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
• 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
Who is who in Phylogenetic Networks?

An interactive bibliographic database started in 2007

See how the community working on phylogenetic networks evolved in the last 10 years with the coauthor graphs!
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 co-authors on each publication)
Who is who in Phylogenetic Networks?

A fresh look in 2015, with new functionalities:

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

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

Who is Who in Phylogenetic Networks

Publications list

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.

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.
### Exploring the research – getting the articles

<table>
<thead>
<tr>
<th>Publication</th>
<th>Title</th>
<th>Authors</th>
<th>Keywords</th>
<th>Note</th>
</tr>
</thead>
</table>
Exploring the research – getting the articles

Who is Who in Phylogenetic Networks


Exploring the research – getting the articles

11
Keywords: duplication, from rooted trees, from species tree, lateral gene transfer, loss, NP complete, phylogenetic network, phylogeny, reconstruction.
Note: http://compbio.engr.uconn.edu/papers/Kordi_ISBRA2015.pdf.

12
Keywords: bootstrap, explicit network, from distances, heuristic, incomplete lineage sorting, phylogenetic network, phylogeny, reconstruction.
Exploring the research – understanding the topics


Keywords: duplication, from rooted trees, from species tree, lateral gene transfer, loss, NP complete, phylogenetic network, phylogeny, reconstruction.


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Note: http://compbio.engr.uconn.edu/papers/Kordi_ISBRA2015.pdf.
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:


2015
Exploring the research – understanding the topics

Main keywords in June 2015: the tree cloud

Built with TreeCloud & SplitsTree

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

NetCloud
Built with TreeCloud & SplitsTree

Gambette & Véronis, 2009 - http://www.treecloud.org
Exploring the research – understanding the topics

Main keywords in June 2015: the network cloud

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

splits not present in the tree cloud
Exploring the research – understanding the topics

All keywords:

- abstract-network
- agreement-forest
- approximation
- APX-hard
- ARG
- bayesian
- block-realization
- bootstrap
- bound
- branch-and-bound
- cactus-graph
- characterization
- circular-split-system
- clustering
- coalescent
- consensus
- consistency
- cophylogeny
- counting
- database
- distance-between-networks
- diversity
- duplication
- dynamic-programming
- enumeration
- evaluation
- explicit-network
- exponential-algorithm
- FPT
- from-clusters
- from-continuous-characters
- from-distances
- from-gene-order
- from-multilabeled-tree
- from-network
- from-NGS-data
- from-quartets
- from-rooted-trees
- from-sequences
- from-species-tree
- from-splits
- from-trees
- from-trinets
- from-triplets
- from-unrooted-trees
- galled-network
- generation
- haplotype-network
- haplotyping
- heuristic
- HMM
- hybridization
- inapproximability
- integer-linear-programming
- isomorphism
- k-reticulated
- kernelization
- labeling
- lateral-gene-transfer
- level-k
- phylogenetic-network
- likelihood
- lineage-sorting
- loss
- MASN
- median
- MedianJoining
- Minimal
- lateral-network
- minimum-contradiction
- minimum-number
- minimum-spanning-network
- model-selection
- mu-distance
- NeighborNet
- nested-network
- netting
- normal-network
- NP-complete
- optimal-realization
- parsimony
- pedigree
- perfect
- phylogenetic-network
- phylogeny
- polynomial
- population-genetics
- Program-AdmixTools
- Program-ALE
- Program-Angst
- Program-Arlequin
- Program-Beagle
- Program-BIMLR
- Program-Bio-PhyloNetwork
- Program-Clustistic
- Program-CMPT
- Program-Combinetrees
- Program-ConsensusNetwork
- Program-constNJ
- Program-CycleKiller
- Program-Dendroscope
- Program-EEEP
- Program-FastHN
- Program-FlatNJ
- Program-Fylogenetica
- Program-GalledTree
- Program-GraphDTL
- Program-HapBound
- Program-HGT_simul
- Program-Hide1
- Program-HorizStory
- Program-Hybrid-Lambda
- Program-HybridInterleave
- Program-HybridNET
- Program-HybridNumber
- Program-Hybroscale
- Program-JML
- Program-LatTrans
- Program-LEV1ATHAN
- Program-Lev1Generator
- Program-Level2
- Program-linpy
- Program-LNetwork
- Program-MafB
- Program-Marlon
- Program-MCNet
- Program-McKitsh
- Program-Movgli
- Program-MovgliNNI
- Program-MPNet
- Program-MY-CLOSURE
- Program-Nepal
- Program-NetGen
- Program-NetTest
- Program-NetView
- Program-Network
- Program-Notung
- Program-PADRE
- Program-Phangorn
- Program-PhippsNetwork
- Program-PhyloNet
- Program-PhyloNet-HMM
- Program-PiRN
- Program-Prunier
- Program-Pyramids
- Program-QNet
- Program-Quartet
- Program-Quartet-Decomposition
- Program-Quartet-Methods
- Program-QuartetNet
- Program-QuickCass
- Program-RANGER-DTL
- Program-RecMin
- Program-Recodon
- Program-Recpars
- Program-Recidic
- Program-SAGE
- Program-SAQ-Net
- Program-Serial-NetEvolve
- Program-SHRUB
- Program-Simplistic
- Program-Sliding-MinPD
- Program-SNSA
- Program-Spectronet
- Program-SplitsTree
- Program-SPNet
- Program-SPDist
- Program-SuperQ
- Program-T-REX
- Program-TCS
- Program-TERA
- Program-TerminusEst
- Program-TreeFix-DTL
- Program-TreeMix
- Program-Treeolve
- Program-TripleNet
- Program-urutan-Net
- Program-Ubranet
- Program-WeakHierarchies
- Program-Xscape
- pyramid
- quasi-median-network
- realization
- recombination
- reconstruction
- regular-network
- reticulogram
- serial-evolutionary-networks
- simulated-annealing
- simulation
- site-consistency
- software
- split
- split-decomposition
- split-network
- SPR-distance
- spread
- statistical-model
- statistical-parsimony
- supernetwork
- survey
- tanglegram
- time-consistent-network
- tree-child
- tree-sibling
- tripartition-distance
- triplet-distance
- unicyclic-network
- visualization
- weak-hierarchy
- weakly-compatible
Exploring the research – understanding the topics
Exploring the research – understanding the topics

→ missing references: ARG, pedigrees, haplotyping, etc...
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Exploring the research – discovering software

Software and input data:

Number of nodes is 42. Number of edges is 71.
Exploring the research – discovering software

Who is Who in Phylogenetic Networks

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.

Order by: Type | Year

Only □ And □ Or □ related to: ---

Show

Associated keywords

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
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Finding experts – In pictures!

The Community
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.

Choose a subcriteria to style nodes accordingly.

agreement forest

Prolificacy (total output)

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

Choose a country to style node borders accordingly.

2 publication(s)

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) BIOT06(1) CIBCB13(1) COCOA07(1) COCOA08(1) COCOODN4(1) COCOODN5(1) COCOON06(1) COCOON07(1) CPM07(1) CPM09(2) CPM10(1) CPM12(1) CPM08(1) CSB03(1) CSB05(1) CSB06(1) CSB10(1) ECCC03(1) ECCC05(1) ECCC06(1) ECCC12(1) ICCAB311(1) IFCS0(1) IFCS04(1) IFCS06(1) GFKL03(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) ISMBECB06(1) ISPAN12(1) IWBR05(1) JOBI04(1) Logic-and-Program-Semantics(1) MCMC11(1) MFCS05(1) MCS05(1) PACB12(1) PADO03(1) PReMI07(1) CATS’04(1) SPIE-BBS-III(1) RECOMB-CG’10(2) Alco09(1) RECOMB-CG’06(1) PPSNIX(1) SEA’10(1) ICTCS05(1) ICDCT05(1) WEA’08(1) RECOMB-CG’08(1) SMBE’05(1) SYRCoDis’08(1) ICTCS’07(1) JCSE’15(1) PSB03(2) PSB04(1) RECOMB-CG’12(1) RECOMB-CG’13(1) RECOMB01(1) RECOMB02(1) RECOMBO4(3) RECOMBO5(4) RECOMBO8(2) RECOMB13(1) RECOMB15(1) RECOMB99(1) SACO05(1) SACO06(1) SODA’05(1) SODA’06(1) SODA04(1) TANC12(1) TCSB2(1) Verhandlungen-des-Naturwissenschaftlichen-Vereins-Hamburg(1) JMDA’06(1) WABI02(1) WABI03(3) WABI05(1) WABI06(1) WABI07(1) WABI08(3) WABI09(1) WABI12(2) W614(1)

**Journals**

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
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Following the community – RSS feeds

Who is Who in Phylogenetic Networks

→ whole website

Publications of Luay Nakhleh

→ this author

Associated keywords


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


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


→ share on social networks or by email
Following the community – Professional networks

→ on Google Scholar

→ download BibTeX basket including Scopus query about the DOIs
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Analyzing the trends – general trends of the field

About 40 publications a year:

Analyzing the trends – general trends of the field

Number of PhD Theses per year

- 1990: 0
- 1995: 1
- 2000: 1
- 2005: 2
- 2010: 4
- 2015: 3
Analyzing the trends – general trends of the field

Explicit networks versus abstract networks?

• **explicit** phylogenetic networks
  
  **model evolution**
  
  [Diagram: Dendroscope]
  
  galled network

• **abstract** phylogenetic networks
  
  **classify, visualize data**
  
  [Diagram: SplitsTree, Minchin, etc.]

TCS

SplitsTree

median network

split network

Synthesis diagram

minimum spanning network

level-2 network

Simplistic
Analyzing the trends – general trends of the field
Analyzing the trends – general trends of the field

Abstract networks

Explicit networks
Analyzing the trends – A less clusterized field?

Gephi visualization of the coauthor network clustering → reflects the history
Analyzing the trends – A less clusterized field?

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
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Subclasses of phylogenetic networks

Huson & Bryant 2006

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

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

What is ISGCI?

ISGCI is an encyclopaedia of graph classes 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

Classic classes

Meyniel
P₄-bipartite
P₄-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
Hamiltonian cycle
ISIPhyNC and subclasses of phylogenetic networks

- binary spread-k
- binary level-k
- binary spread-3
- binary spread-2
- binary spread-1
- binary level-3
- binary level-2
- binary level-1
- binary 3-nested
- binary 2-nested
- binary leaf outerplanar
- binary galled network
- binary galled tree
- binary unicyclic
- binary phylogenetic tree
- binary tree-based
- binary nested
- binary compressed
- binary tree-sibling
- binary genetically stable
- binary nearly stable
- binary MUL-stable
- binary CLS
- binary distinct-cluster
- binary tree-child
- binary regular
- binary normal

Internship of Maxime Morgado, 2015
ISIPhyNC and subclasses of phylogenetic networks
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(n²) time [reference]
- Tree Containment: Solvable in O(n log n) time [reference]
ISIPhyNC – The problems

**ISIPhyNC - Problem: Tree Containment**

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**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 $O(2^k \cdot n)$ 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

Possibility 2: stick with definition

is a binary regular network

are not

ARE not
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 ?
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/

Thank you for your attention!