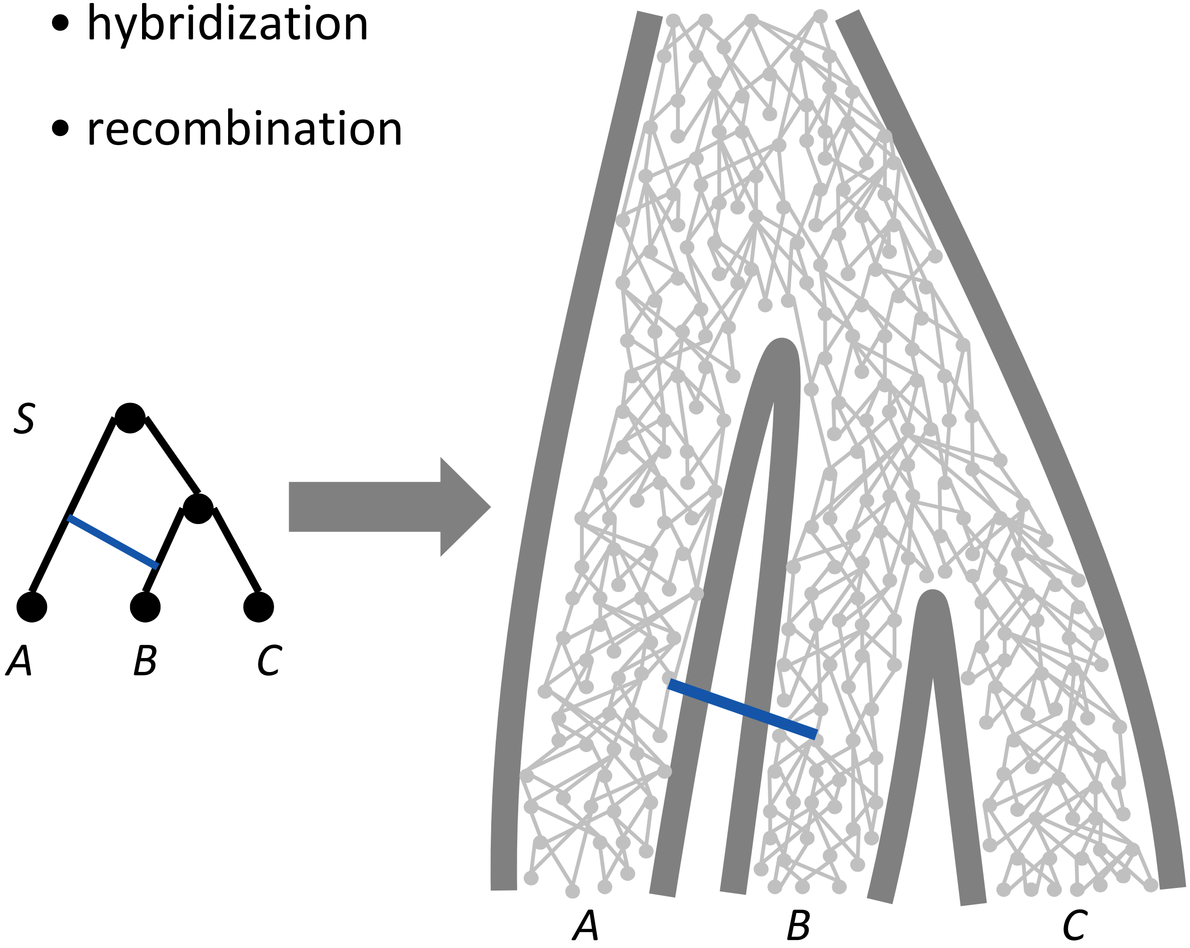
Phylogenetic tree of a set of species



Genetic material transfers

Transfers of genetic material between coexisting species:

- lateral gene transfer
- hybridization
- recombination



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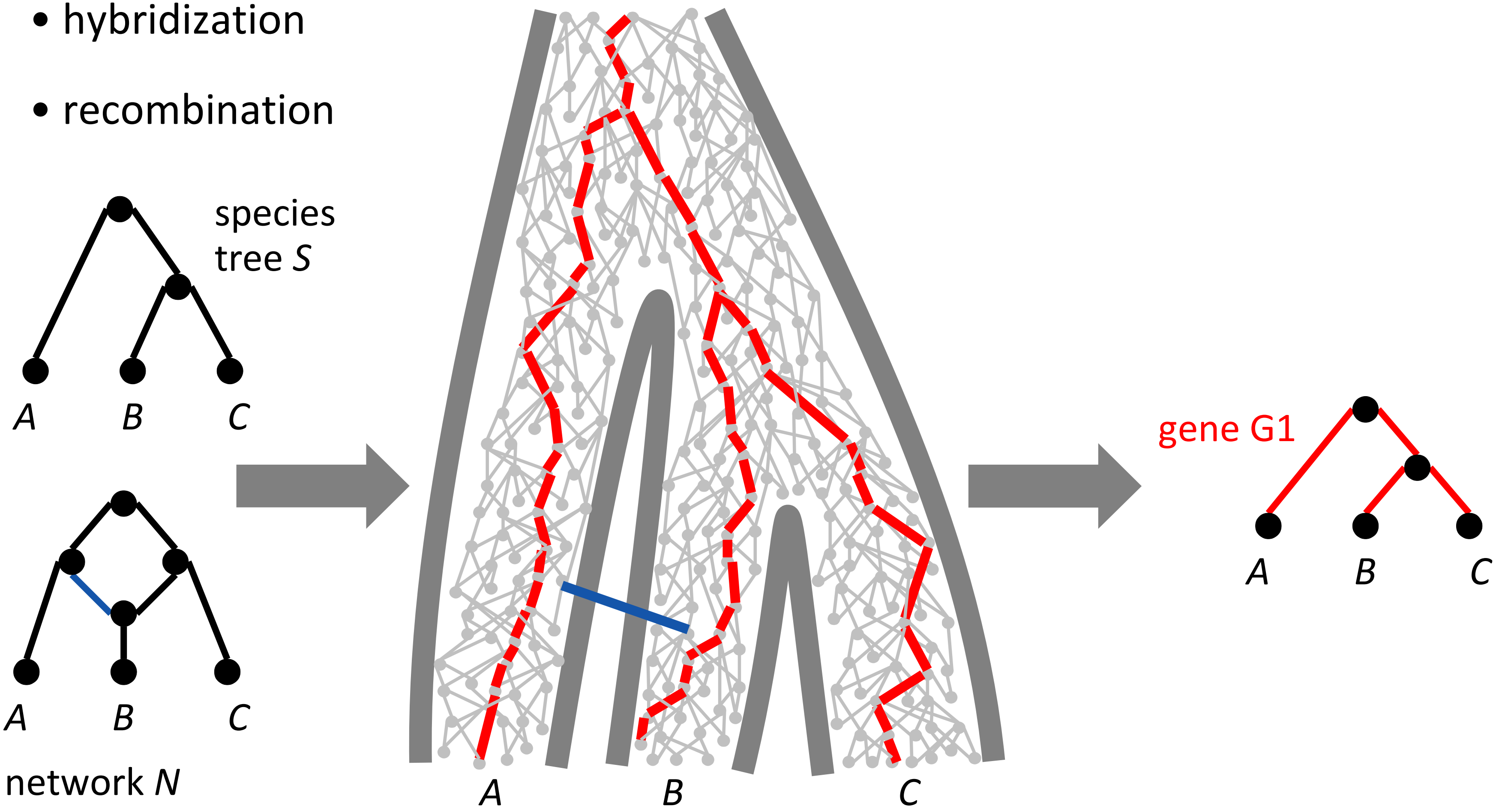

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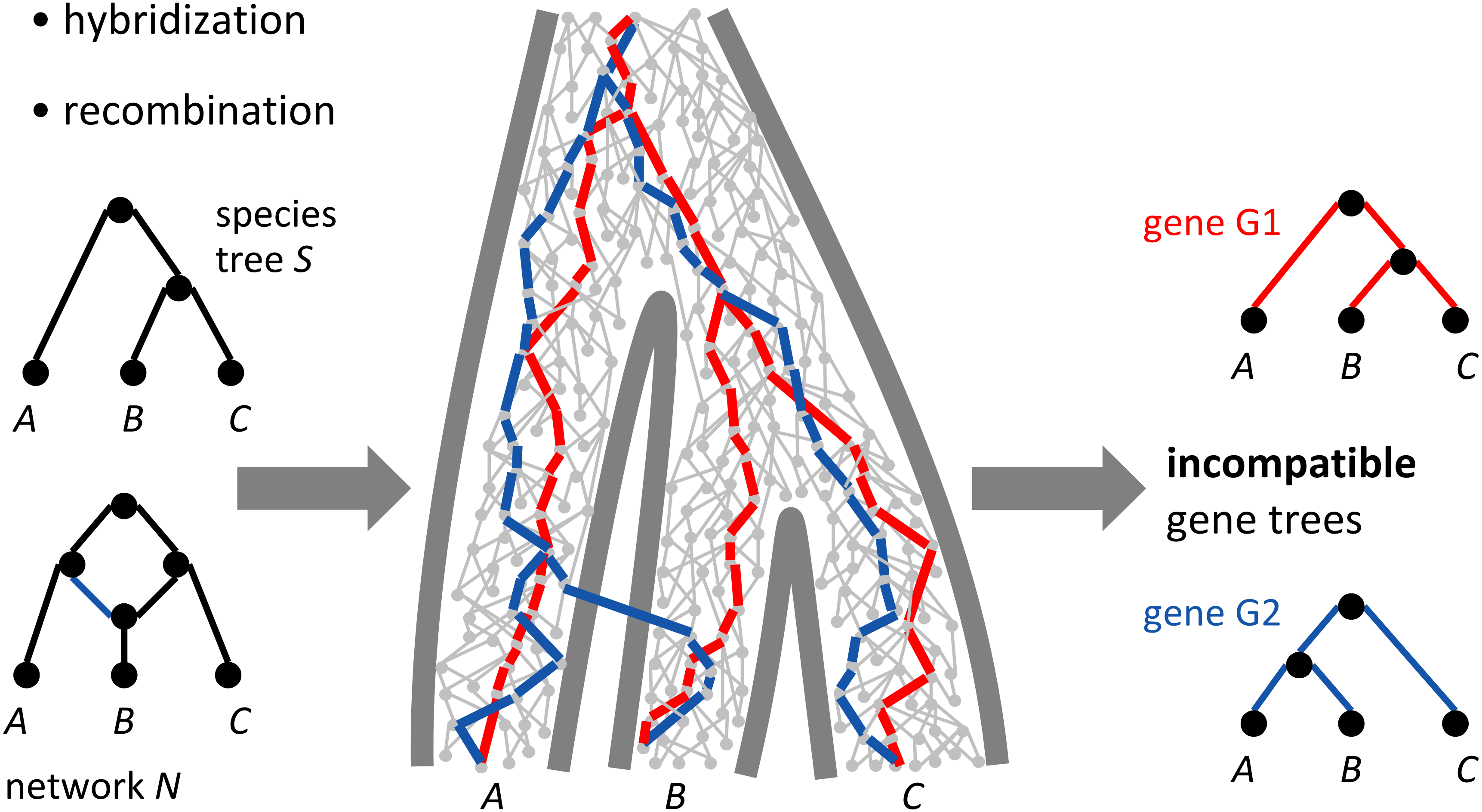


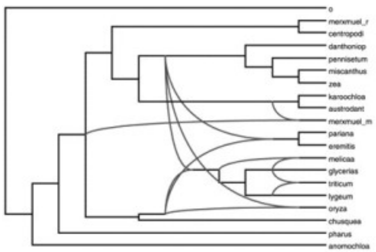
incompatible gene trees

Phylogenetic networks

Phylogenetic network: network representing evolution data

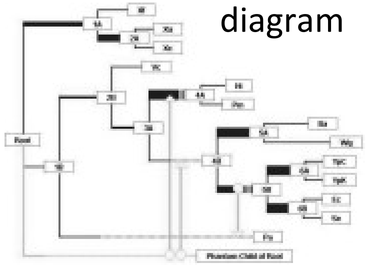
- **explicit** phylogenetic networks

model evolution



galled
network

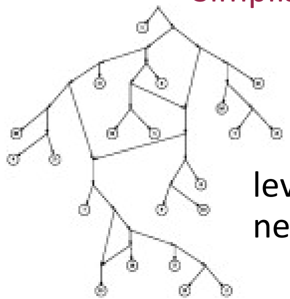
Dendroscope



synthesis
diagram

HorizStory

Simplistic

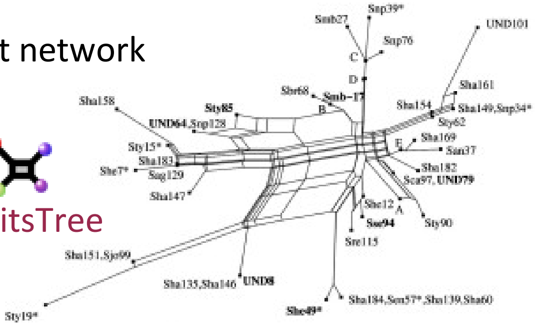


level-2
network

- **abstract** phylogenetic networks

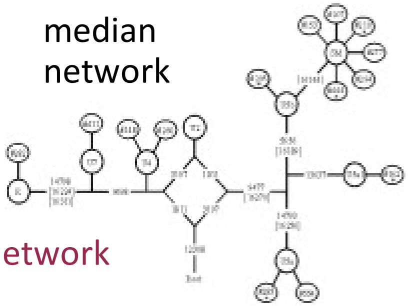
classify, **visualize** data

split network



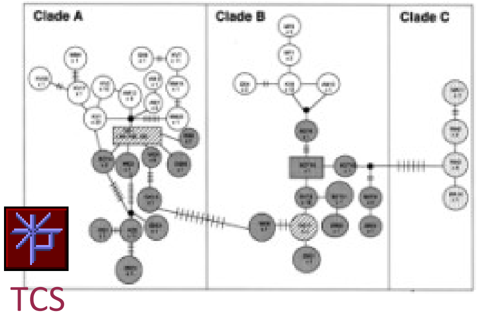
SplitsTree

median
network



Network

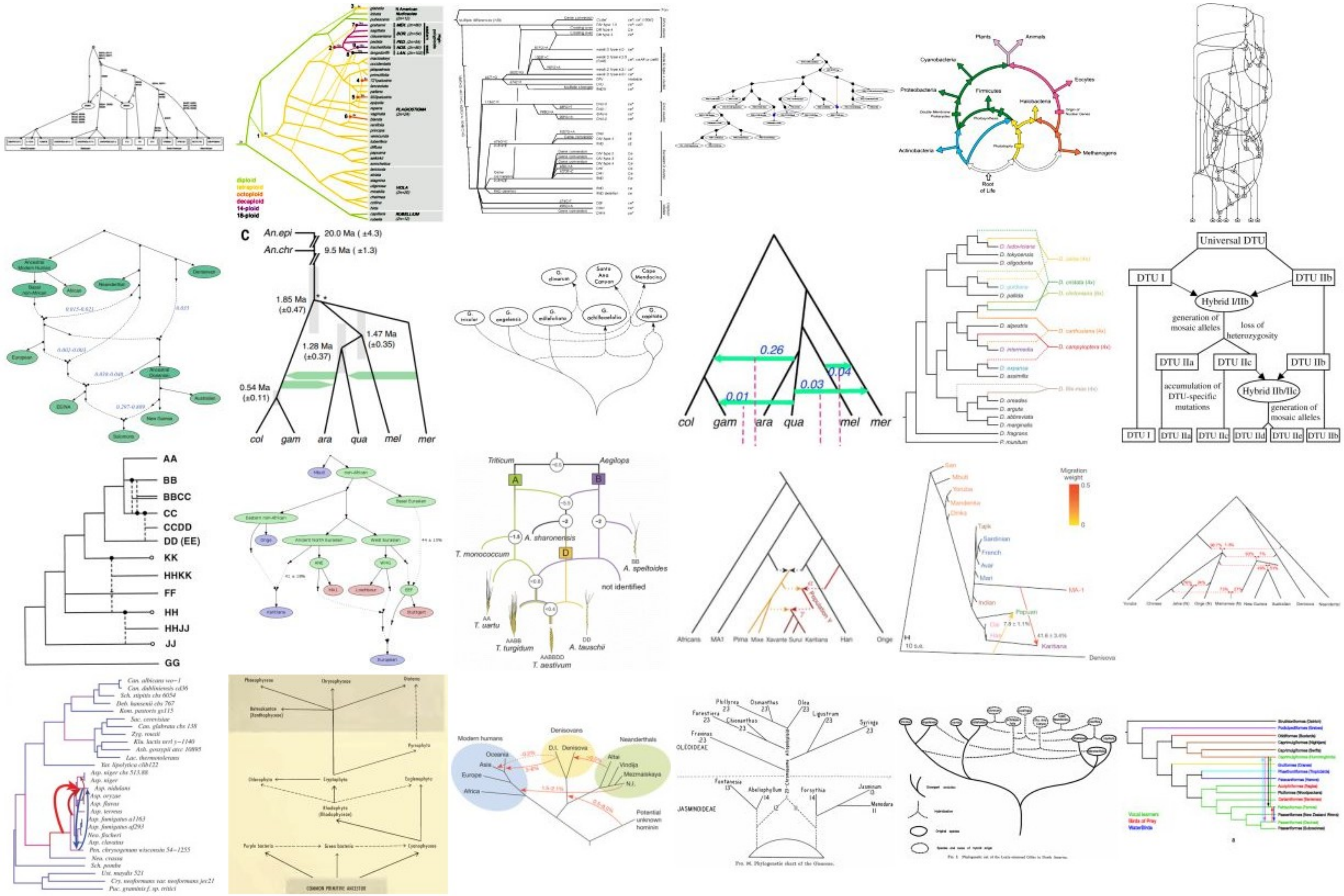
minimum spanning network



TCS

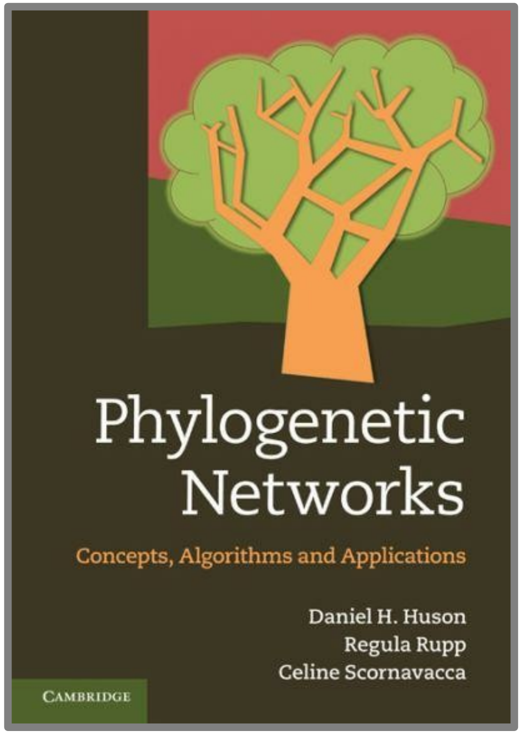
Today: focus on explicit phylogenetic networks

A gallery of explicit phylogenetic networks :

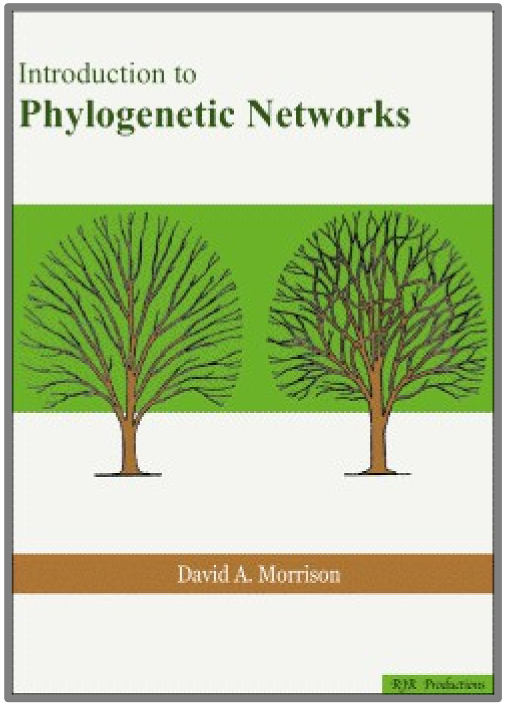


http://phylnet.univ-mlv.fr/recophync/networkDraw.php

Books about phylogenetic networks

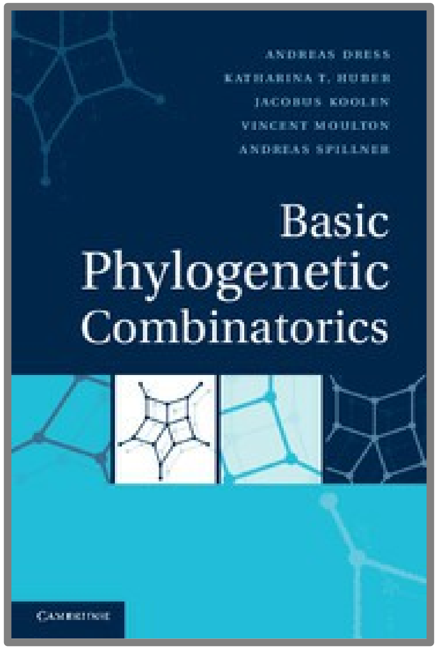


Huson, Rupp,
Scornavacca, 2011

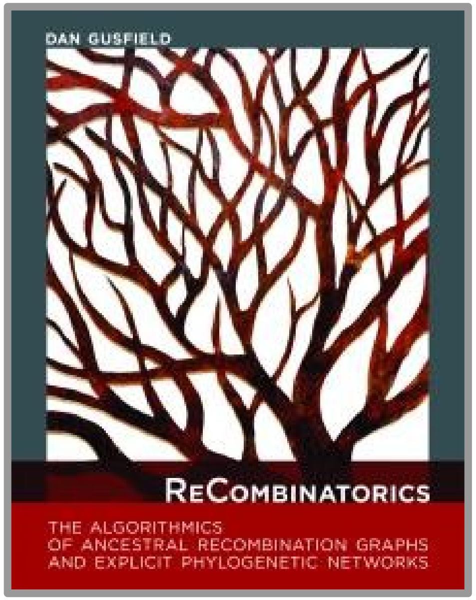


Morrison, 2011

Dress, Huber,
Koolen, Moulton,
Spillner, 2012



Gusfield, 2014



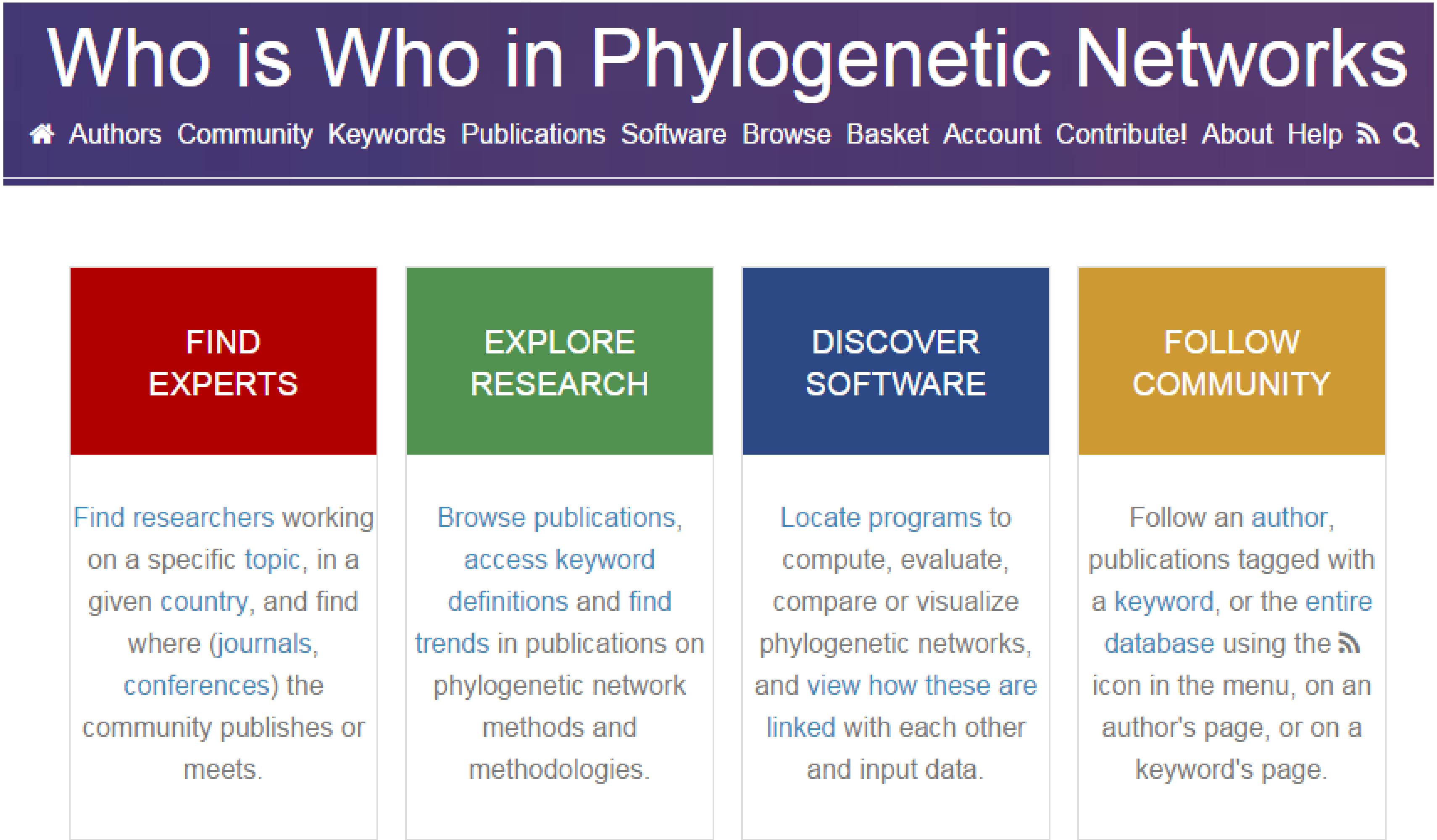
Workshops about phylogenetic networks

The Future of Phylogenetic Networks, 15-19 October **2012**,
Lorentz Center,
Leiden, The Netherlands

Utilizing Genealogical Phylogenetic Networks in Evolutionary Biology: Touching the Data,
7-11 July **2014**, Lorentz Center,
Leiden, The Netherlands

The Phylogenetic Network Workshop, 27 - 31 Jul **2015**,
Institute for Mathematical Science
(National University of Singapore)

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.

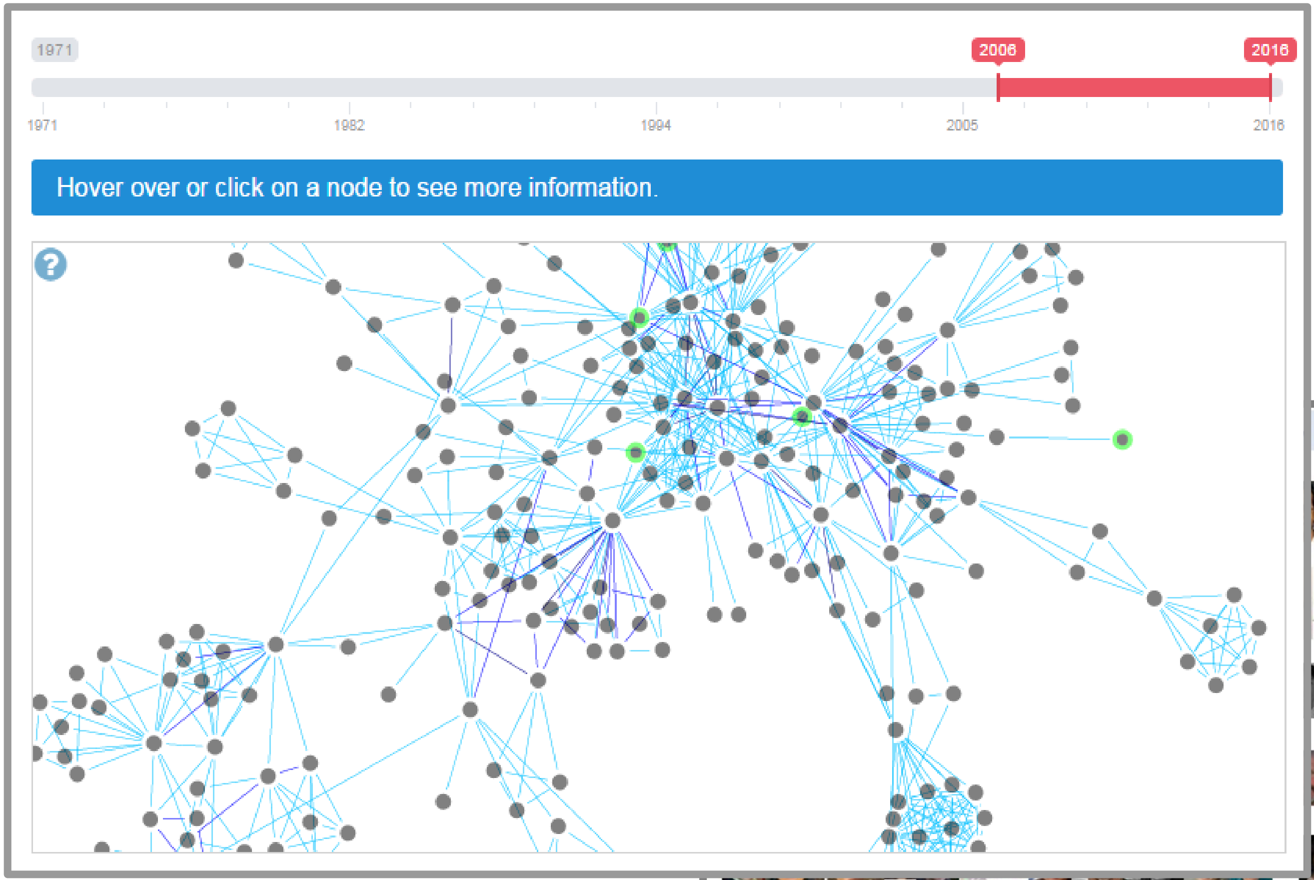
FOLLOW COMMUNITY

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.

Based on BibAdmin by Sergiu Chelcea
+ tag clouds, date histograms, journal lists,
keyword definitions, co-author graphs

http://phylnet.univ-mlv.fr

Who is who in Phylogenetic Networks?



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

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

Analysis of the co-author and keyword graphs: internship of **Tushar Agarwal**

Agarwal, Gambette & Morrison, arXiv, 2017

http://phylnet.univ-mlv.fr

Who is who in Phylogenetic Networks?

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)

Who is who in Phylogenetic Networks?

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input

software

Who is who in Phylogenetic Networks?

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input

software

classes

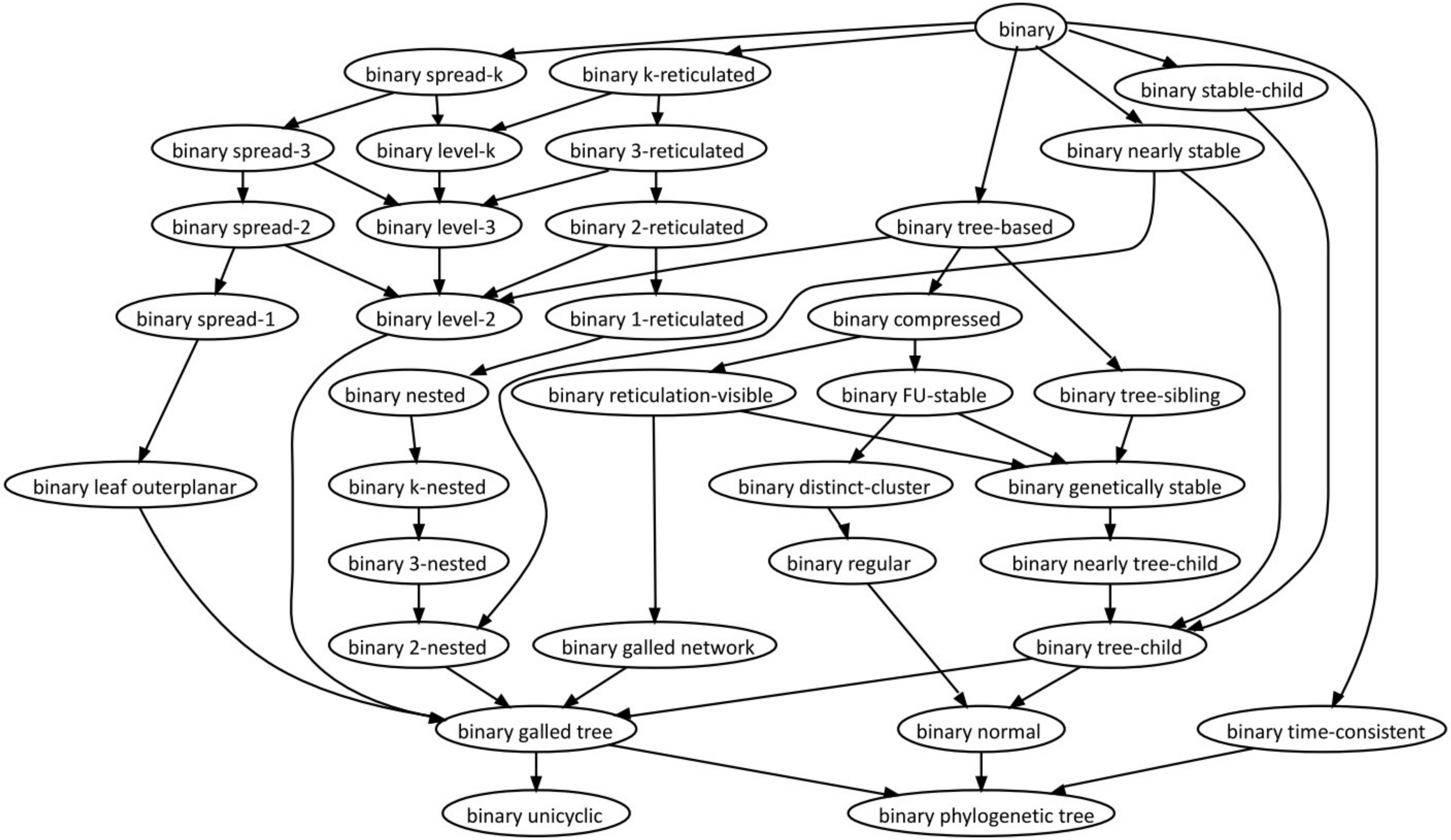
problems

algorithmic properties

Outline

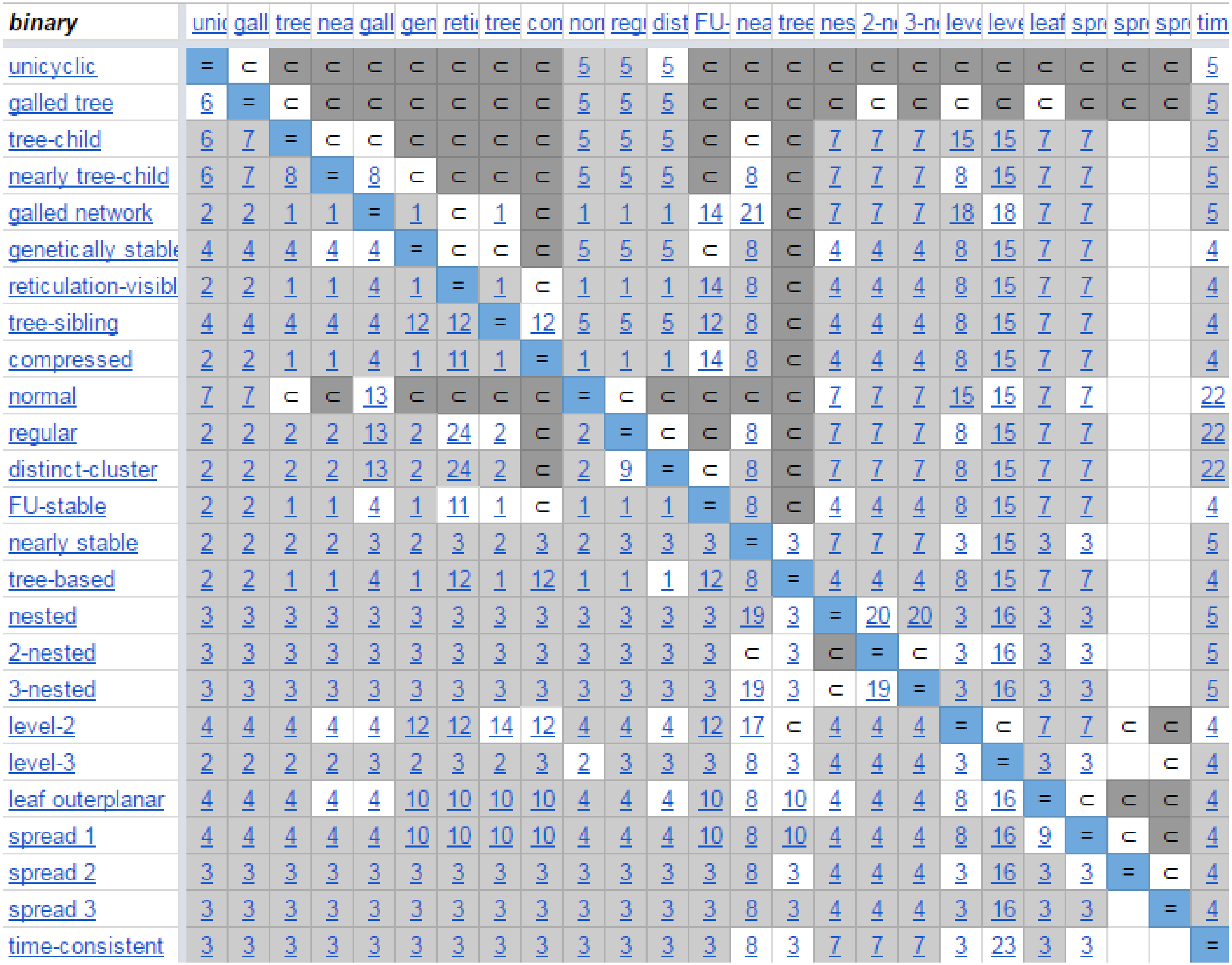
- Phylogenetic networks
- Classes of phylogenetic networks
- The Tree Containment Problem

Classes of phylogenetic networks


binary
binary spread-k
binary k-reticulated
binary stable-child
binary spread-3
binary level-k
binary 3-reticulated
binary nearly stable
binary spread-2
binary level-3
binary 2-reticulated
binary tree-based
binary spread-1
binary level-2
binary 1-reticulated
binary compressed
binary nested
binary reticulation-visible
binary FU-stable
binary tree-sibling
binary leaf outerplanar
binary k-nested
binary distinct-cluster
binary genetically stable
binary 3-nested
binary regular
binary nearly tree-child
binary 2-nested
binary galled network
binary tree-child
binary galled tree
binary normal
binary time-consistent
binary unicyclic
binary phylogenetic tree

joint work with Maxime Morgado and Narges Tavassoli
http://phylnet.univ-mlv.fr/isiphync/

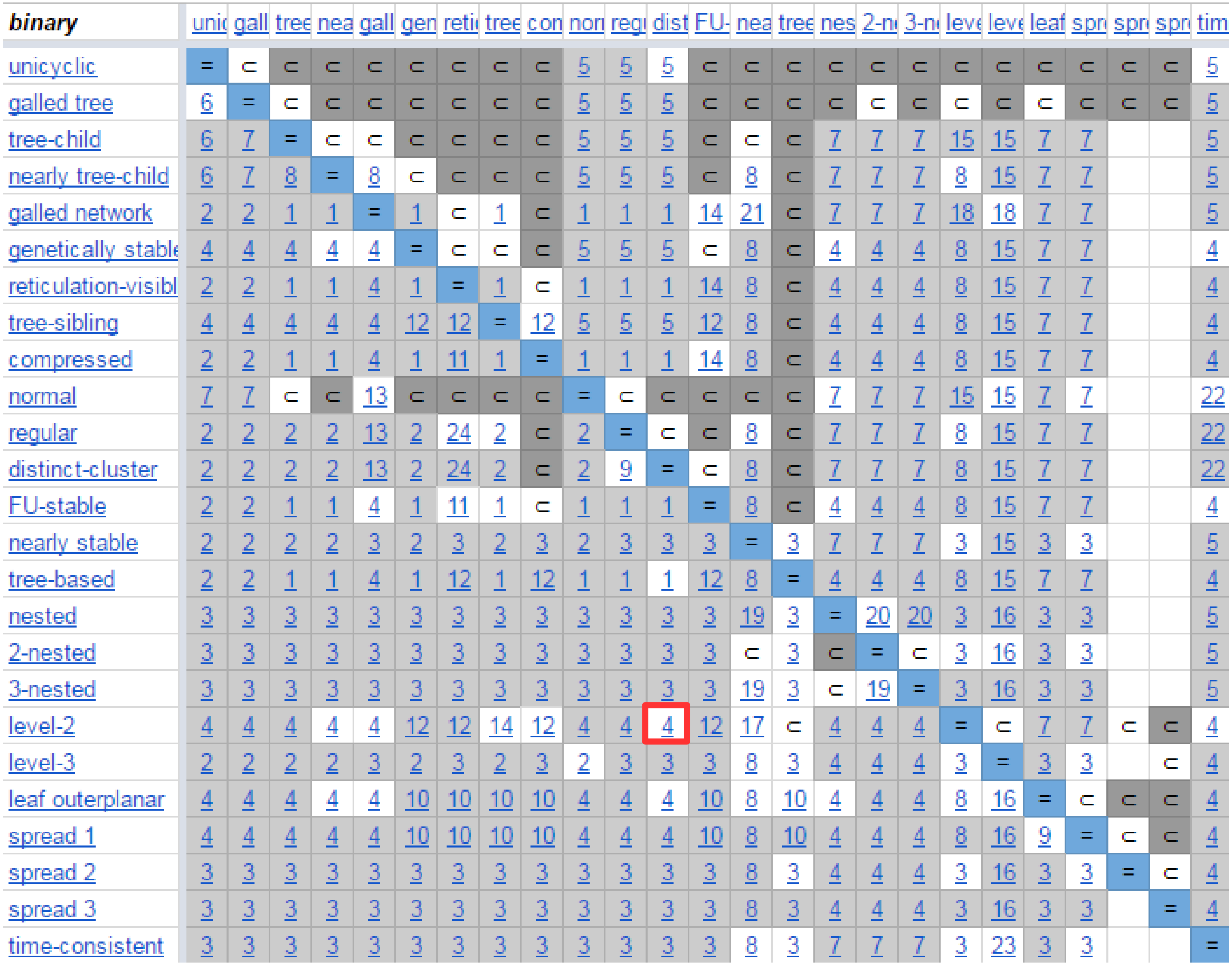
Classes of phylogenetic networks: inclusions



binary	unic	gall	tree	nea	gall	gen	reti	tree	con	nor	reg	dist	FU-	nea	tree	nes	2-n	3-n	leve	leve	leaf	spr	spr	spr	tim
unicyclic	=	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5	5	5	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5
galled tree	6	=	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5	5	5	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5
tree-child	6	7	=	⊂	⊂	⊂	⊂	⊂	⊂	5	5	5	⊂	⊂	⊂	7	7	7	15	15	7	7			5
nearly tree-child	6	7	8	=	8	⊂	⊂	⊂	⊂	5	5	5	⊂	8	⊂	7	7	7	8	15	7	7			5
galled network	2	2	1	1	=	1	⊂	1	⊂	1	1	1	14	21	⊂	7	7	7	18	18	7	7			5
genetically stable	4	4	4	4	4	=	⊂	⊂	⊂	5	5	5	⊂	8	⊂	4	4	4	8	15	7	7			4
reticulation-visibl	2	2	1	1	4	1	=	1	⊂	1	1	1	14	8	⊂	4	4	4	8	15	7	7			4
tree-sibling	4	4	4	4	4	12	12	=	12	5	5	5	12	8	⊂	4	4	4	8	15	7	7			4
compressed	2	2	1	1	4	1	11	1	=	1	1	1	14	8	⊂	4	4	4	8	15	7	7			4
normal	7	7	⊂	⊂	13	⊂	⊂	⊂	⊂	=	⊂	⊂	⊂	⊂	⊂	7	7	7	15	15	7	7			22
regular	2	2	2	2	13	2	24	2	⊂	2	=	⊂	⊂	8	⊂	7	7	7	8	15	7	7			22
distinct-cluster	2	2	2	2	13	2	24	2	⊂	2	9	=	⊂	8	⊂	7	7	7	8	15	7	7			22
FU-stable	2	2	1	1	4	1	11	1	⊂	1	1	1	=	8	⊂	4	4	4	8	15	7	7			4
nearly stable	2	2	2	2	3	2	3	2	3	2	3	3	3	=	3	7	7	7	3	15	3	3			5
tree-based	2	2	1	1	4	1	12	1	12	1	1	1	12	8	=	4	4	4	8	15	7	7			4
nested	3	3	3	3	3	3	3	3	3	3	3	3	3	19	3	=	20	20	3	16	3	3			5
2-nested	3	3	3	3	3	3	3	3	3	3	3	3	3	⊂	3	⊂	=	⊂	3	16	3	3			5
3-nested	3	3	3	3	3	3	3	3	3	3	3	3	3	19	3	⊂	19	=	3	16	3	3			5
level-2	4	4	4	4	4	12	12	14	12	4	4	4	12	17	⊂	4	4	4	=	⊂	7	7	⊂	⊂	4
level-3	2	2	2	2	3	2	3	2	3	2	3	3	3	8	3	4	4	4	3	=	3	3		⊂	4
leaf outerplanar	4	4	4	4	4	10	10	10	10	4	4	4	10	8	10	4	4	4	8	16	=	⊂	⊂	⊂	4
spread 1	4	4	4	4	4	10	10	10	10	4	4	4	10	8	10	4	4	4	8	16	9	=	⊂	⊂	4
spread 2	3	3	3	3	3	3	3	3	3	3	3	3	3	8	3	4	4	4	3	16	3	3	=	⊂	4
spread 3	3	3	3	3	3	3	3	3	3	3	3	3	3	8	3	4	4	4	3	16	3	3		=	4
time-consistent	3	3	3	3	3	3	3	3	3	3	3	3	3	8	3	7	7	7	3	23	3	3			=

joint work with Maxime Morgado and Narges Tavassoli

Classes of phylogenetic networks: inclusions



binary	unic	gall	tree	nea	gall	gen	reti	tree	con	non	regi	dist	FU-	nea	tree	nes	2-n	3-n	leve	leve	leaf	spr	spr	spr	tim
unicyclic	=	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5	5	5	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5
galled tree	6	=	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5	5	5	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	⊂	5
tree-child	6	7	=	⊂	⊂	⊂	⊂	⊂	⊂	5	5	5	⊂	⊂	⊂	7	7	7	15	15	7	7			5
nearly tree-child	6	7	8	=	8	⊂	⊂	⊂	⊂	5	5	5	⊂	8	⊂	7	7	7	8	15	7	7			5
galled network	2	2	1	1	=	1	⊂	1	⊂	1	1	1	14	21	⊂	7	7	7	18	18	7	7			5
genetically stabl	4	4	4	4	4	=	⊂	⊂	⊂	5	5	5	⊂	8	⊂	4	4	4	8	15	7	7			4
reticulation-visibl	2	2	1	1	4	1	=	1	⊂	1	1	1	14	8	⊂	4	4	4	8	15	7	7			4
tree-sibling	4	4	4	4	4	12	12	=	12	5	5	5	12	8	⊂	4	4	4	8	15	7	7			4
compressed	2	2	1	1	4	1	11	1	=	1	1	1	14	8	⊂	4	4	4	8	15	7	7			4
normal	7	7	⊂	⊂	13	⊂	⊂	⊂	⊂	=	⊂	⊂	⊂	⊂	⊂	7	7	7	15	15	7	7			22
regular	2	2	2	2	13	2	24	2	⊂	2	=	⊂	⊂	8	⊂	7	7	7	8	15	7	7			22
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nested	3	3	3	3	3	3	3	3	3	3	3	3	3	19	3	=	20	20	3	16	3	3			5
2-nested	3	3	3	3	3	3	3	3	3	3	3	3	3	⊂	3	⊂	=	⊂	3	16	3	3			5
3-nested	3	3	3	3	3	3	3	3	3	3	3	3	3	19	3	⊂	19	=	3	16	3	3			5
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spread 2	3	3	3	3	3	3	3	3	3	3	3	3	3	8	3	4	4	4	3	16	3	3	=	⊂	4
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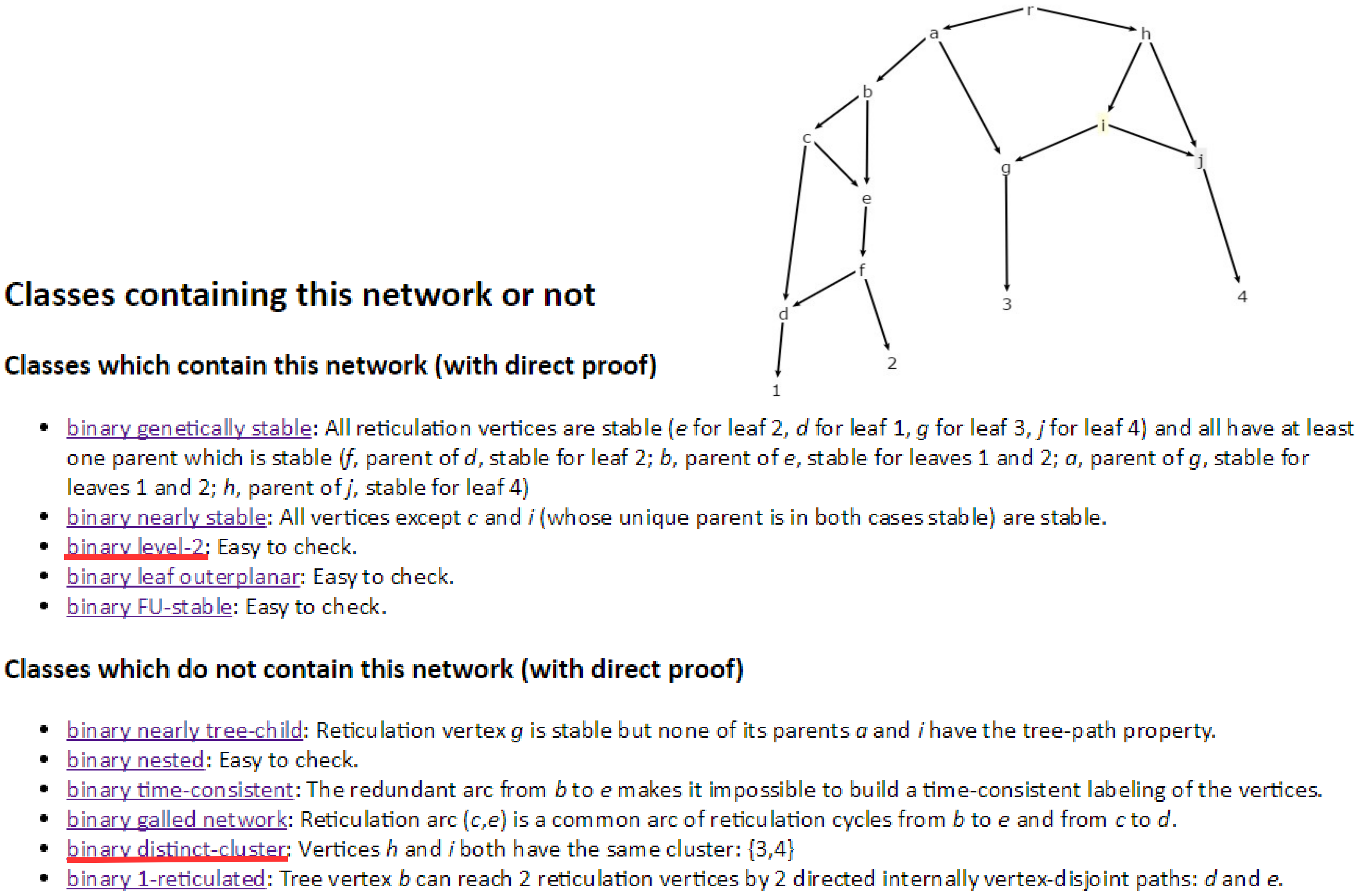
time-consistent	3	3	3	3	3	3	3	3	3	3	3	3	3	8	3	7	7	7	3	23	3	3			=

joint work with Maxime Morgado and Narges Tavassoli

Classes of phylogenetic networks: inclusions



Classes containing this network or not

Classes which contain this network (with direct proof)

- binary genetically stable: All reticulation vertices are stable (*e* for leaf 2, *d* for leaf 1, *g* for leaf 3, *j* for leaf 4) and all have at least one parent which is stable (*f*, parent of *d*, stable for leaf 2; *b*, parent of *e*, stable for leaves 1 and 2; *a*, parent of *g*, stable for leaves 1 and 2; *h*, parent of *j*, stable for leaf 4)
- binary nearly stable: All vertices except *c* and *i* (whose unique parent is in both cases stable) are stable.
- binary level-2: Easy to check.
- binary leaf outerplanar: Easy to check.
- binary FU-stable: Easy to check.

Classes which do not contain this network (with direct proof)

- binary nearly tree-child: Reticulation vertex *g* is stable but none of its parents *a* and *i* have the tree-path property.
- binary nested: Easy to check.
- binary time-consistent: The redundant arc from *b* to *e* makes it impossible to build a time-consistent labeling of the vertices.
- binary galled network: Reticulation arc (*c*,*e*) is a common arc of reticulation cycles from *b* to *e* and from *c* to *d*.
- binary distinct-cluster: Vertices *h* and *i* both have the same cluster: {3,4}
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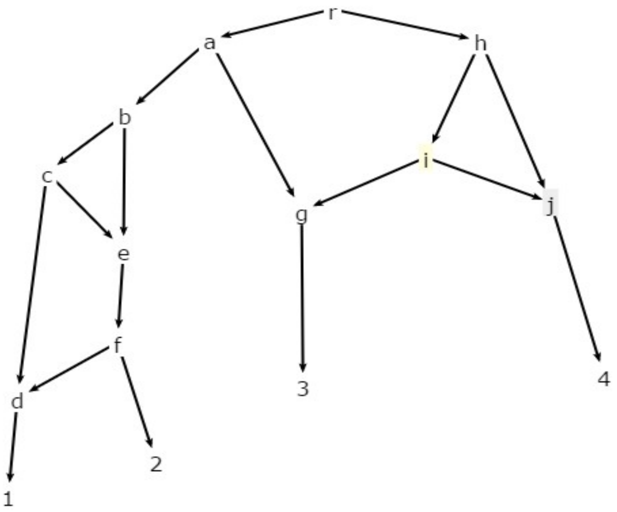
joint work with Maxime Morgado and Narges Tavassoli
http://phylnet.univ-mlv.fr/isiphync/network.php?id=4

Classes of phylogenetic networks: inclusions

level = maximum number of reticulation vertices among all bridgeless components in the network
cluster = set of leaves below a vertex



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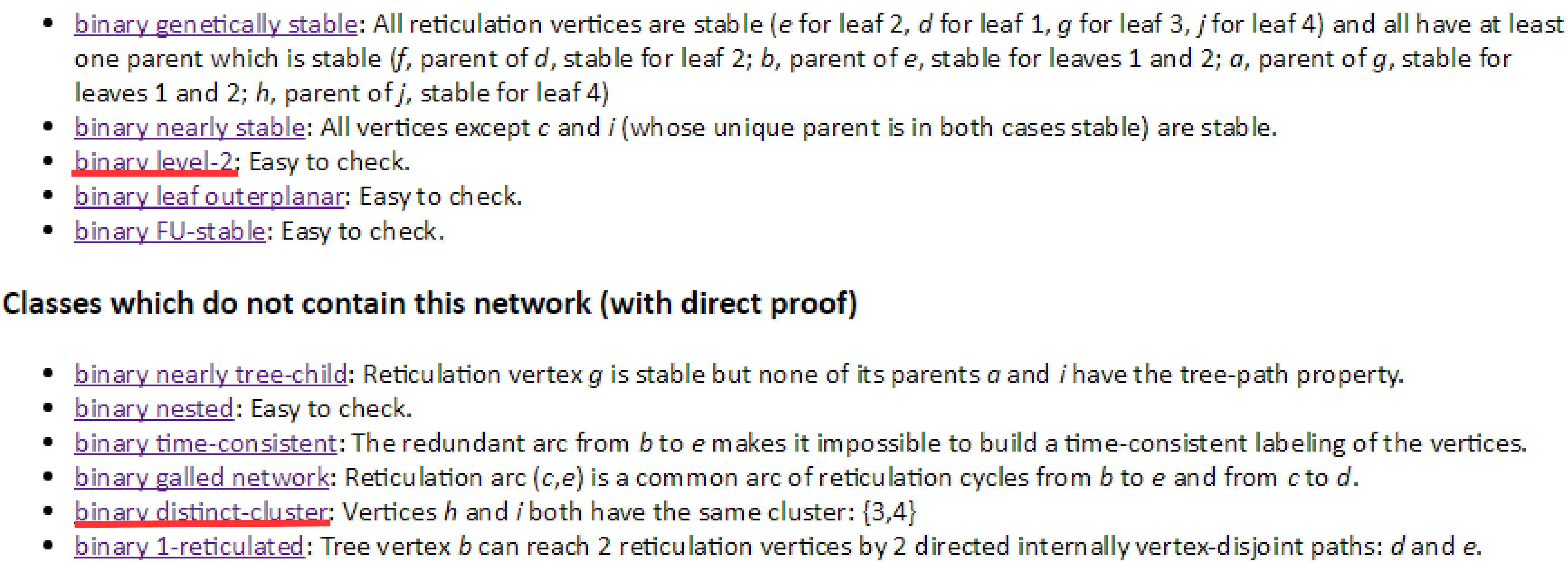

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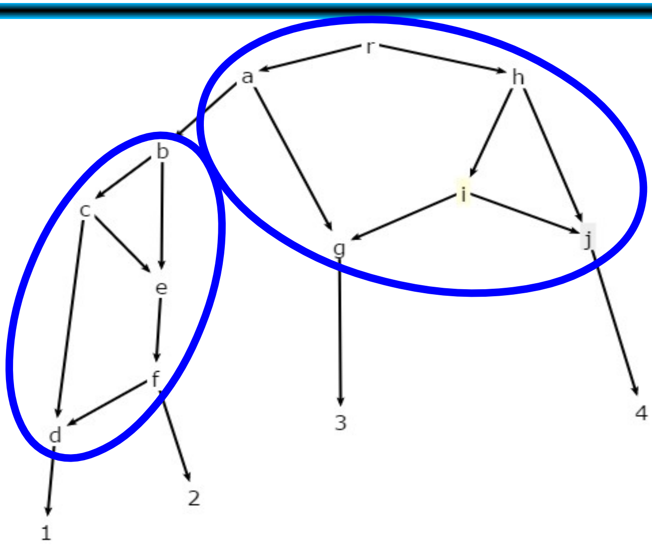

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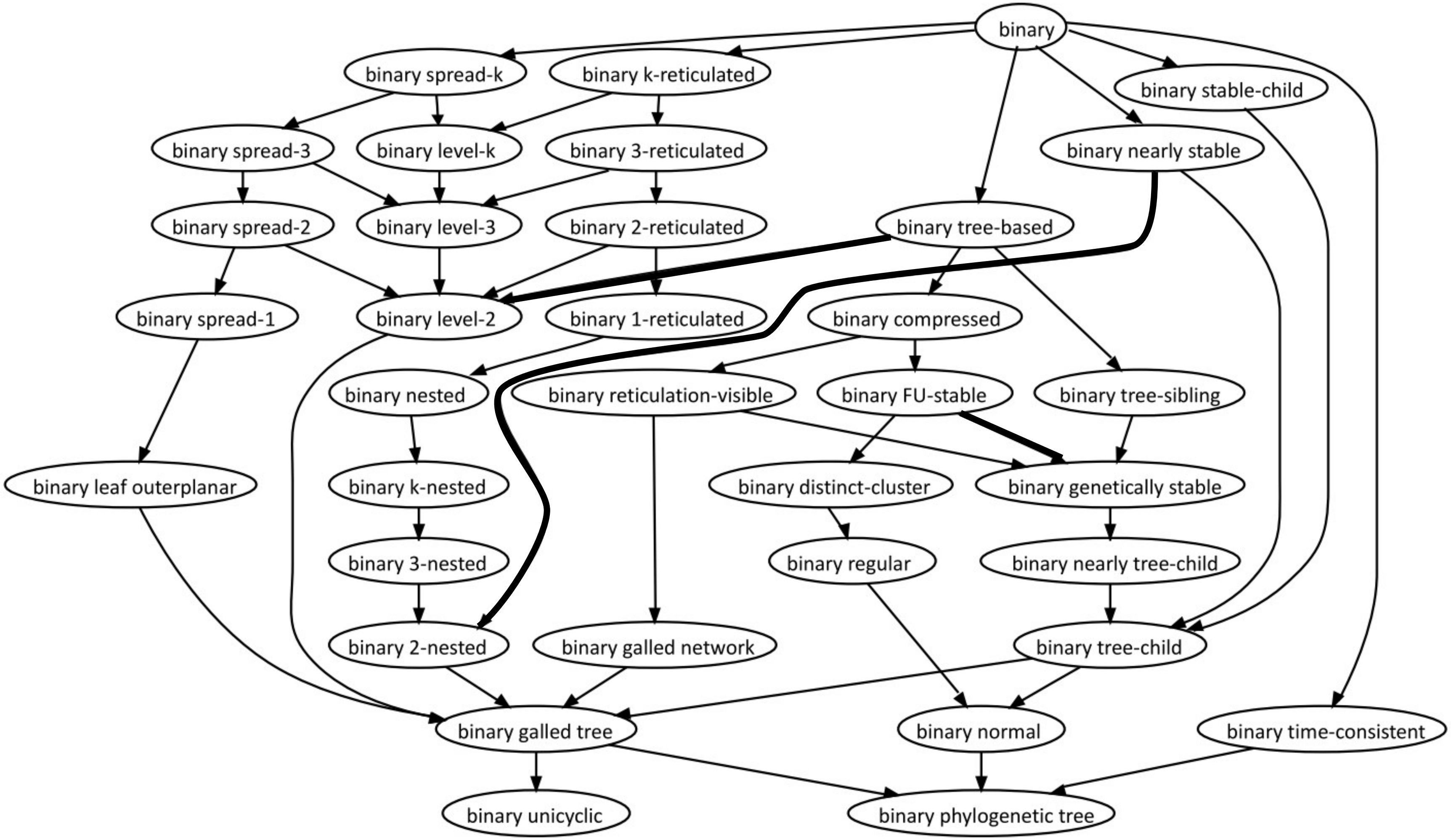
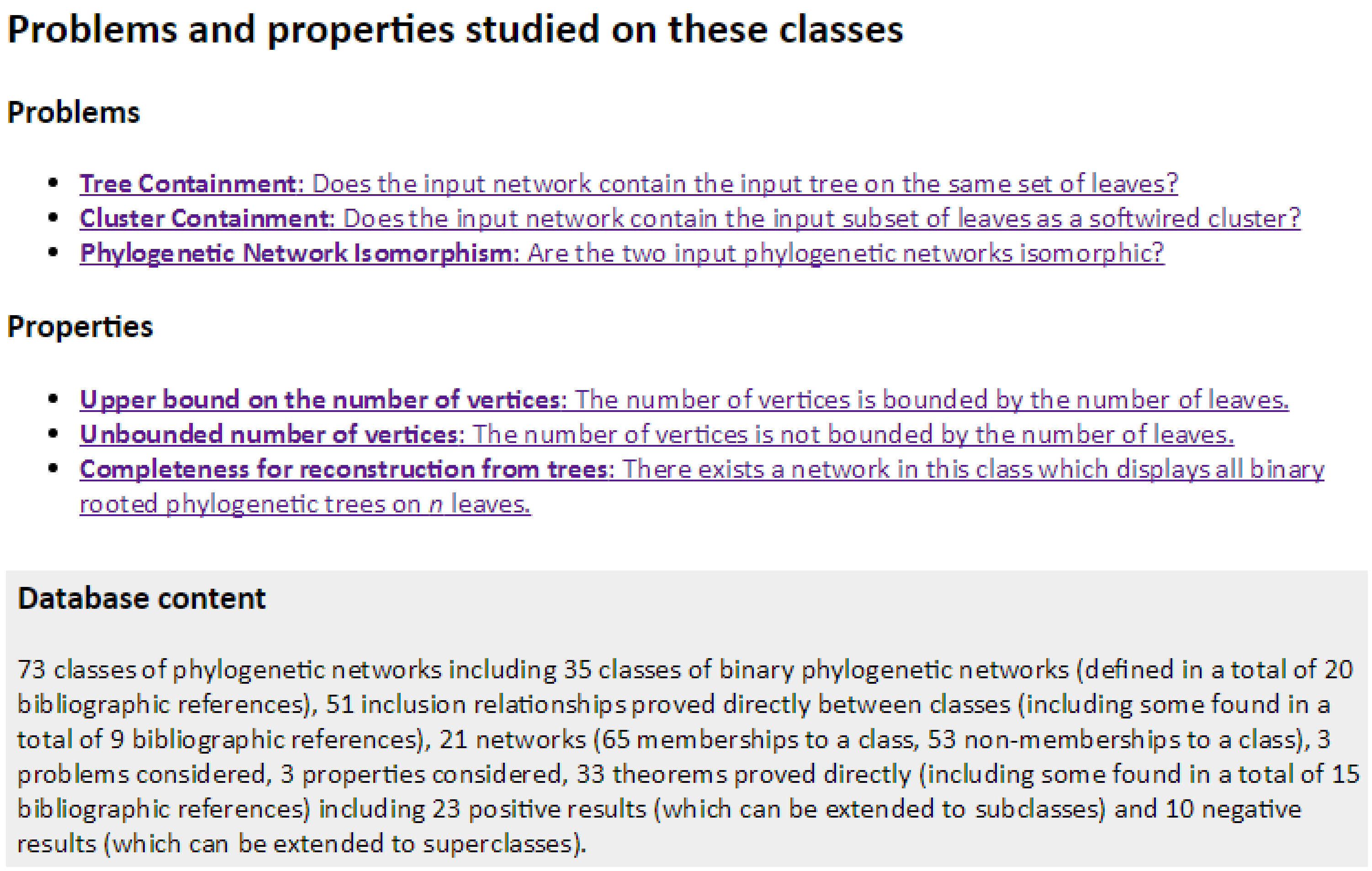
Classes of phylogenetic networks: new inclusions



joint work with Maxime Morgado and Narges Tavassoli

Classes of phylogenetic networks



Problems and properties studied on these classes

Problems

- **Tree Containment**: Does the input network contain the input tree on the same set of leaves?
- **Cluster Containment**: Does the input network contain the input subset of leaves as a softwired cluster?
- **Phylogenetic Network Isomorphism**: Are the two input phylogenetic networks isomorphic?

Properties

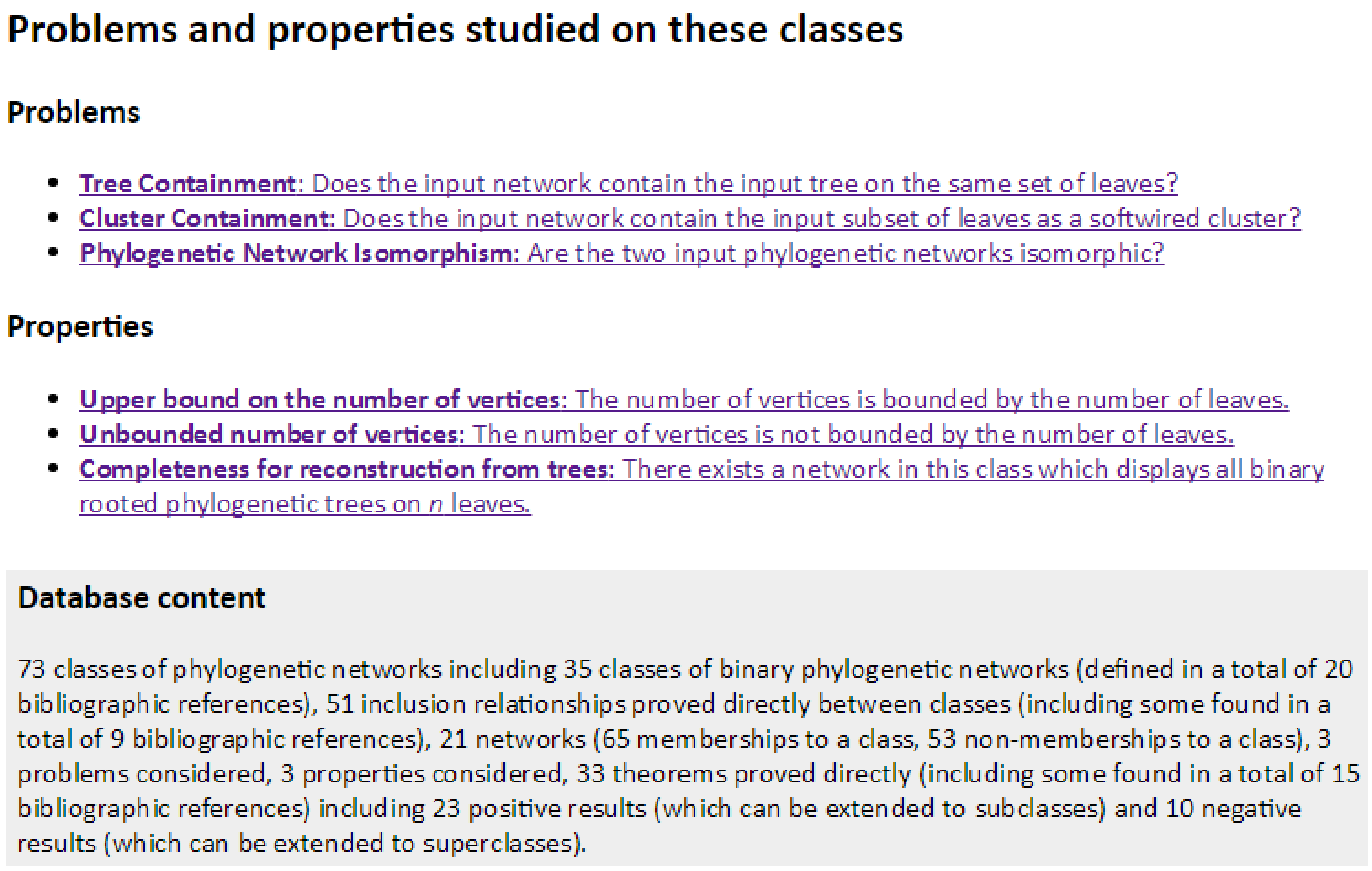
- **Upper bound on the number of vertices:** The number of vertices is bounded by the number of leaves.
- **Unbounded number of vertices:** The number of vertices is not bounded by the number of leaves.
- **Completeness for reconstruction from trees:** There exists a network in this class which displays all binary rooted phylogenetic trees on *n* leaves.

Database content

73 classes of phylogenetic networks including 35 classes of binary phylogenetic networks (defined in a total of 20 bibliographic references), 51 inclusion relationships proved directly between classes (including some found in a total of 9 bibliographic references), 21 networks (65 memberships to a class, 53 non-memberships to a class), 3 problems considered, 3 properties considered, 33 theorems proved directly (including some found in a total of 15 bibliographic references) including 23 positive results (which can be extended to subclasses) and 10 negative results (which can be extended to superclasses).

joint work with Maxime Morgado and Narges Tavassoli

Classes of phylogenetic networks



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Polynomial time algorithm available on class A → works on **subclass** B
NP-completeness on class B → NP-completeness on **superclass** A
(similar to ISGCI)

joint work with Maxime Morgado and Narges Tavassoli

Outline

- Phylogenetic networks
- Classes of phylogenetic networks
- The Tree Containment Problem

Phylogenetic network reconstruction

```
espèce 1 : AATTGCAG TAGCCCAAAAT
espèce 2 : ACCTGCAG TAGACCAAT
espèce 3 : GCTTGCCG TAGACAAGAAT
espèce 4 : ATTTGCAG AAGACCAAAT
espèce 5 :          TAGACAAGAAT
espèce 6 : ACTTGCAG TAGCACAAAAT
espèce 7 : ACCTGGTG TAAAAT
```

G1 G2

{gene sequences}

distance methods

Bandelt & Dress 1992 - Legendre & Makarenkov 2000 - Bryant & Moulton 2002 - Chan, Jansson, Lam & Yiu 2006

parsimony methods

Hein 1990 - Kececioglu & Gusfield 1994 - Jin, Nakhleh, Snir, Tuller 2009 - Park, Jin & Nakhleh 2010 - Kannan & Wheeler, 2012

likelihood methods

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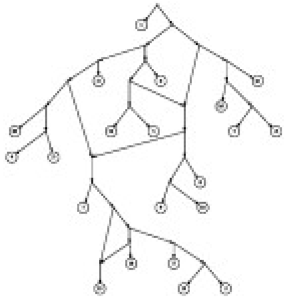

network *N*

Phylogenetic network reconstruction

**Problem: methods are usually slow,
especially with rapidly increasing sequence length.**

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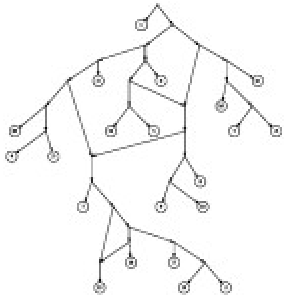

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G1 G2

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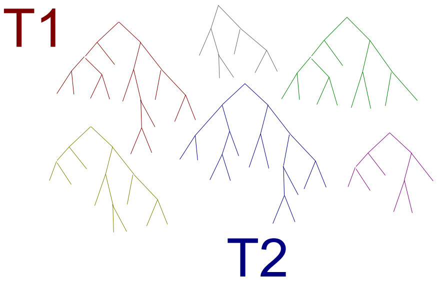
Reconstruction of a tree for each gene present in several species

Guindon & Gascuel, SB, 2003

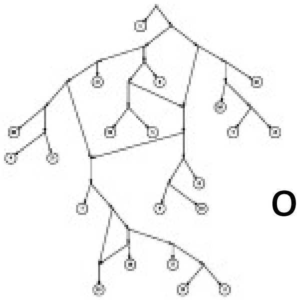


{trees}

HOGENOM Database

Dufayard, Duret, Penel, Gouy, Rechenmann & Perrière, BioInf, 2005

Tree reconciliation or consensus



explicit network

optimal super-network *N*:

- contains the input trees
- has the smallest number of reticulations

http://doua.prabi.fr/databases/hogenom/home.php?contents=hogenom4

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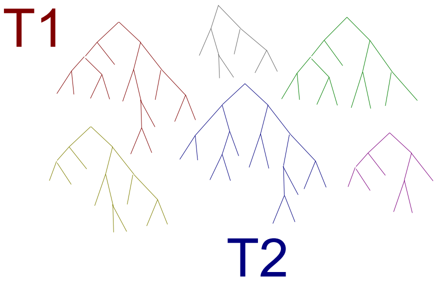

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1470 species, >290 000 trees

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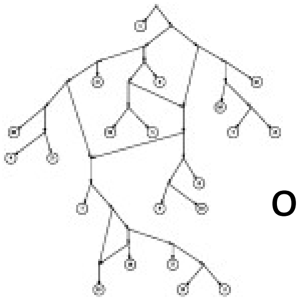

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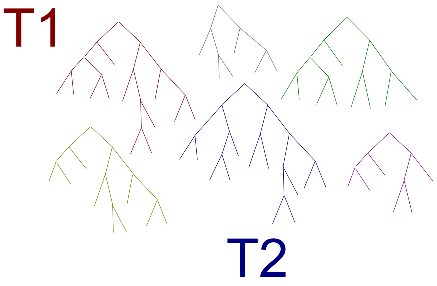

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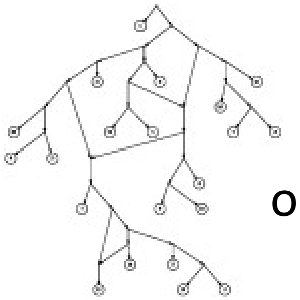
Tree Containment Problem



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The Tree Containment Problem (T.C.P.)

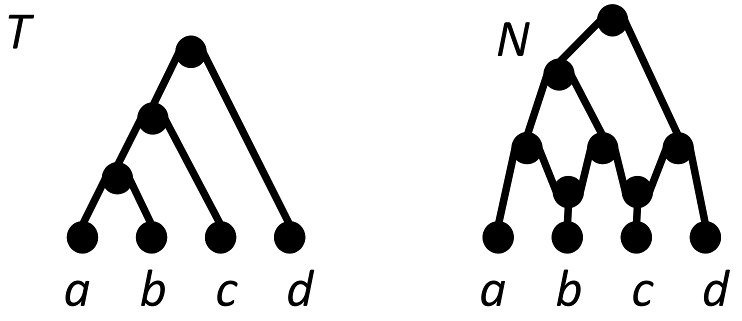
Input:	A binary phylogenetic network *N* and a tree *T* over the same set of taxa.
Question:	Does *N* display *T*?

The Tree Containment Problem (T.C.P.)

Input: A binary phylogenetic network *N* and a tree *T* over the same set of taxa.

Question: Does *N* display *T*?

→ Can we remove one incoming arc, for each vertex with >1 parent in *N*, such that the obtained tree is equivalent to *T*?



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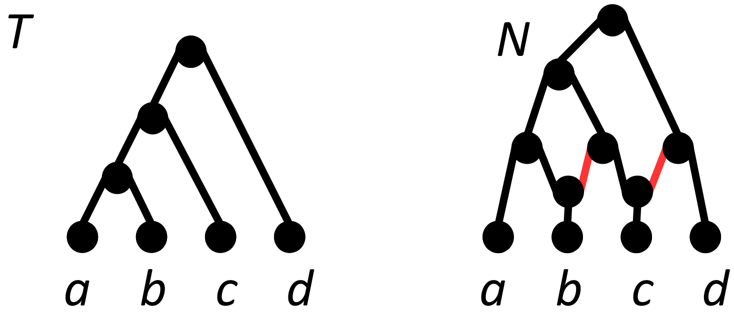


The Tree Containment Problem (T.C.P.)

Input: A binary phylogenetic network *N* and
a tree *T* over the same set of taxa.

Question: Does *N* display *T*?

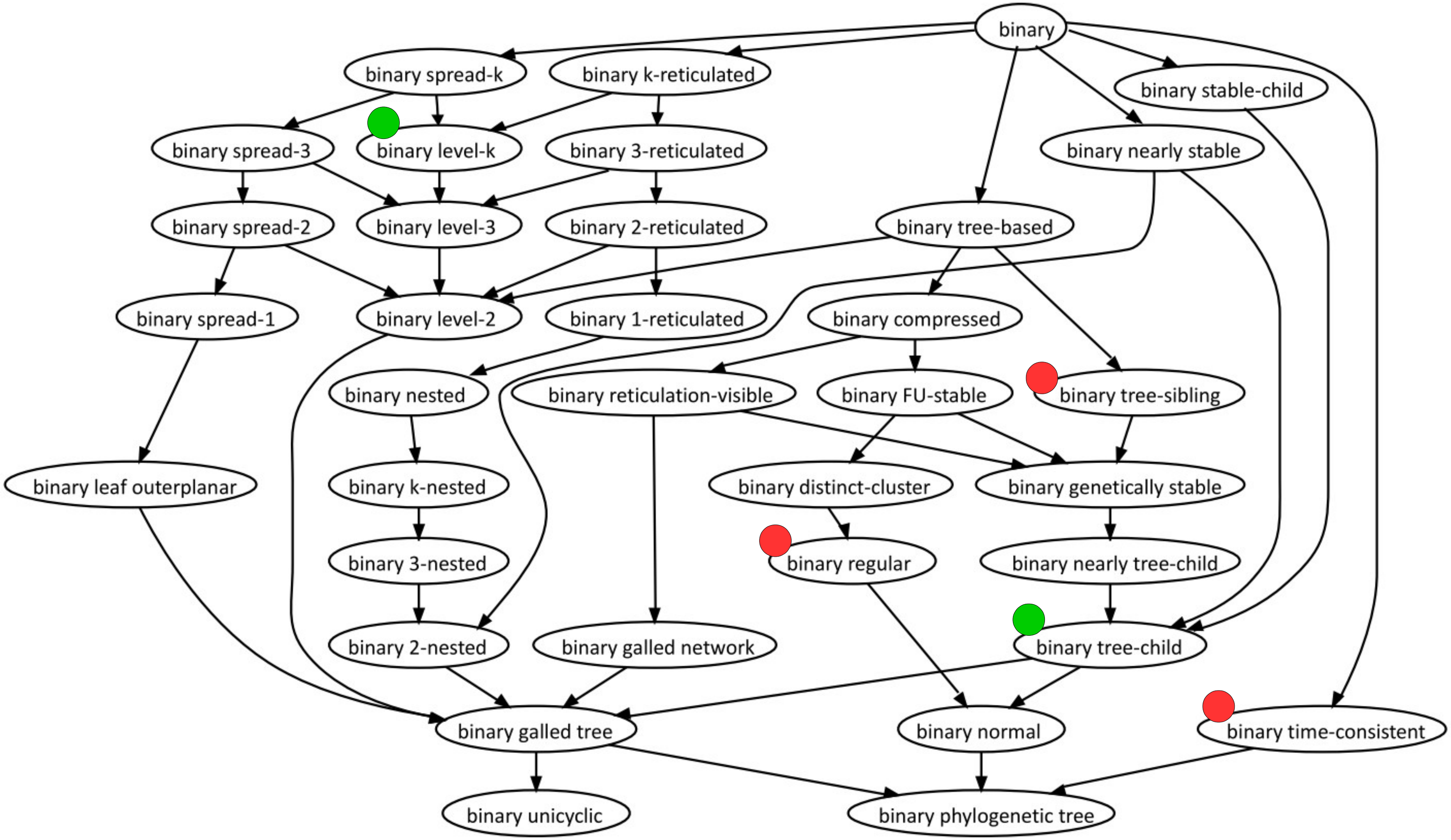
- **NP-complete** in general (Kanj, Nakhleh, Than & Xia, 2008)

- **NP-complete** for tree-sibling, time-consistent, regular networks (Iersel, Semple & Steel, 2010)

- **Polynomial-time solvable** for normal networks, for binary tree-child networks, and for level-k networks (Iersel, Semple & Steel, 2010)

Classes of phylogenetic networks and the T.C.P.

State of the art



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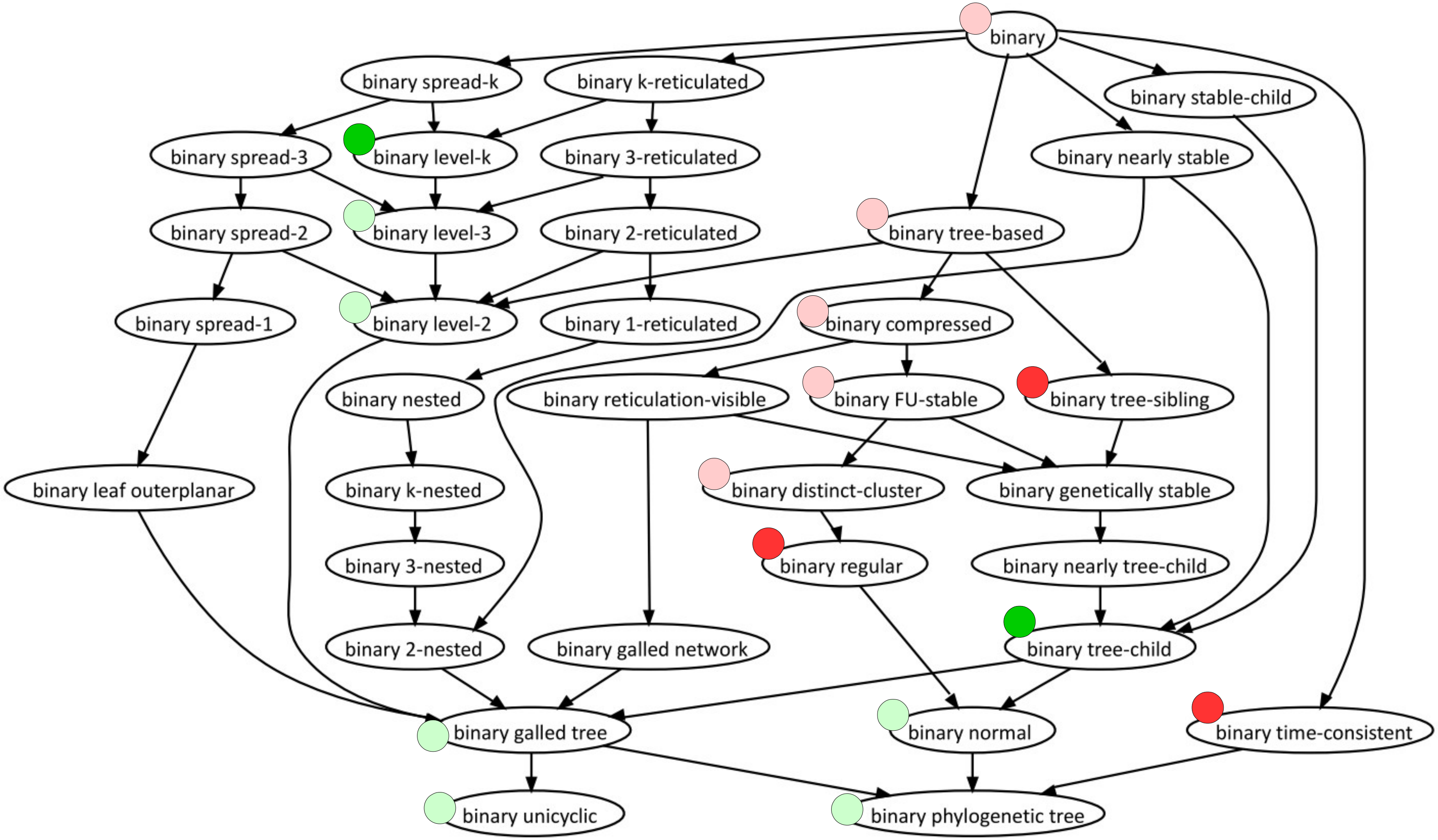
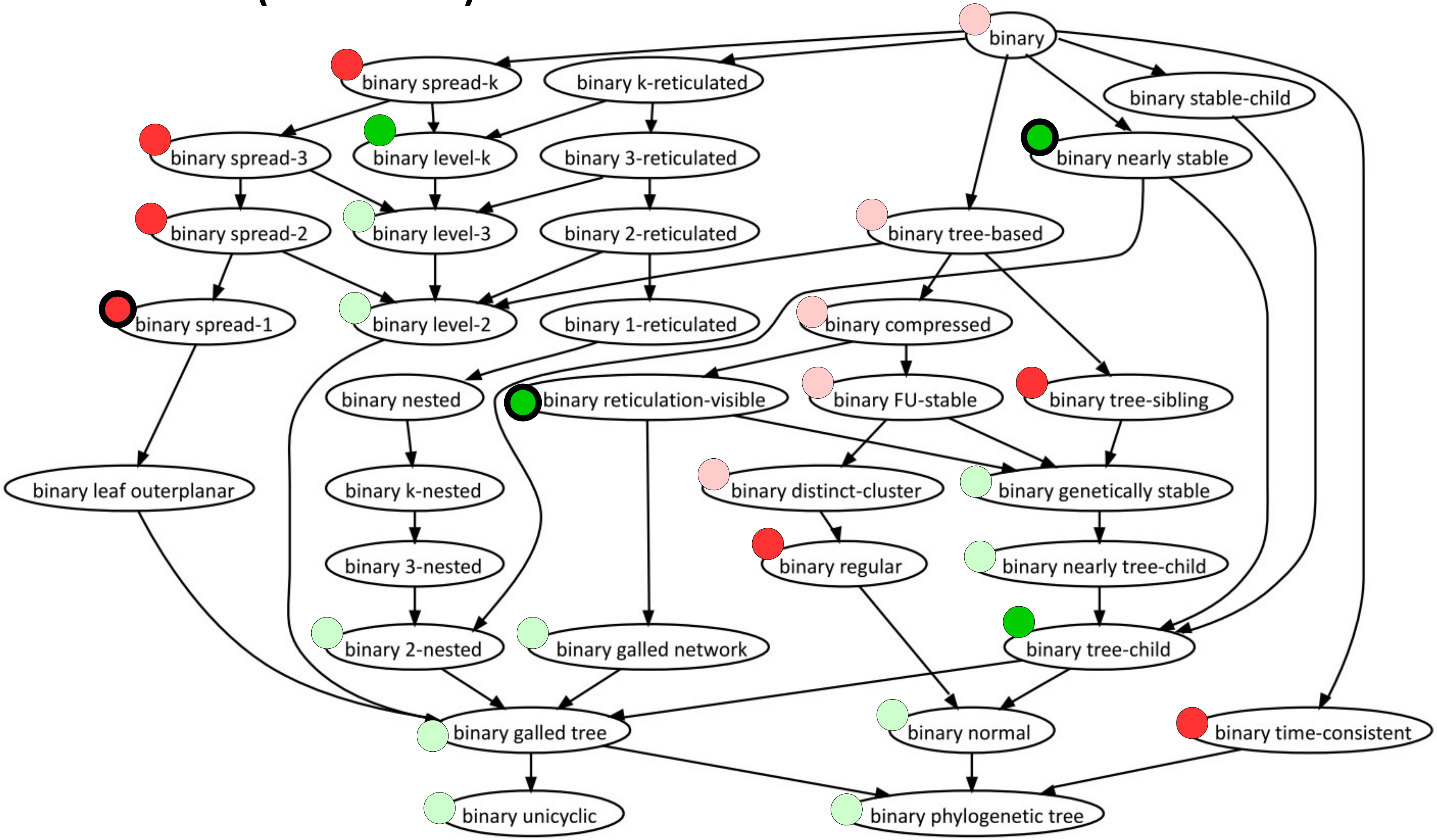
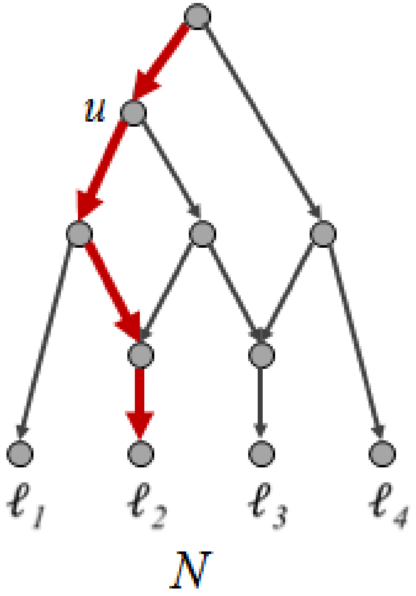


Classes of phylogenetic networks and the T.C.P.

Recent results (since 2015):

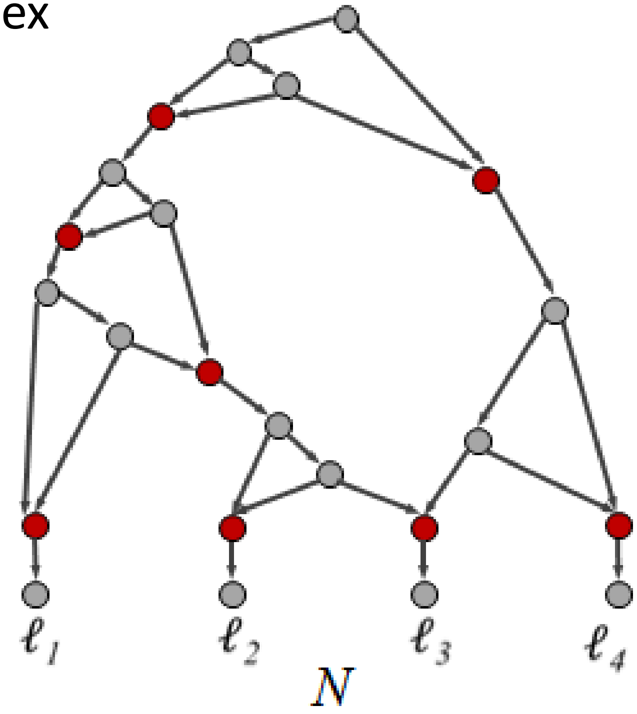


Reticulation-visible and nearly-stable networks



A vertex *u* is **stable** if there exists a leaf *l* such that all paths from the root to *l* go through *u*.

A phylogenetic network is **reticulation-visible** if every reticulation vertex is stable.



A phylogenetic network is **nearly-stable** if for each vertex, either it is stable or its parents are.

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

Strategy to get a quadratic time algorithm for T.C.P.

Given *N*, a phylogenetic network with *n* leaves and the input tree *T* of the T.C.P.

Theorem 1: If *N* is reticulation-visible then: #{reticulation vertices of *N*} ≤ 4(*n*-1)
#{vertices of *N*} ≤ 9*n*

Theorem 2: If *N* is nearly-stable then #{reticulation vertices of *N*} ≤ 12(*n*-1)

Theorem 3: Considering a longest path in *N* (nearly stable), it is possible, in constant time:

- either to realize that *T* is not contained in *N*
- or to build a network *N'* with less arcs than *N* such that *T* contained in *N* if and only if *T* contained in *N'*

Number of reticulations of a reticulation-visible network

Decompose *N* into **2*n*-2 paths**:

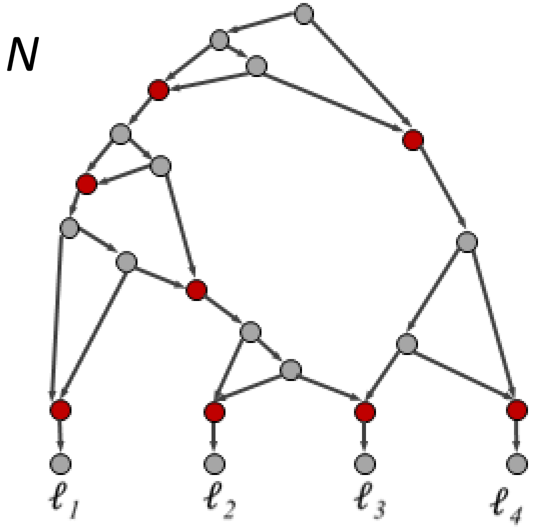
- remove one reticulation arc per reticulation,

ensuring we get no « dummy leaf », to get a tree *T* with *n* leaves

- summarize *T* into a rooted binary tree *T*' with *n* leaves... and 2*n*-2 arcs

We can prove (technical) that:

each path contains at most 2 reticulation vertices



Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

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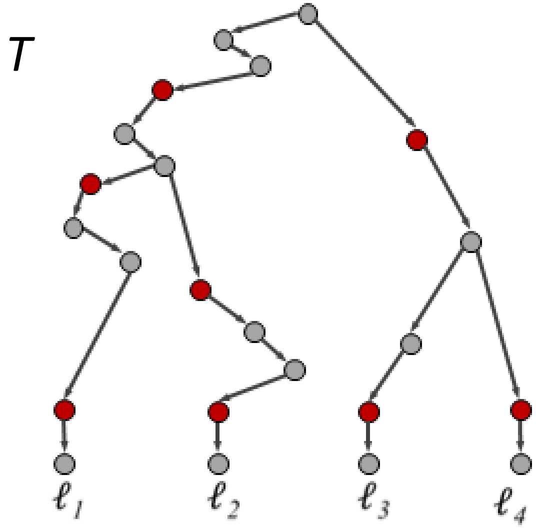

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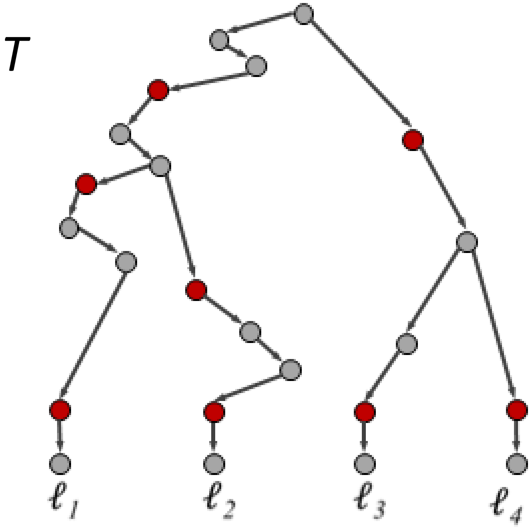

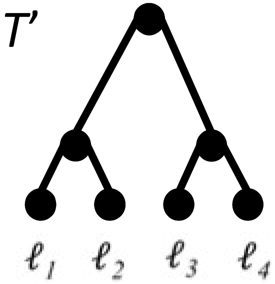

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

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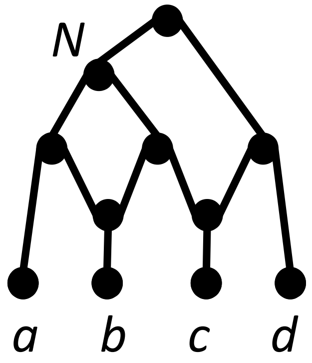
→ *N* contains at most 4(*n*-1) reticulation vertices

Number of reticulations of a reticulation-visible network

« Dummy leaves »?



Deleting reticulation arcs can create « **dummy leaves** »

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

Number of reticulations of a reticulation-visible network

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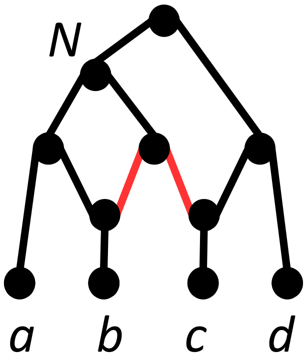

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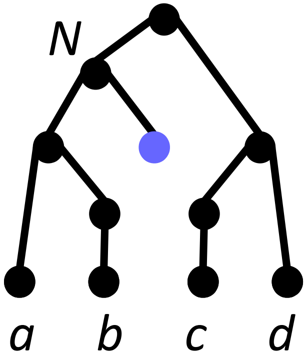

Number of reticulations of a reticulation-visible network

Possible to avoid creating « dummy leaves »?

Number of reticulations of a reticulation-visible network

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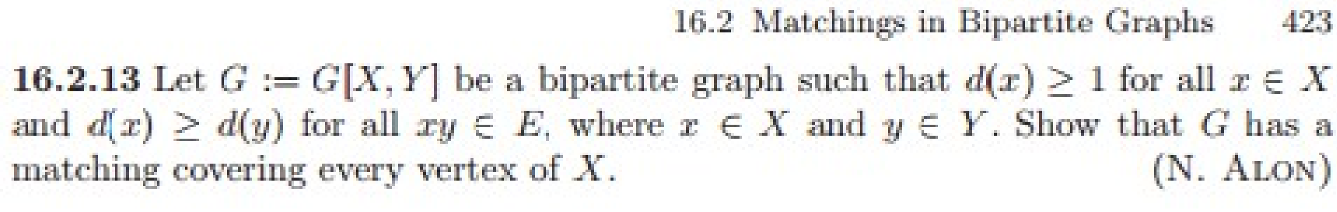
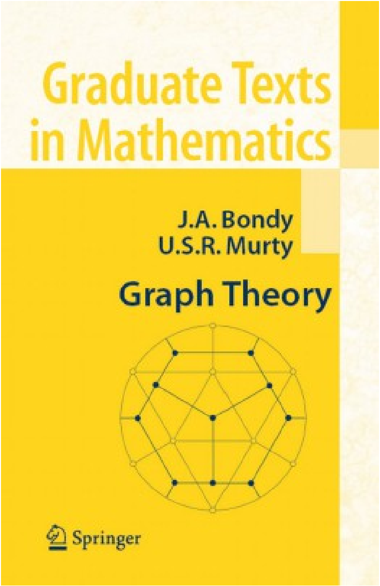


16.2 Matchings in Bipartite Graphs 423

16.2.13 Let $G := G[X, Y]$ be a bipartite graph such that $d(x) \geq 1$ for all $x \in X$ and $d(x) \geq d(y)$ for all $xy \in E$, where $x \in X$ and $y \in Y$. Show that G has a matching covering every vertex of X. (N. ALON)



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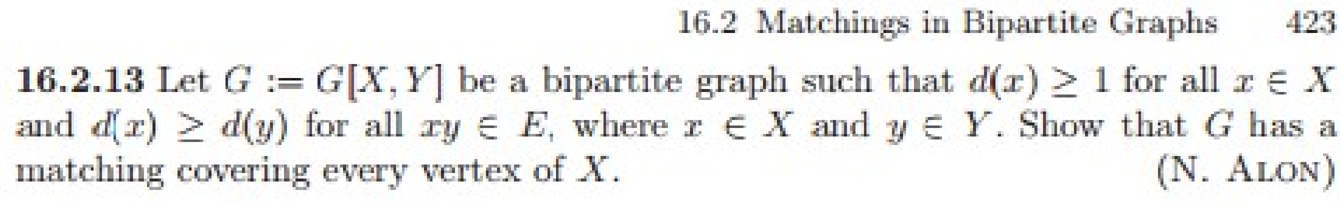

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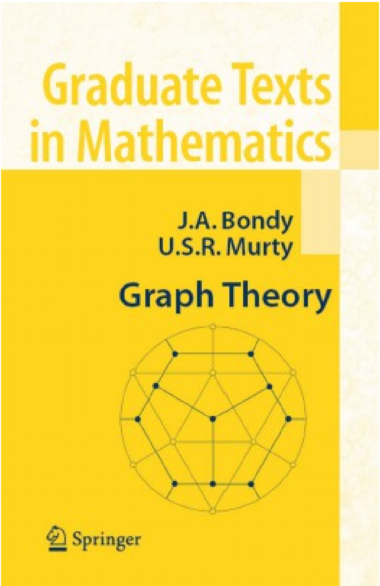


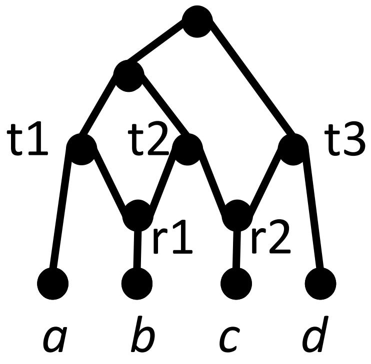
Graduate Texts in Mathematics

J.A. Bondy
U.S.R. Murty

Graph Theory

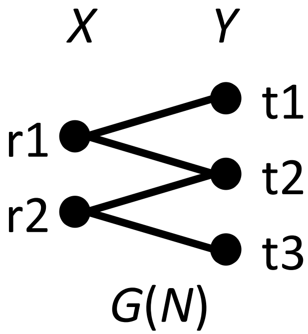
Springer

Given N



Build $G(N)$, bipartite graph such that:

- X = reticulation vertices of N
  - → all vertices in X have degree 2
- Y = tree vertices of N with at least one reticulation child
  - → all vertices in Y have degree 1 or 2
- edge between x and y iff x is a child of y



Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

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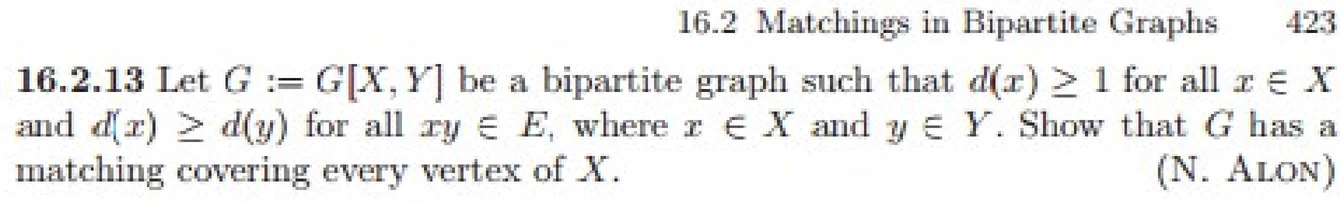

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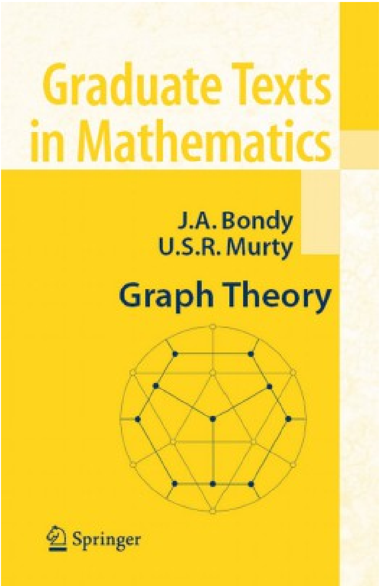
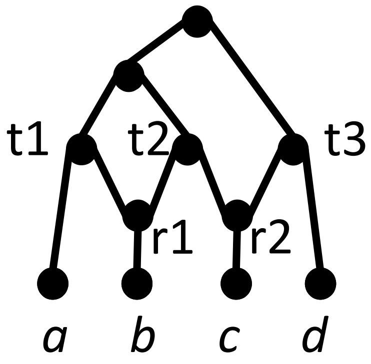


Given *N*



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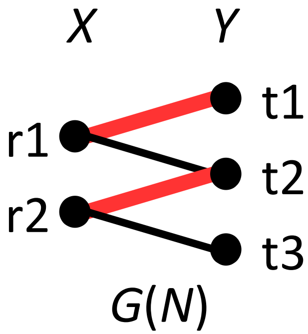
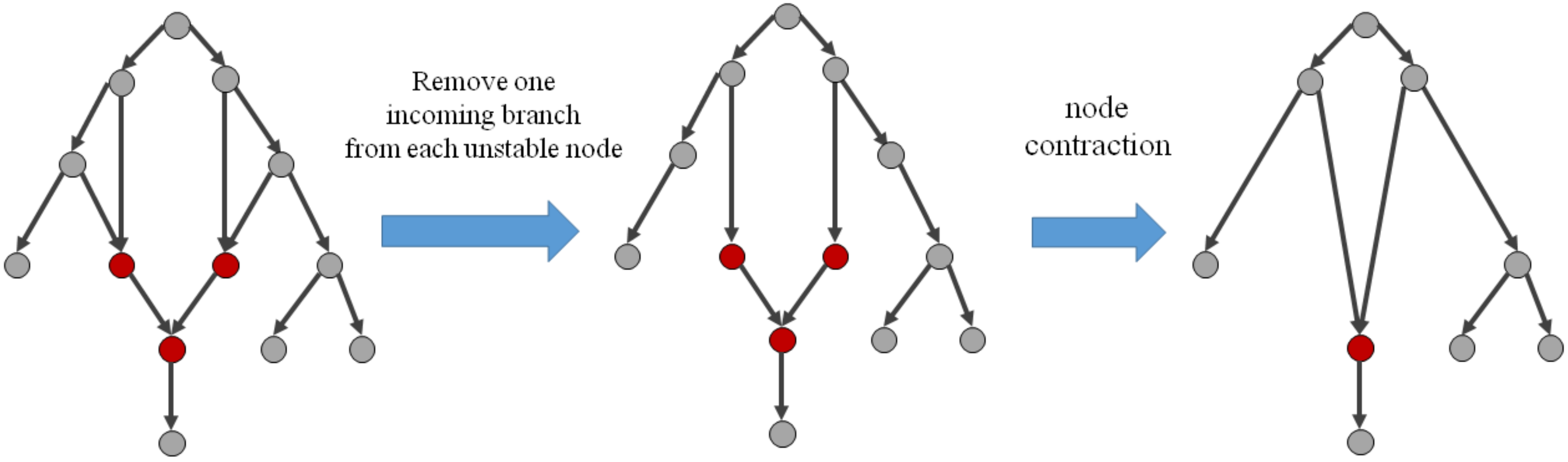


→ **matching covering every vertex of *X*** → **edges to remove from *N***

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

Number of reticulations of a nearly-stable network

Reduce nearly-stable networks to stable networks



Remove one incoming branch from each unstable node

node contraction

nearly-stable network

reticulation-visible network

Claim: #unstableReticulations ≤ 2 #stableReticulations

Proof:
Each unstable reticulation must have a stable reticulation child.
At most two unstable reticulations may have the same reticulation child.

Number of reticulations of a nearly-stable network

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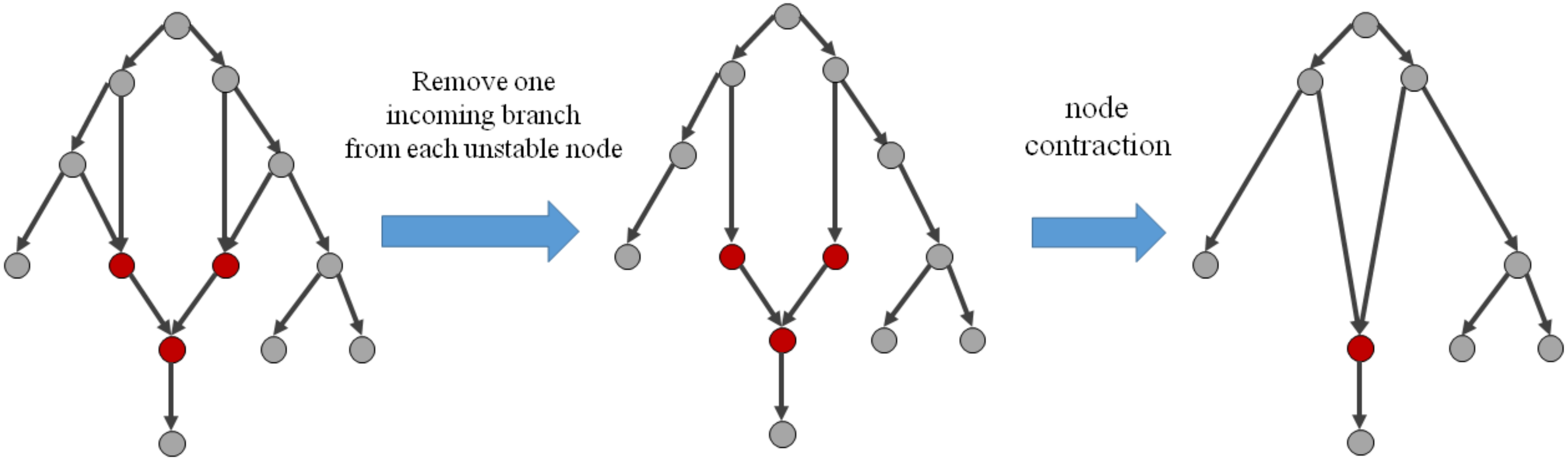


#unstableReticulations ≤ 2 #stableReticulations

#stableReticulations ≤ 4(n-1)

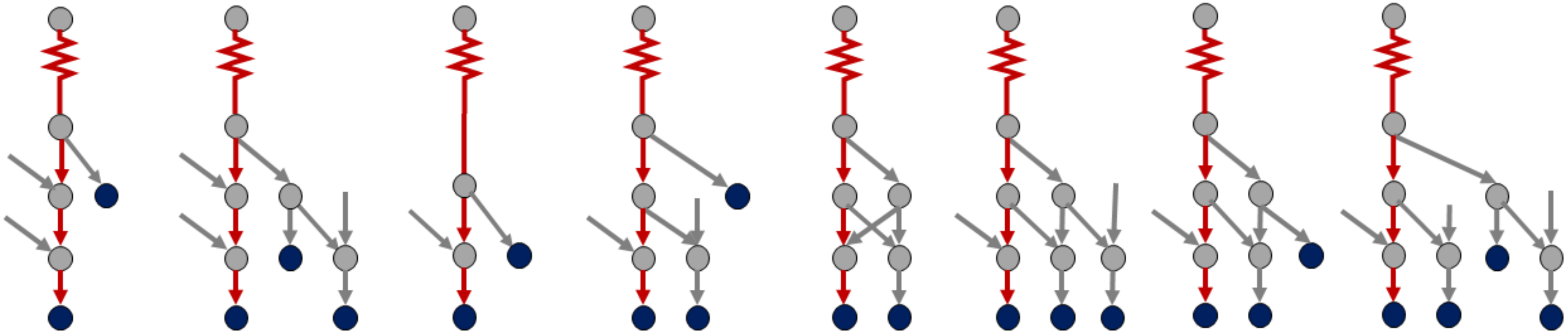
→ #reticulations ≤ 12(n-1)

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

Deleting reticulation arcs to simplify the question

Simplify *N* by removing an arc near the end of a **longest path *P*.**

Case analysis (8 cases):



Algorithm for nearly-stable networks:

Repeat:

- Compute a longest path *P* in *N*
- Simplify *N* by considering the subnetwork at the end of *P* according to the 8 cases above (arc removal + contraction)
- Replace a «cherry» (2 leaves + their common parent) appearing in both *N* and *T* by a new leaf

Finally check that the obtained network is identical to *T*

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

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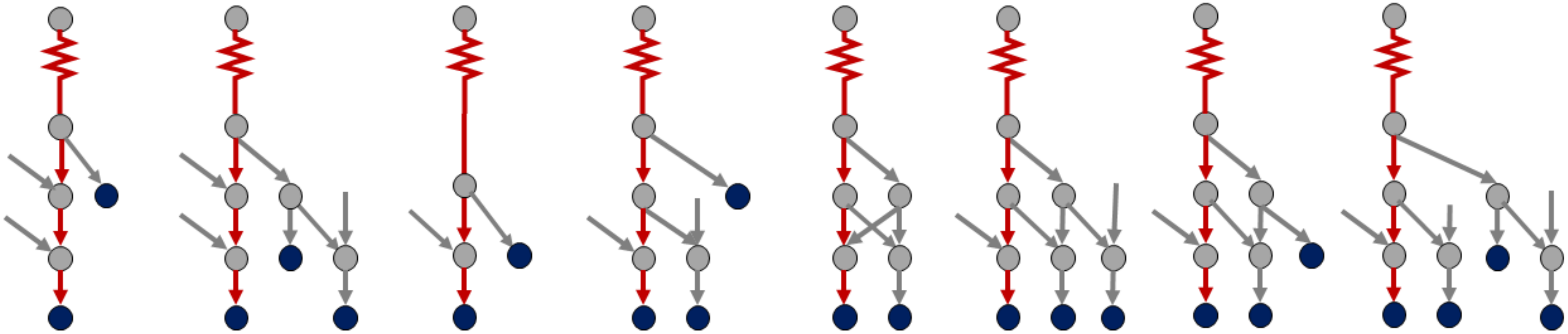

Algorithm for nearly-stable networks:

Repeat: O(*n*) times:

- Compute a longest path *P* in *N* → O(*n*)
- Simplify *N* by considering the subnetwork at the end of *P* according to the 8 cases above (arc removal + contraction) → O(1)
- Replace a «cherry» (2 leaves + their common parent) appearing in both *N* and *T* by a new leaf → O(1)

Finally check that the obtained network is identical to *T* → O(*n*)

Gambette, Gunawan, Labarre, Vialette & Zhang, RECOMB 2015

Improved algorithms

O($n \log n$)-time algorithm for nearly-stable networks

Fakcharoenphol, Kumpijit & Putwattana, JCSSE 2015

Cubic-time algorithm for reticulation-visible networks

Gunawan, DasGupta & Zhang, RECOMB 2016
Bordewich & Semple, Advances in Applied Mathematics, 2016

#reticulations ≤ $3(n-1)$ for reticulation-visible networks

Bordewich & Semple, Advances in Applied Mathematics, 2016

Perspectives...

- Provide a practical algorithmic toolbox using network classes

  → http://phylnet.info/tools/

- Combine the combinatorial and statistical approaches to reconstruct phylogenetic networks

  → CNRS PICS project with L. van Iersel, S. Kelk, F. Pardi & C. Scornavacca

- Develop interactions with related fields:

  → host/parasite relationships

  → population genetics

  → stemmatology