Department of Physics and Astronomy - Northwestern University

Abstract

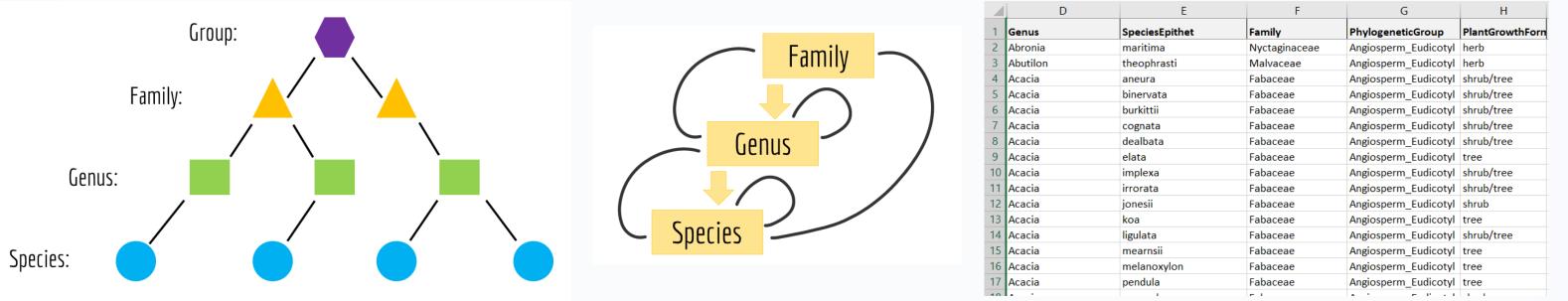
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

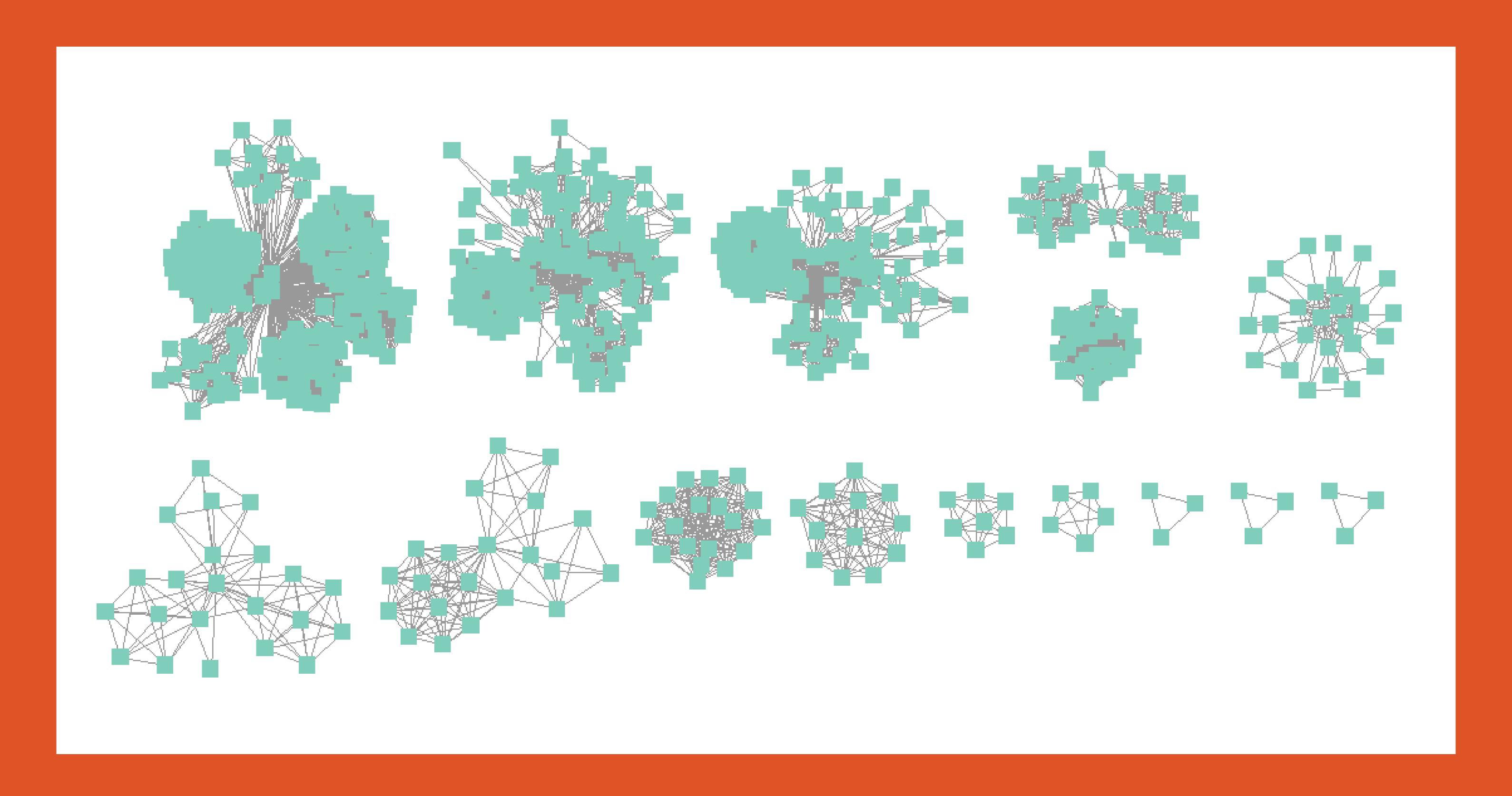
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the TRY Plant Trait Database. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

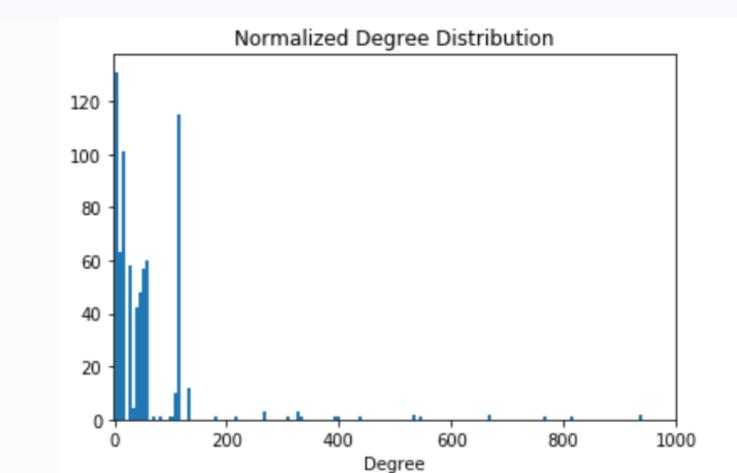


12	Acacia	Jonesii	Fabaceae	Angiosperin_Edulcoty	sinub
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10			e 1	A PERSON NEW YORK AND	1 1



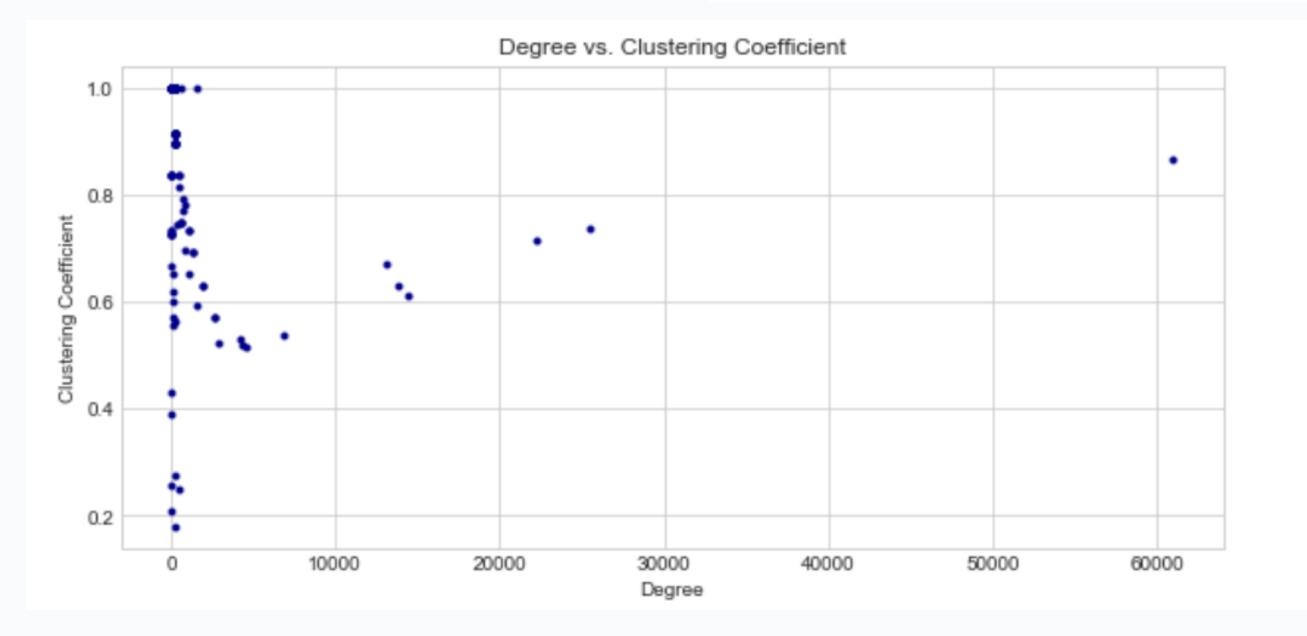
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



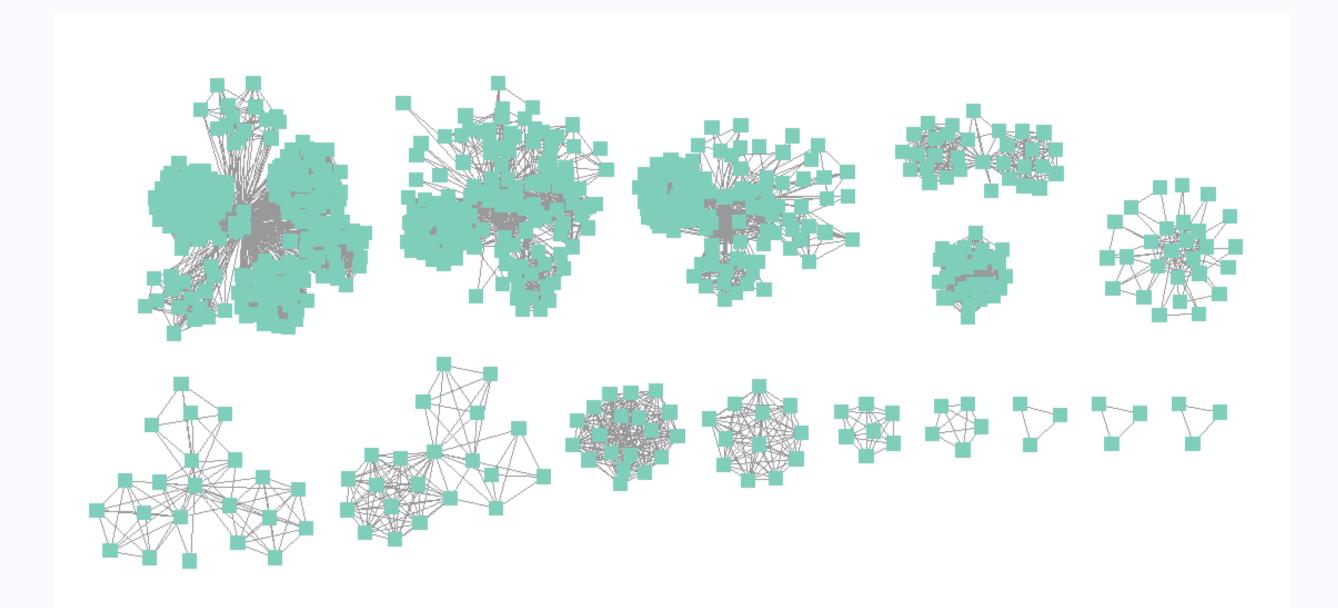
Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

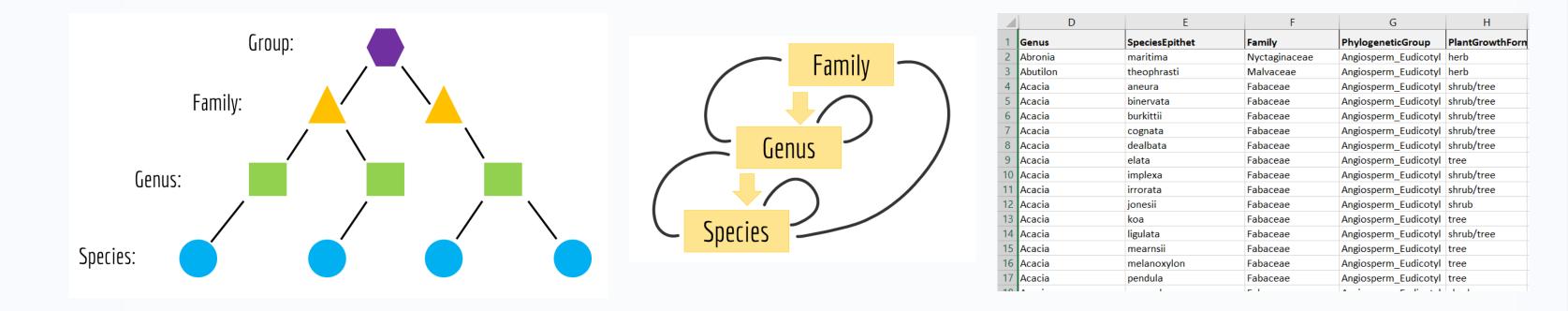
The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University



Method

We began with data from the *TRY Plant Trait Database*. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.



Abstract

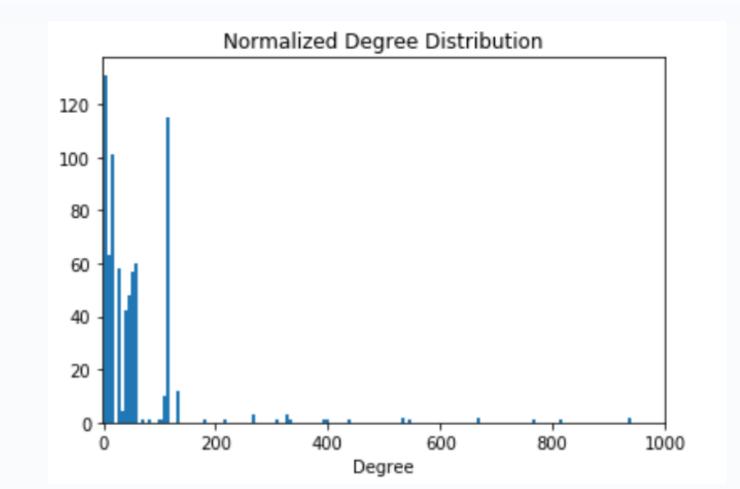
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

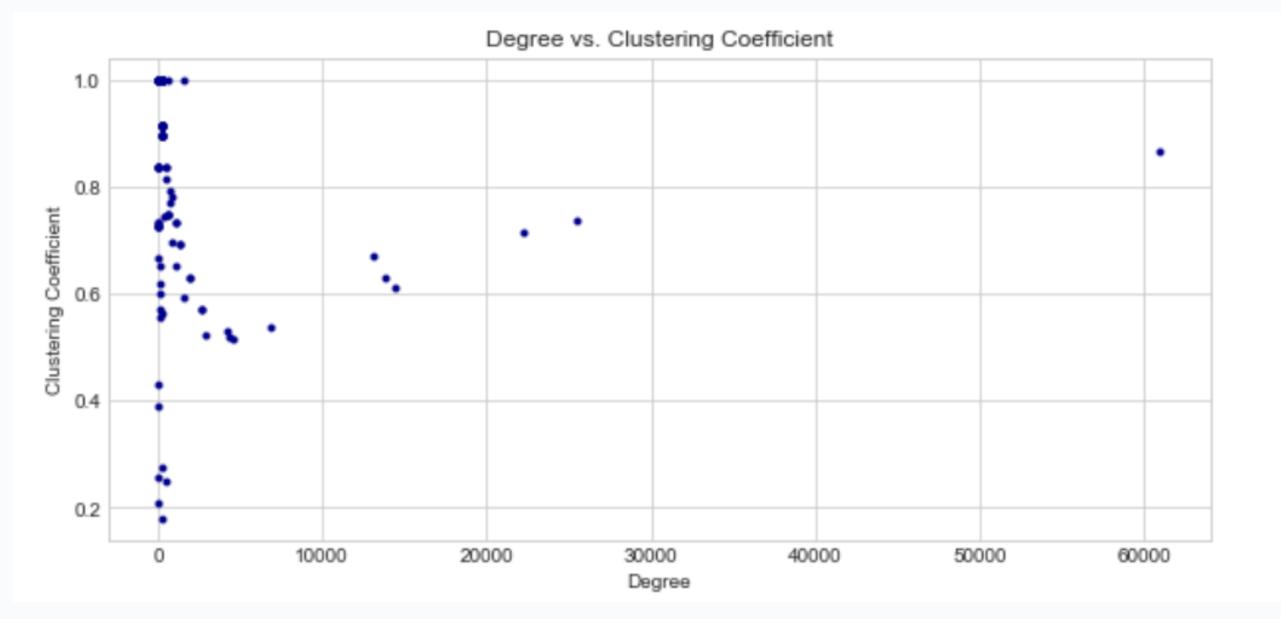
Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950

Results



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not



give us the most useful information.

Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

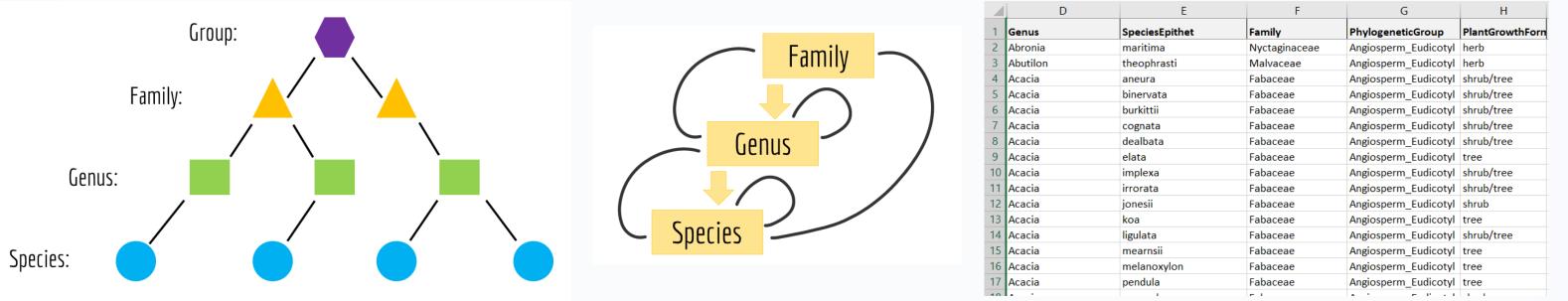
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

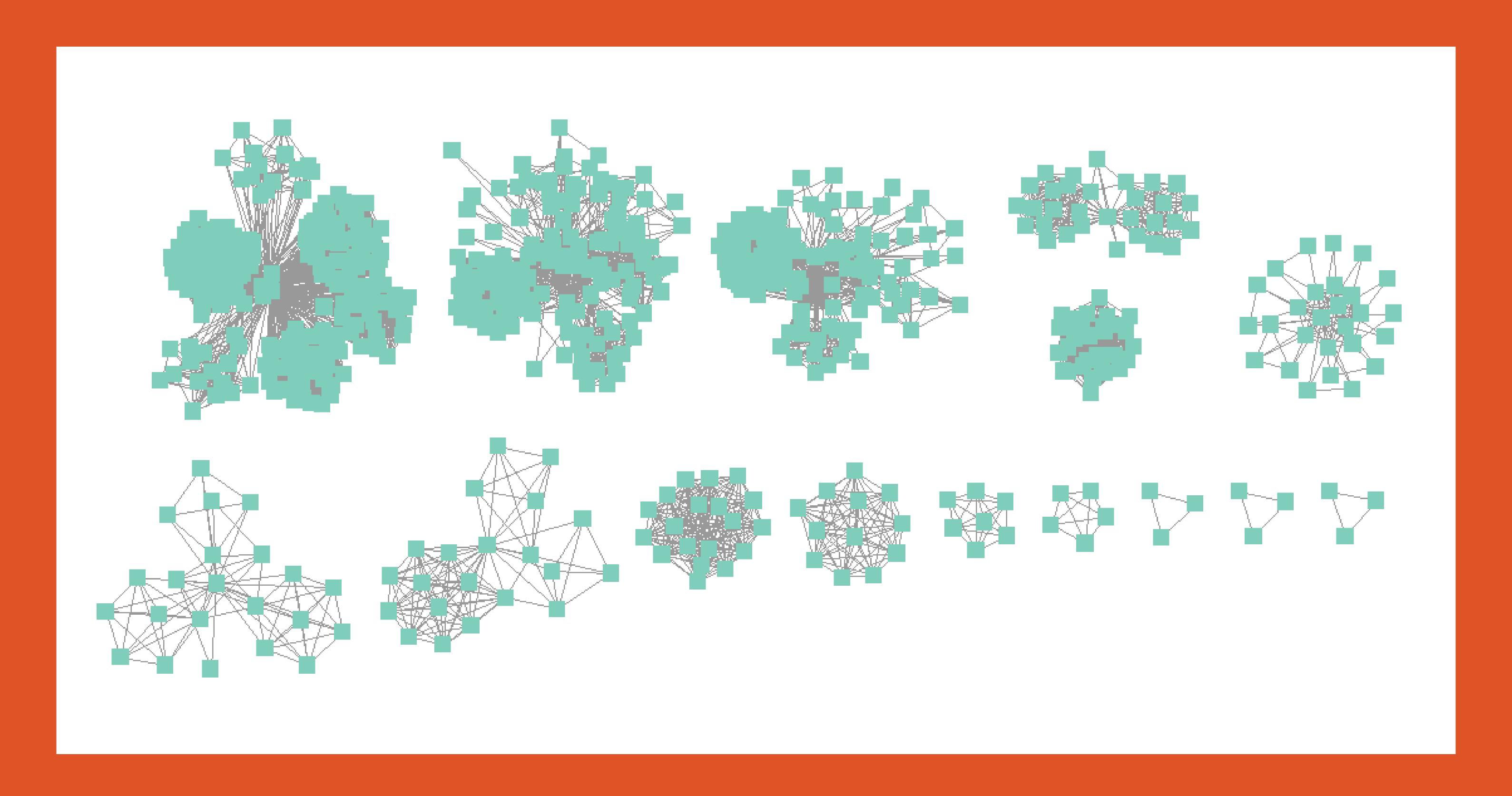
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the TRY Plant Trait Database. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

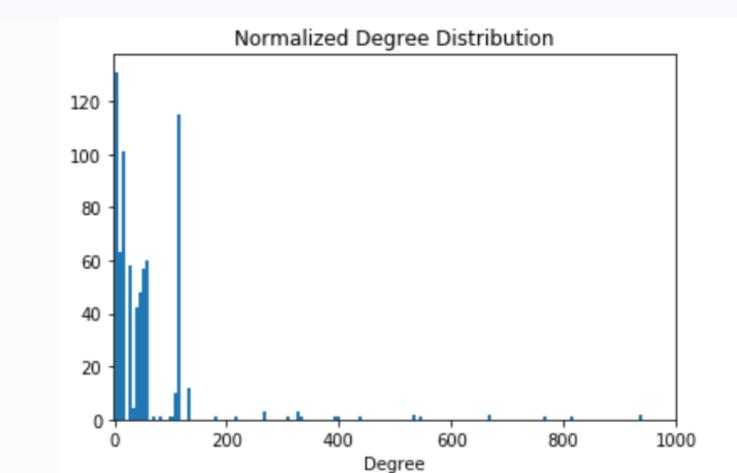


12	Acacia	Jonesii	Fabaceae	Angiosperin_Edulcoty	sinub
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10			e 1	A PERSON NEW YORK AND	1 1



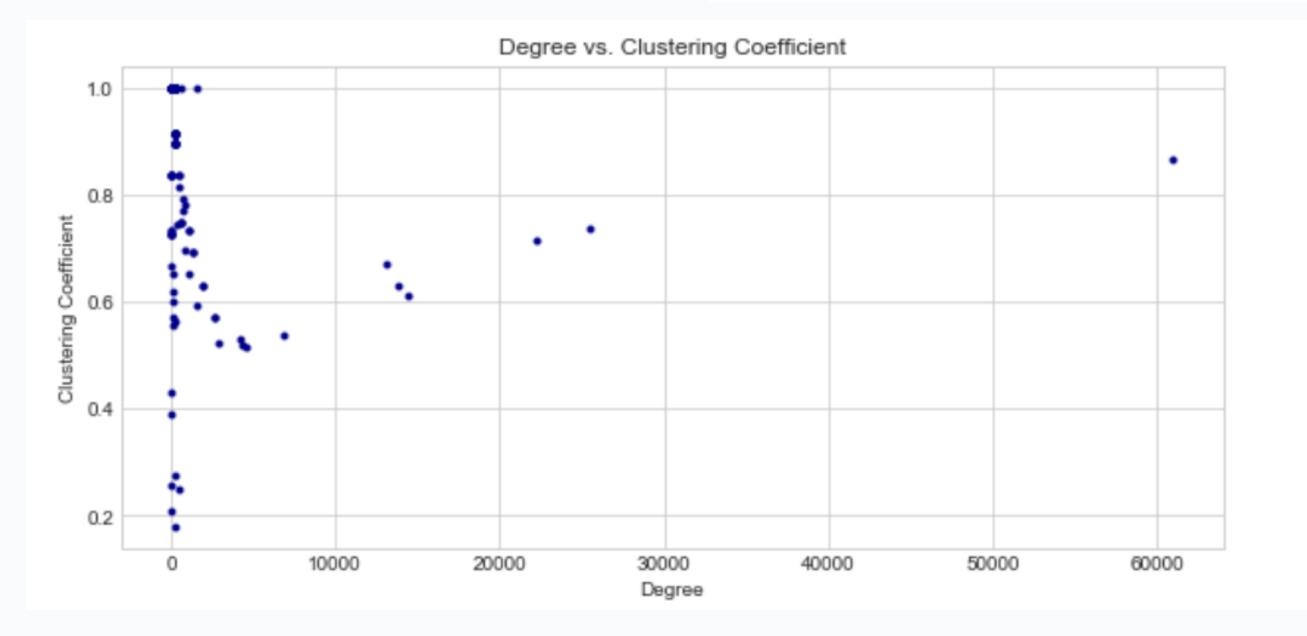
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

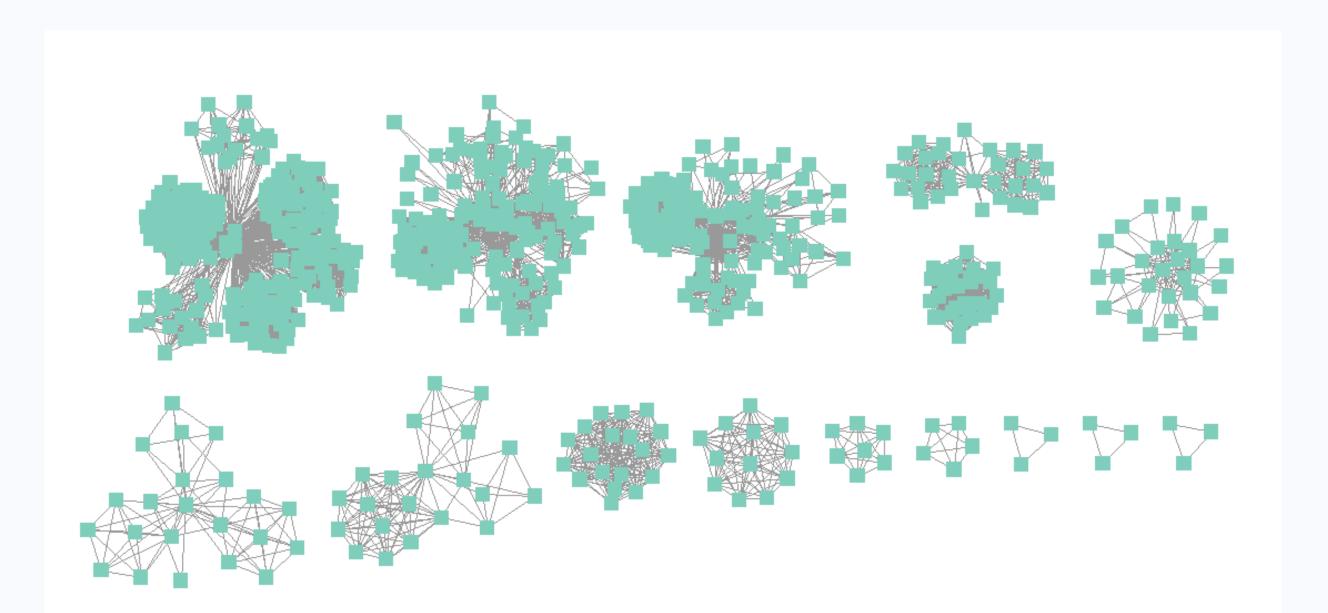
Department of Physics and Astronomy - Northwestern University

Abstract

Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

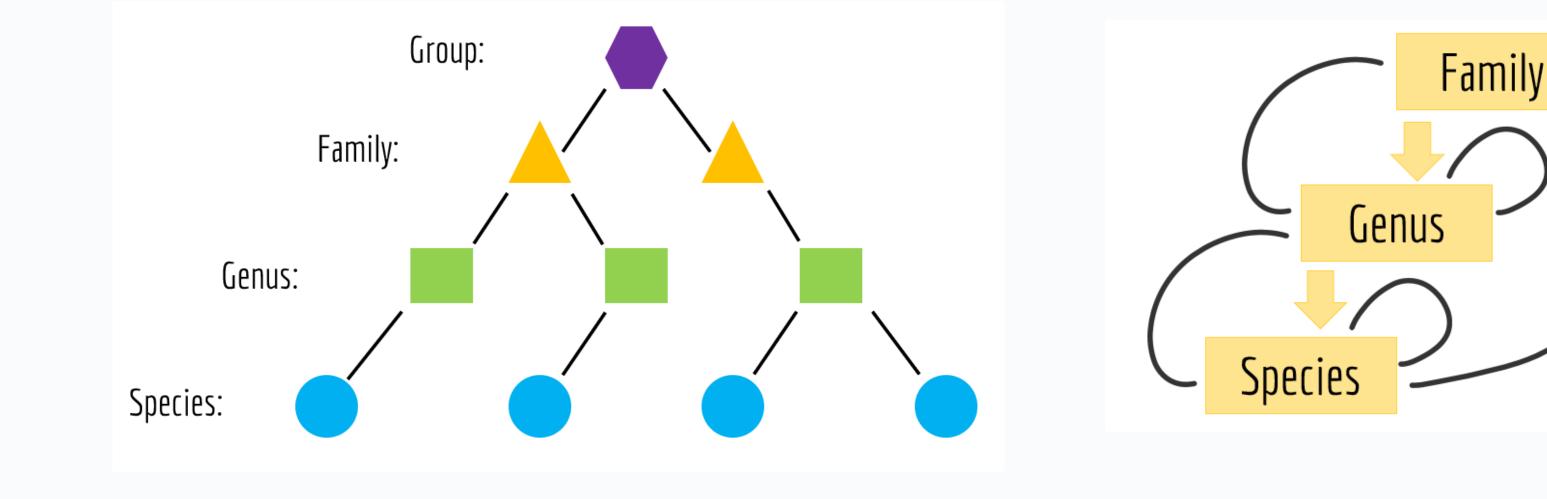
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.



Method

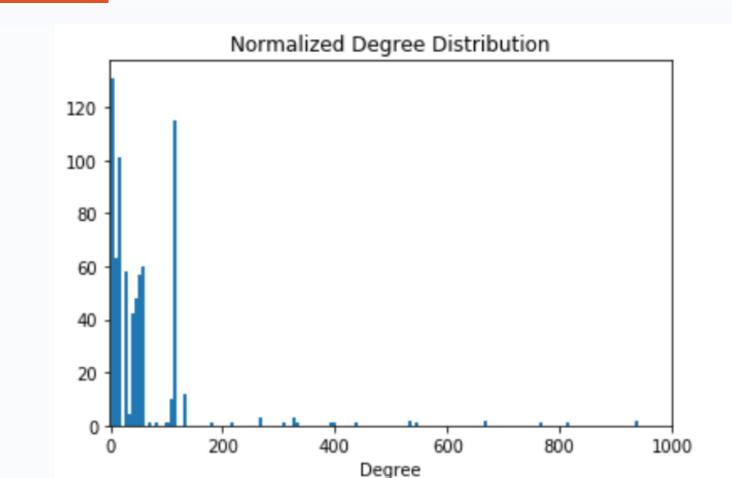
We began with data from the *TRY Plant Trait Database*. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

	D	E	F	G	Н
1	Genus	SpeciesEpithet	Family	PhylogeneticGroup	PlantGrowthForn
2	Abronia	maritima	Nyctaginaceae	Angiosperm_Eudicotyl	herb
3	Abutilon	theophrasti	Malvaceae	Angiosperm_Eudicotyl	herb
4	Acacia	aneura	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
5	Acacia	binervata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
6	Acacia	burkittii	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
7	Acacia	cognata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
8	Acacia	dealbata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
9	Acacia	elata	Fabaceae	Angiosperm_Eudicotyl	tree
10	Acacia	implexa	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
11	Acacia	irrorata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
12	Acacia	jonesii	Fabaceae	Angiosperm_Eudicotyl	shrub
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
17	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10	· ·	1	e 1	A 1	1 1



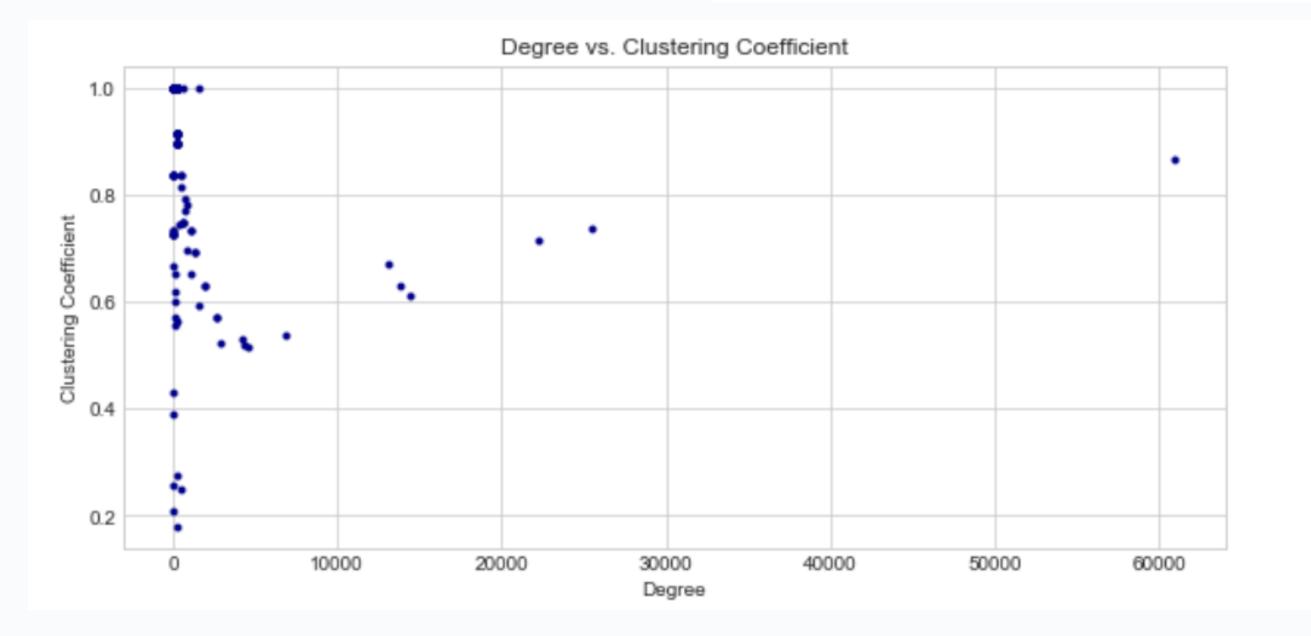
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

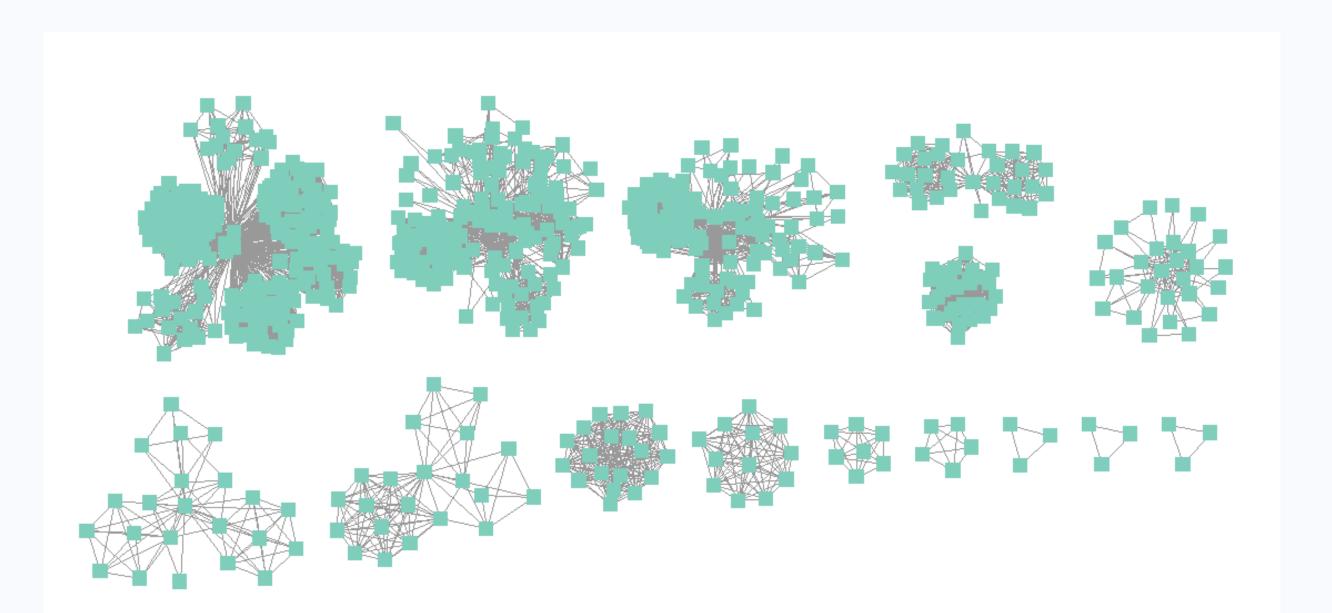
Department of Physics and Astronomy - Northwestern University

Abstract

Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

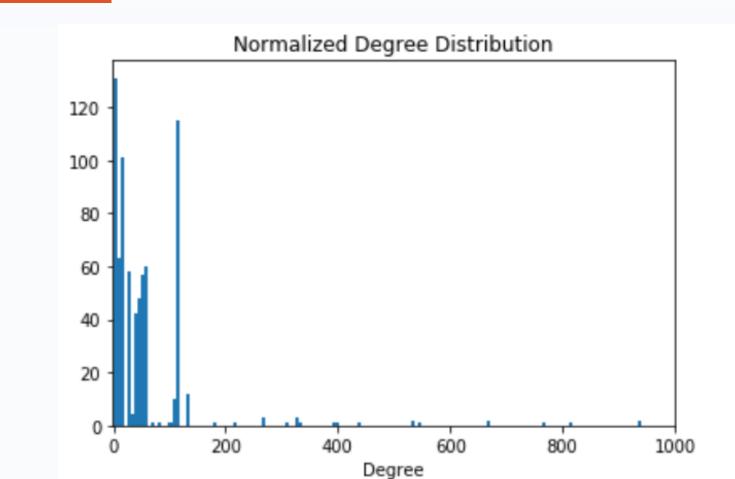


Method

	D	E	F	G	н
1	Genus	SpeciesEpithet	Family	PhylogeneticGroup	PlantGrowthForn
2	Abronia	maritima	Nyctaginaceae	Angiosperm_Eudicotyl	herb
3	Abutilon	theophrasti	Malvaceae	Angiosperm_Eudicotyl	herb
4	Acacia	aneura	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
5	Acacia	binervata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
6	Acacia	burkittii	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
7	Acacia	cognata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
8	Acacia	dealbata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
9	Acacia	elata	Fabaceae	Angiosperm_Eudicotyl	tree
10	Acacia	implexa	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
11	Acacia	irrorata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
12	Acacia	jonesii	Fabaceae	Angiosperm_Eudicotyl	shrub
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
17	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10					

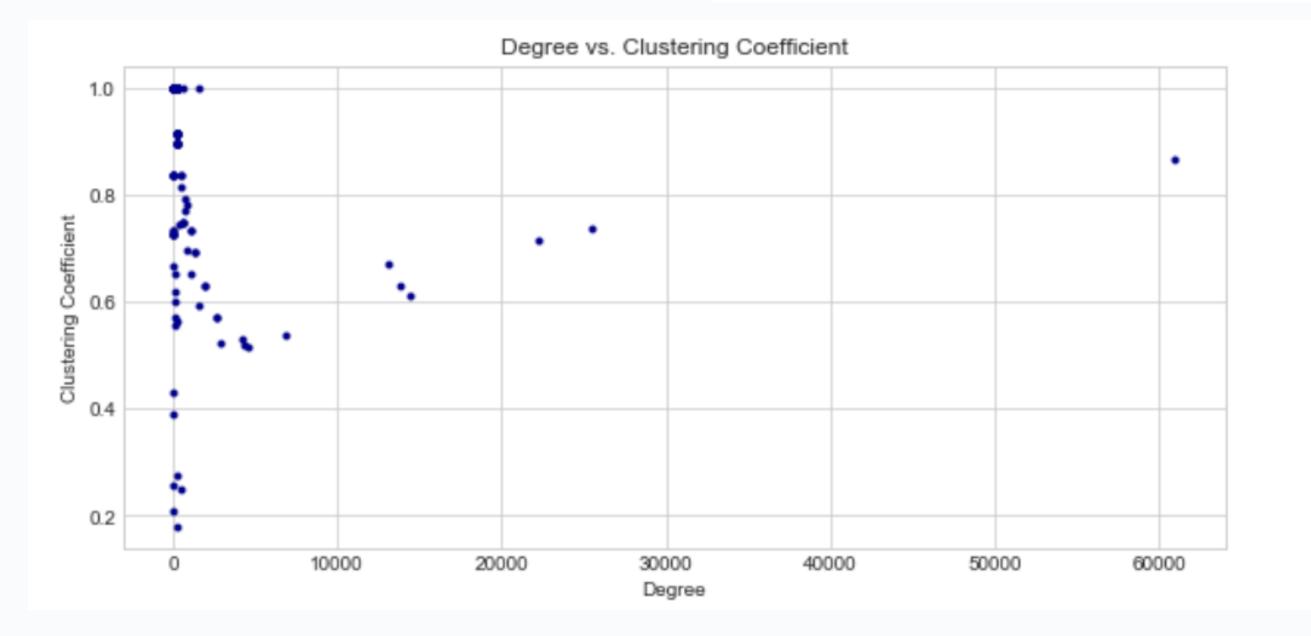
Results

Number of Nodes: 739
Number of Links: 131,321
Connected Components: 15
Clustering Coefficient: 0.986
Smallest Degree: 2
Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not



give us the most useful information.

Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

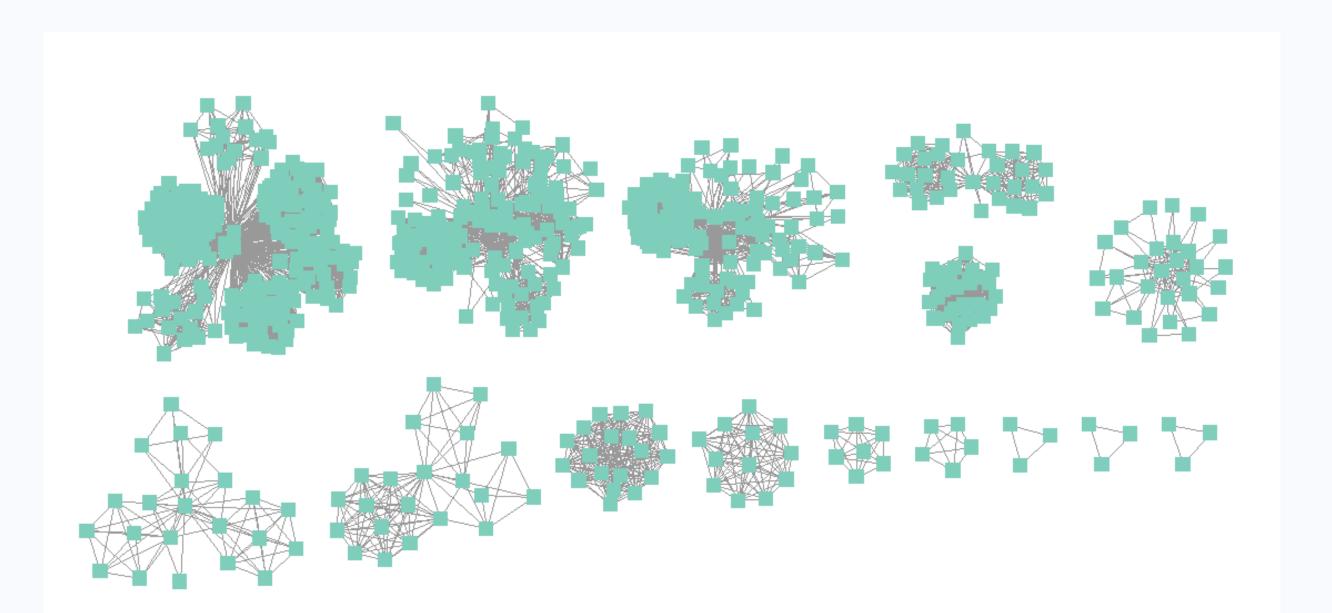
Department of Physics and Astronomy - Northwestern University

Abstract

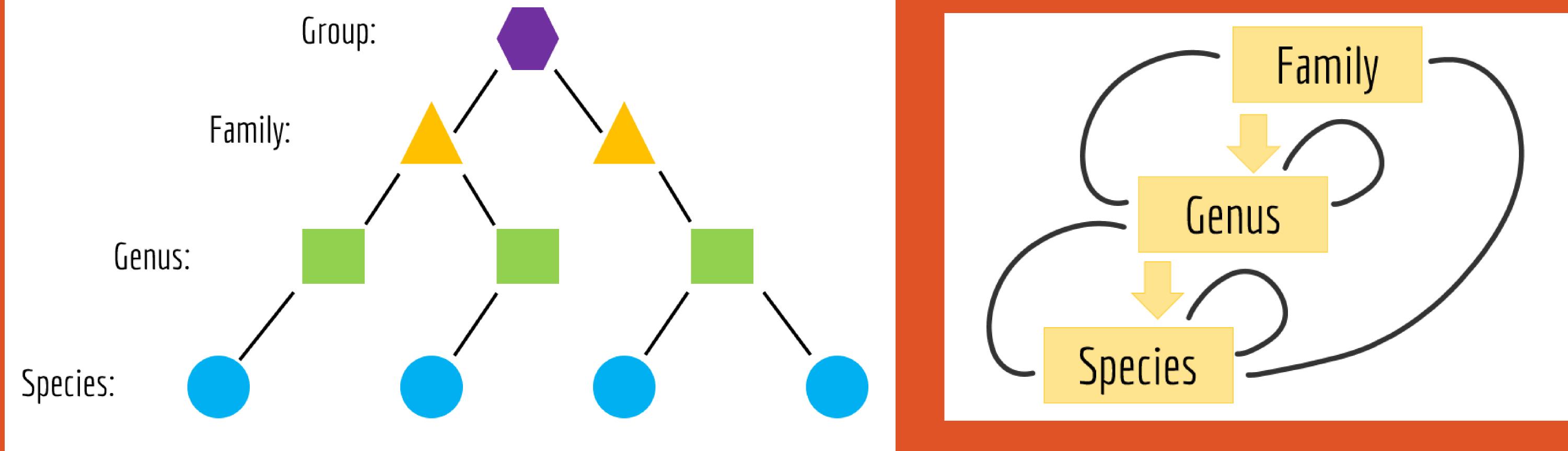
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

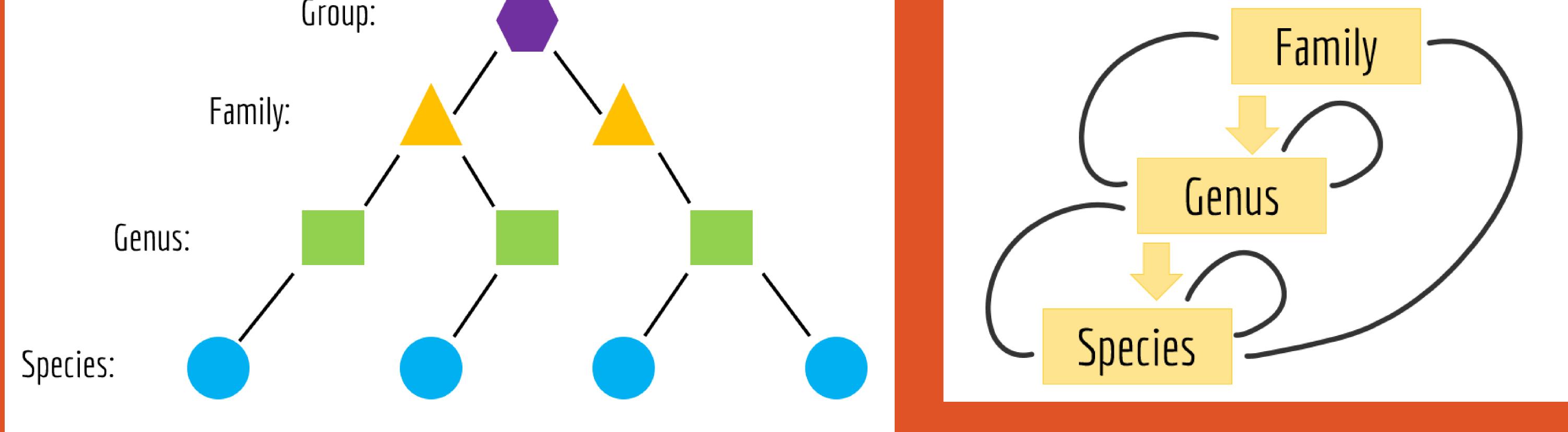
What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.



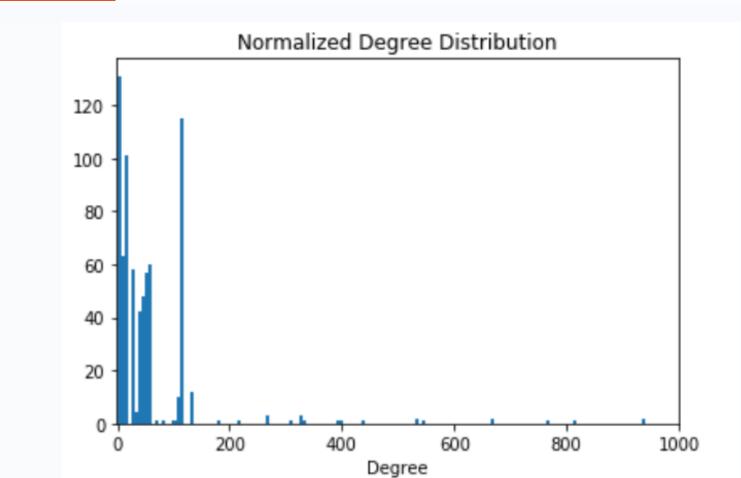
Method





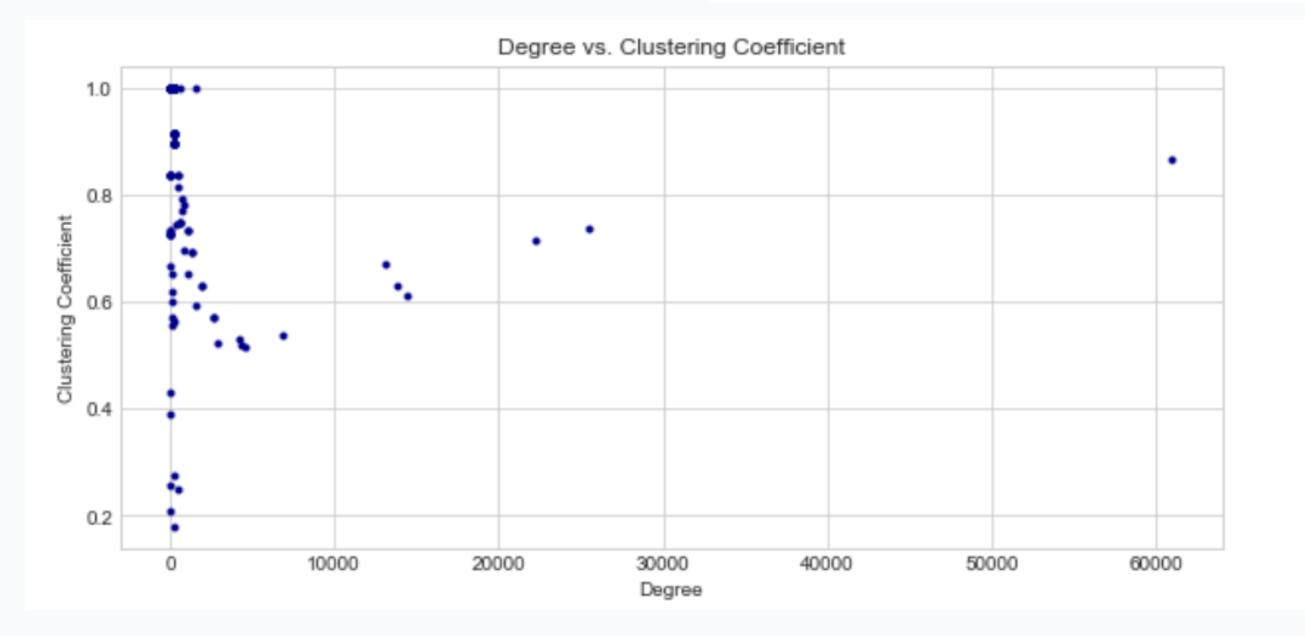
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

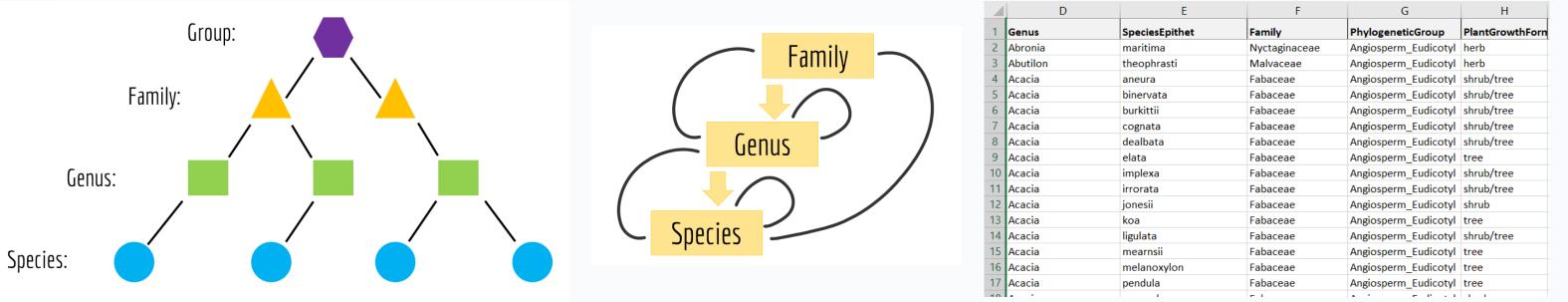
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

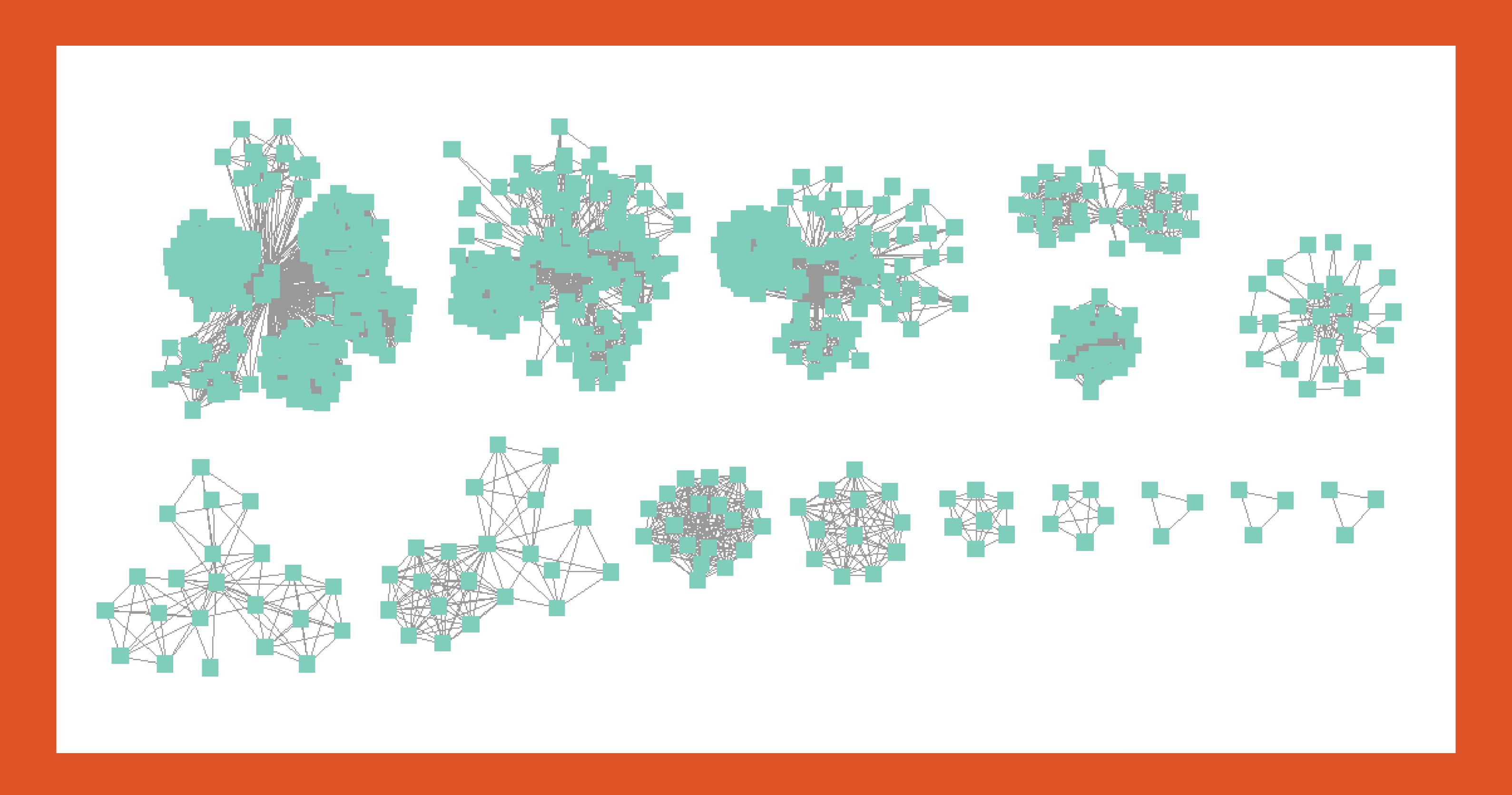
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the TRY Plant Trait Database. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

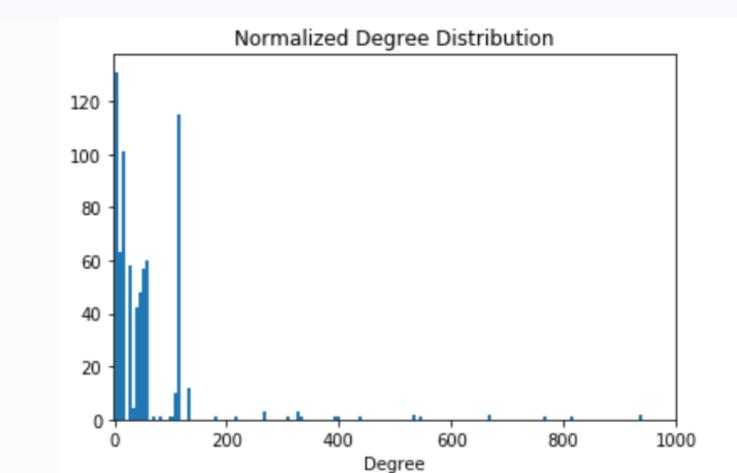


12	Acacia	Jonesii	Fabaceae	Angiosperm_Eudicotyi	shrub
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10	· ·	1	e 1	A 1	1.1.1



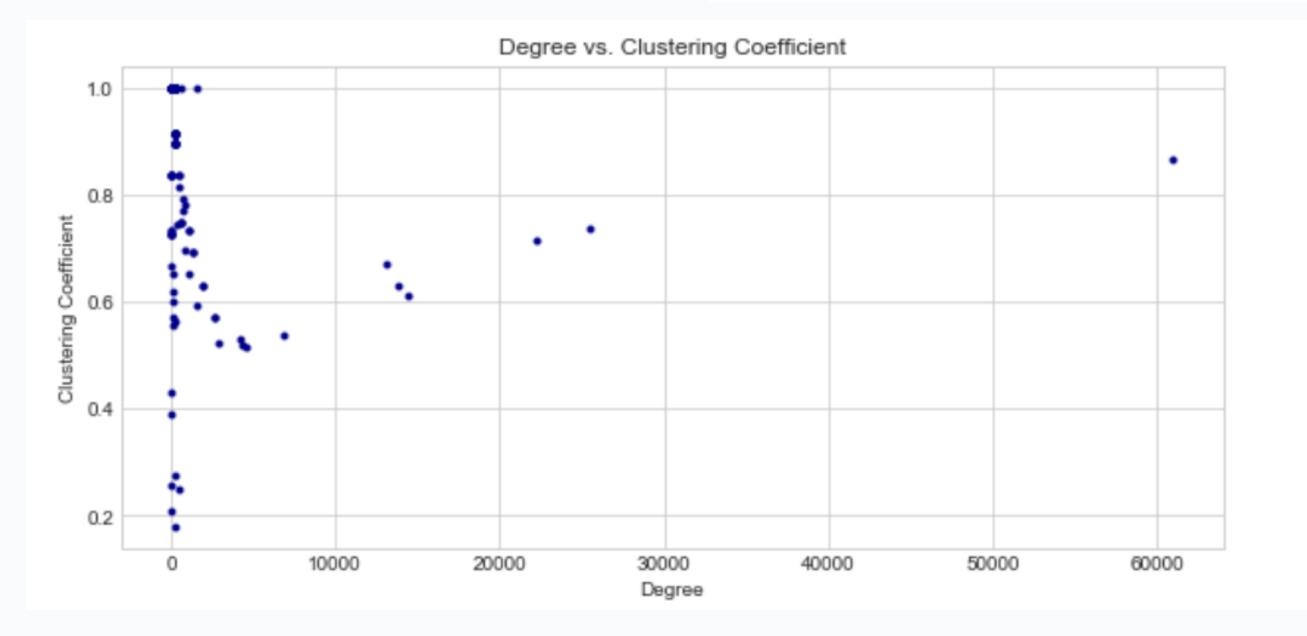
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

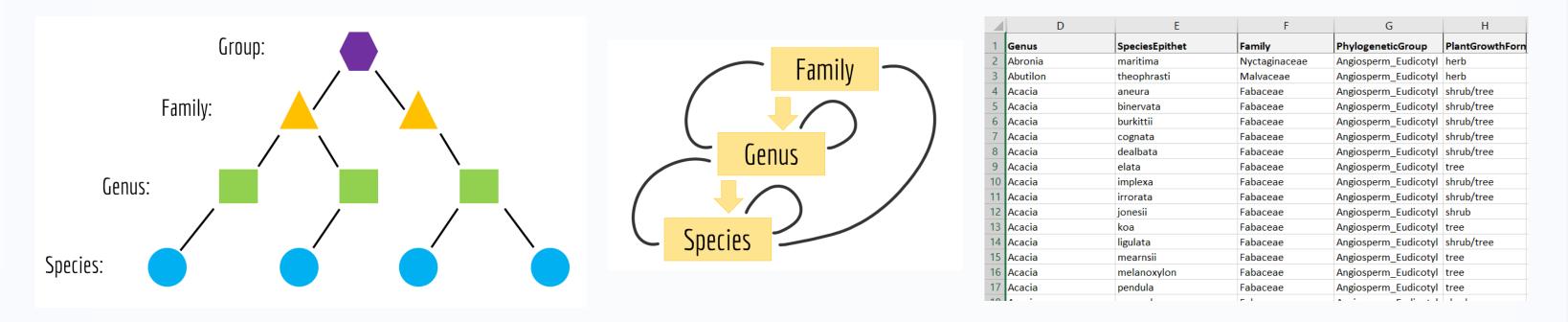
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

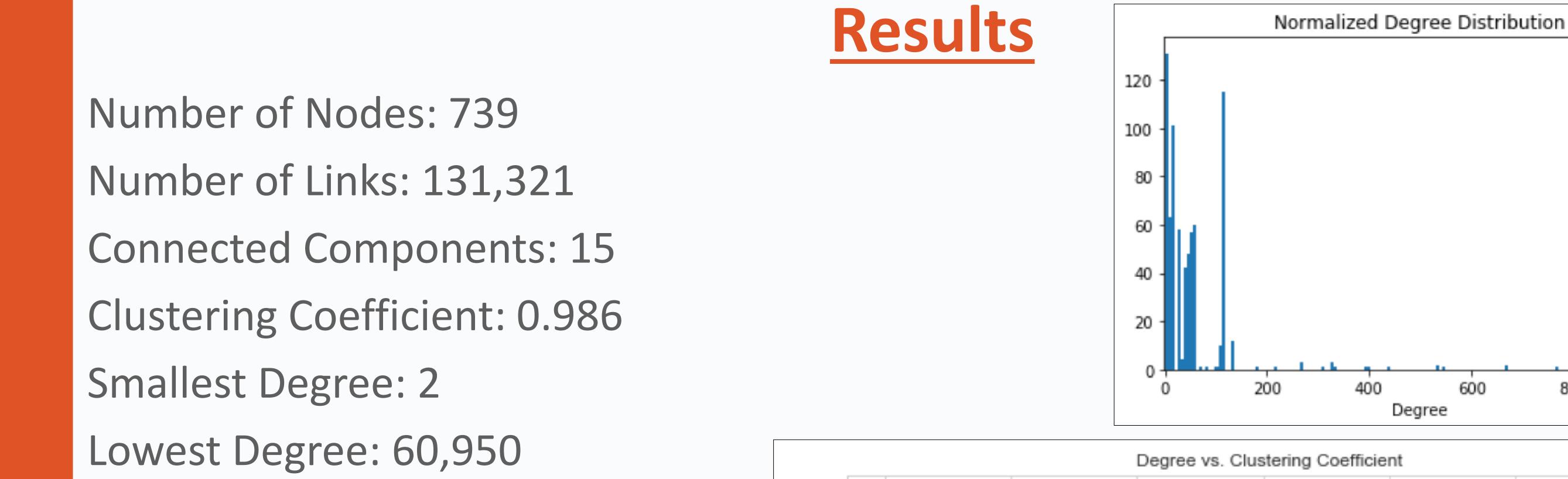
What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

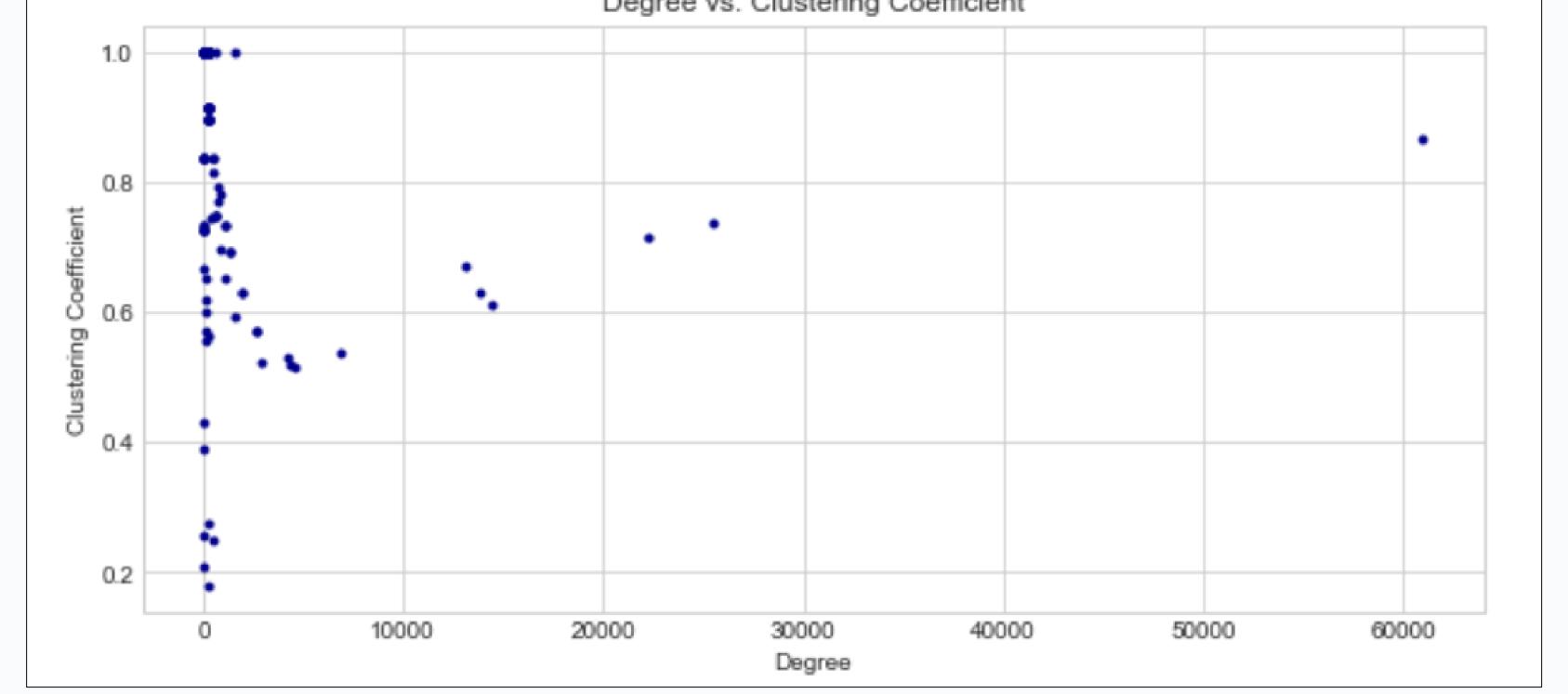
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

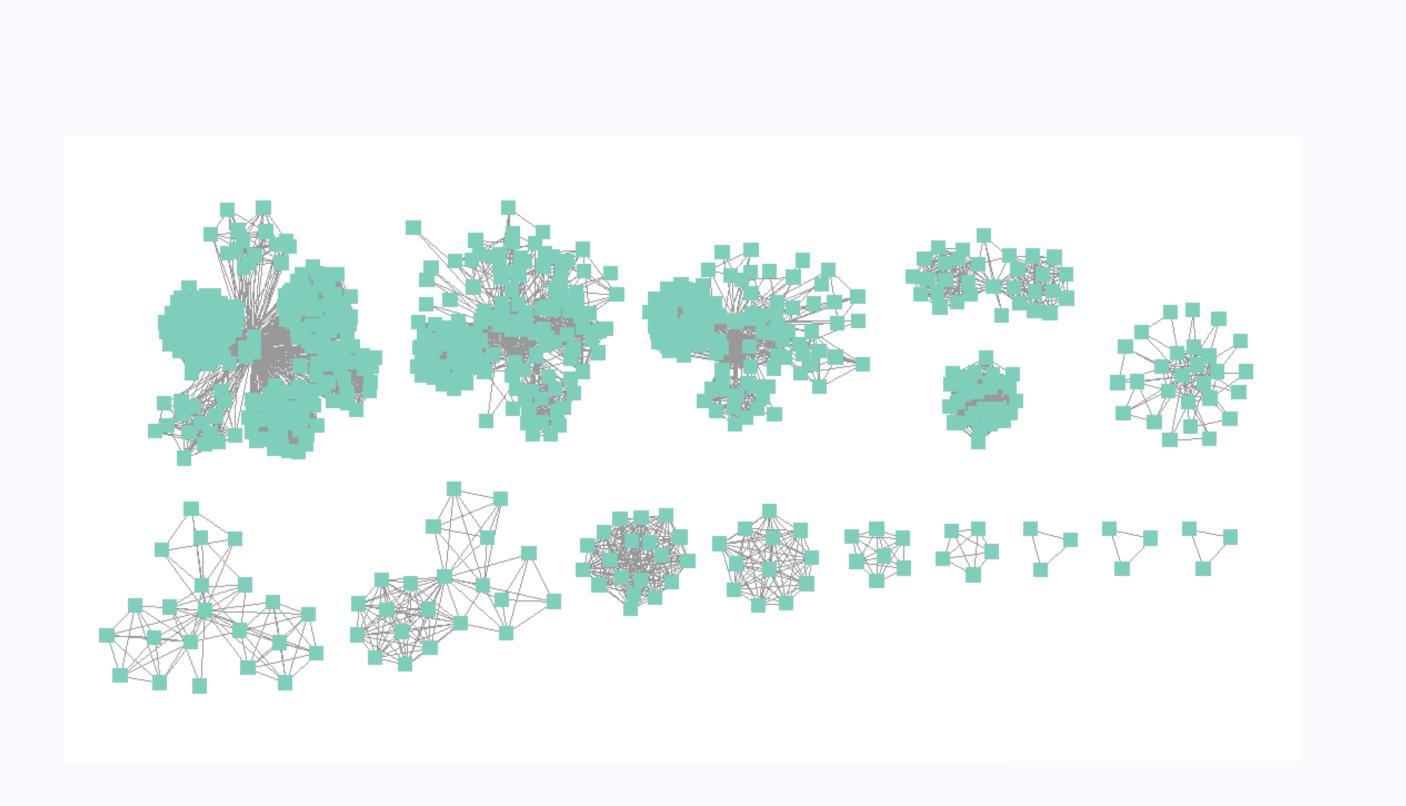
Method

We began with data from the *TRY Plant Trait Database*. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.









Discussion

800

1000

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not

give us the most useful information.

Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

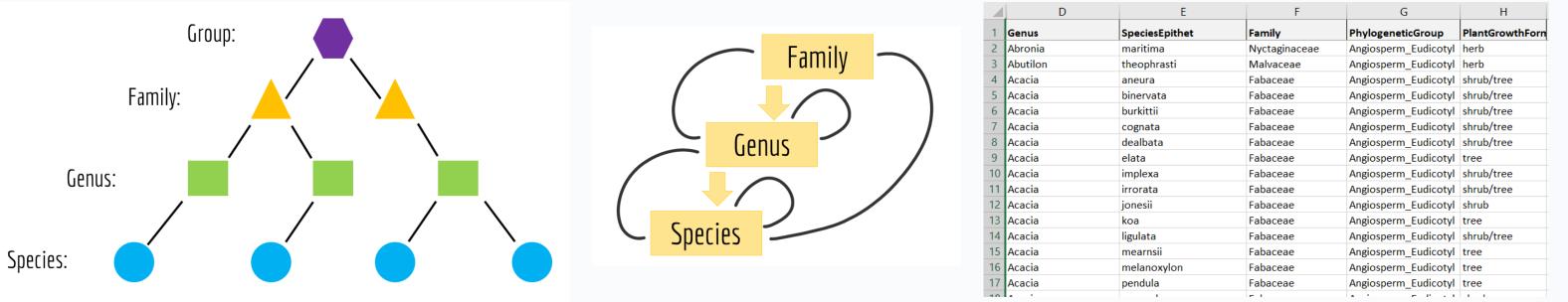
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

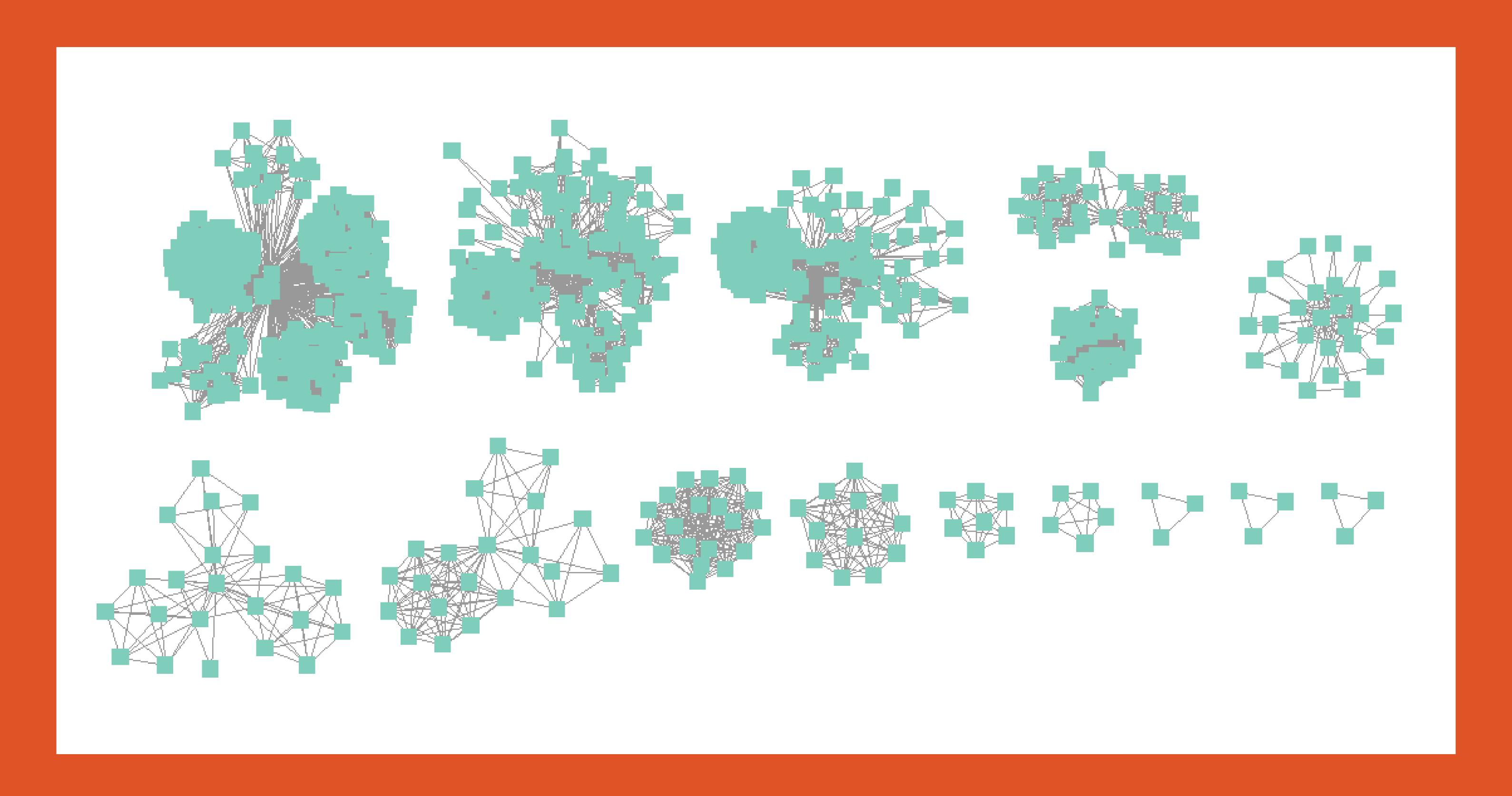
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the TRY Plant Trait Database. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

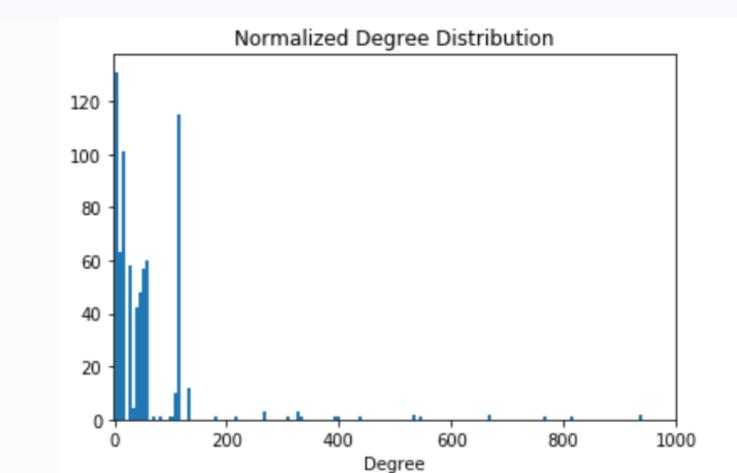


12	Acacia	Jonean	Tabaccac	Angiosperin_Educedy	SHIUD
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10	· ·		e 1	A 1	



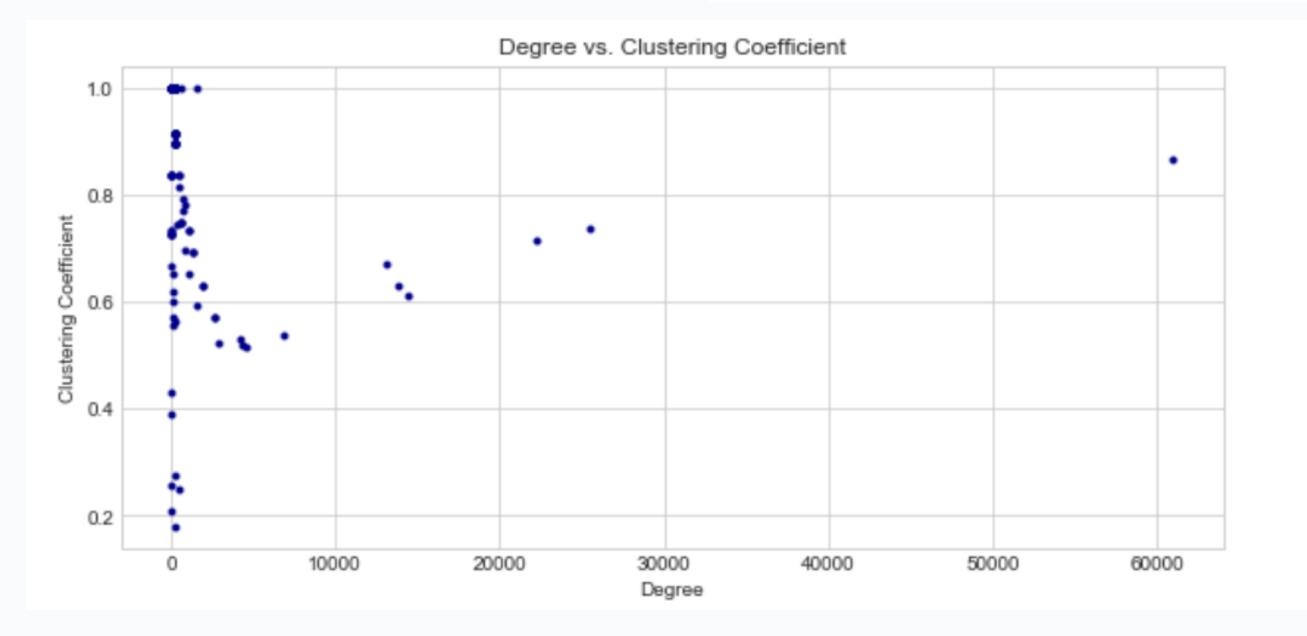
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

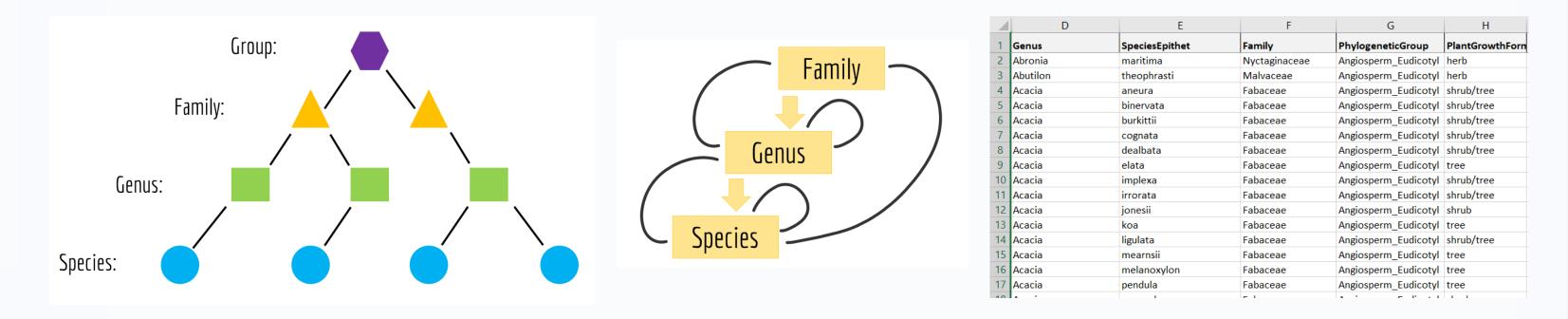
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the *TRY Plant Trait Database*. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

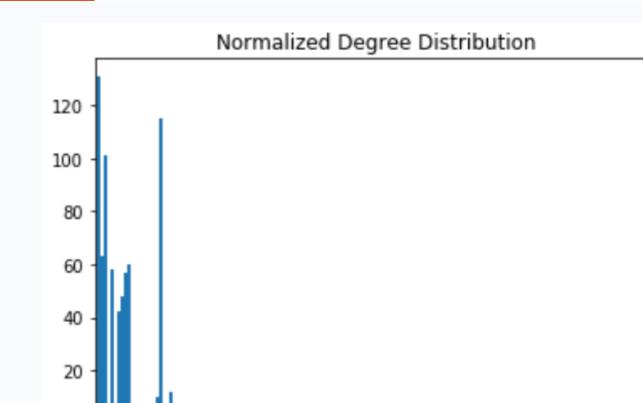


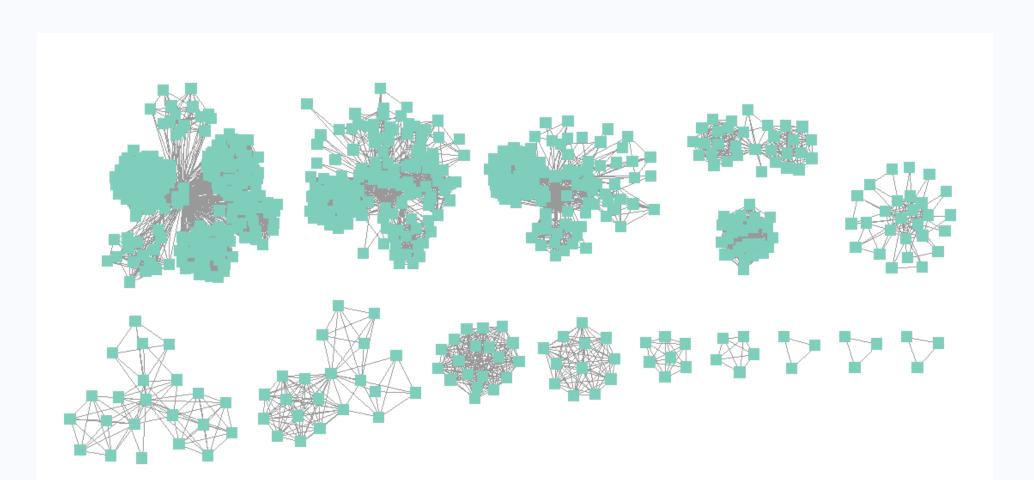
Discussion

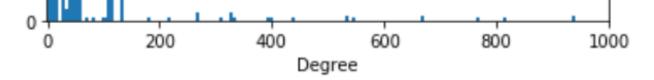
For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.

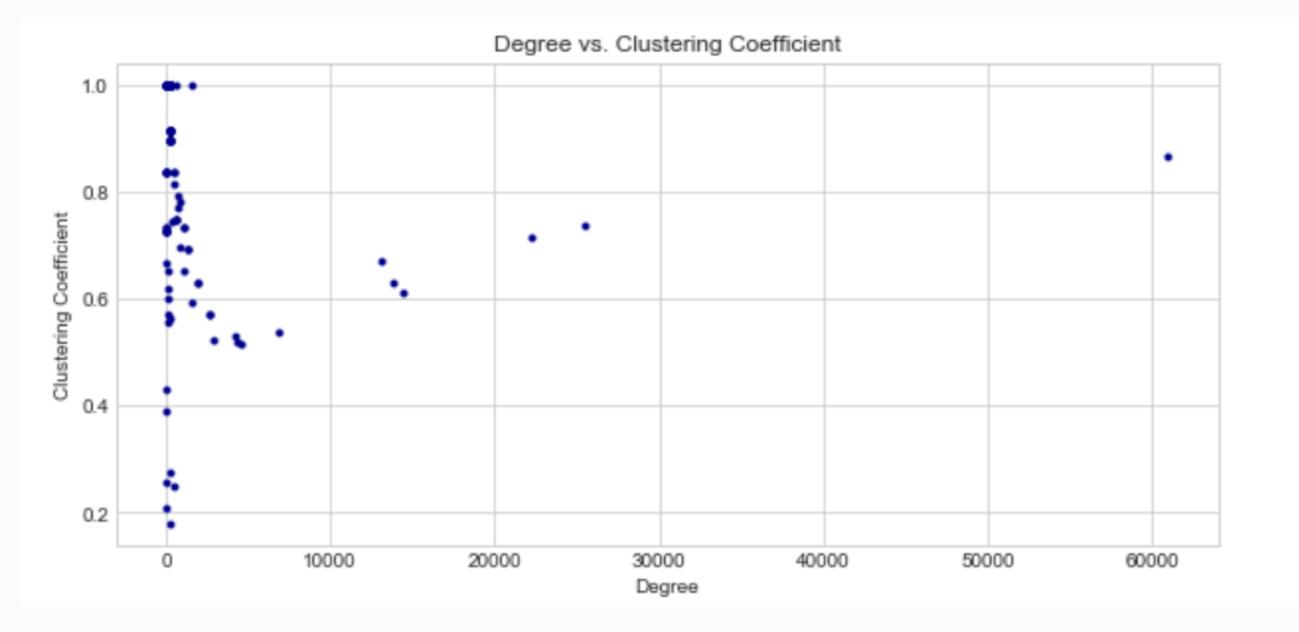
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950









Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

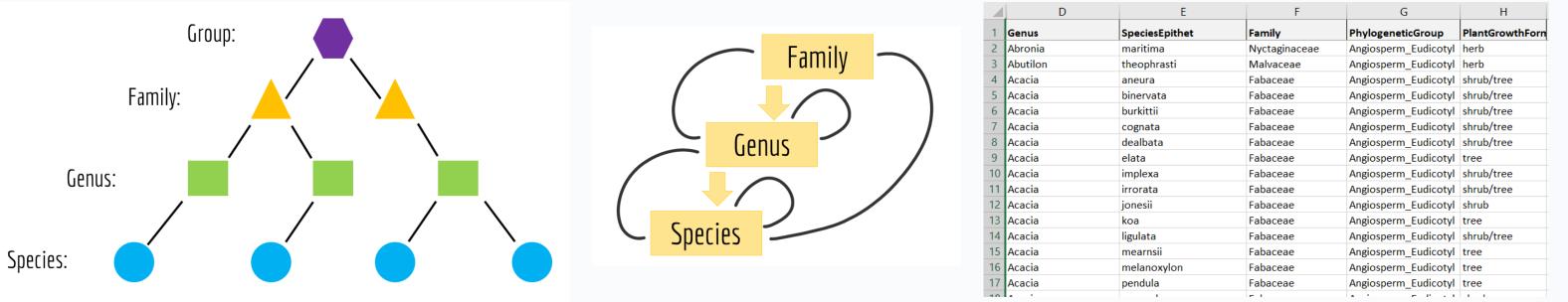
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

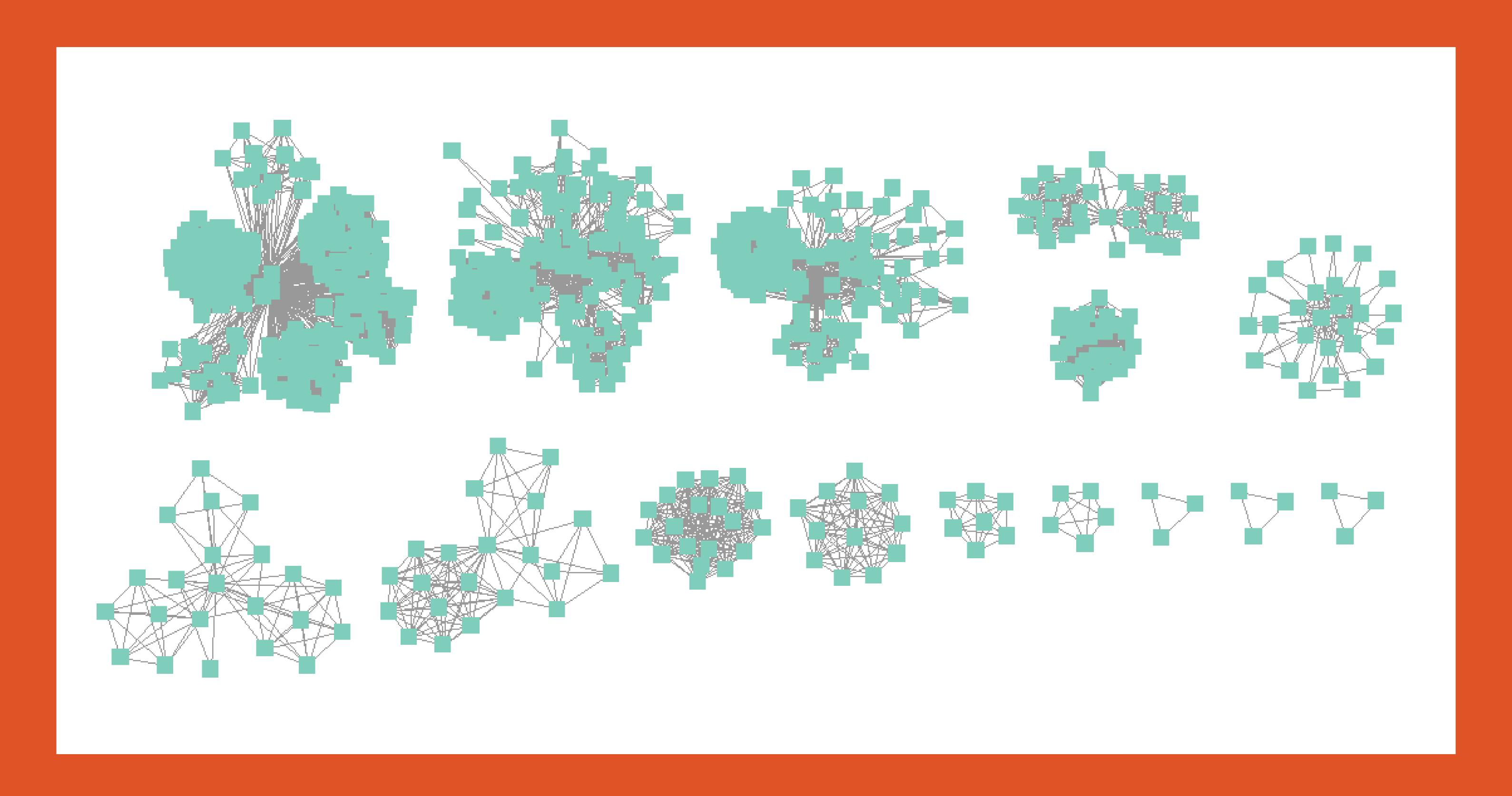
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the TRY Plant Trait Database. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

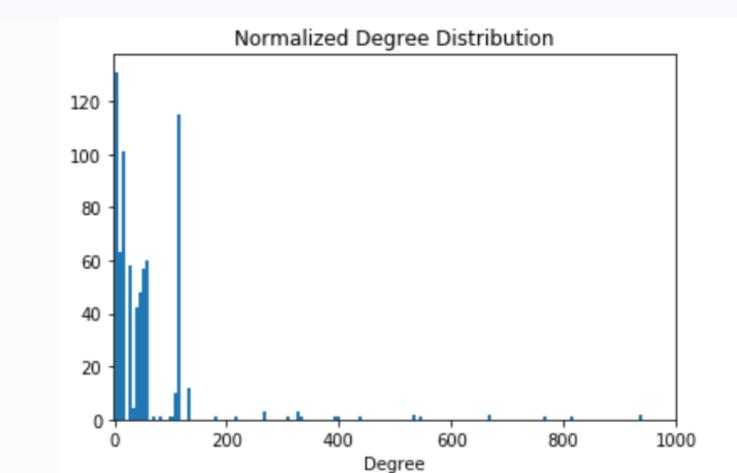


12	Acacia	Jonean	Tabaccac	Angiosperin_Educedy	SHIUD
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10	· ·		e 1	A 1	



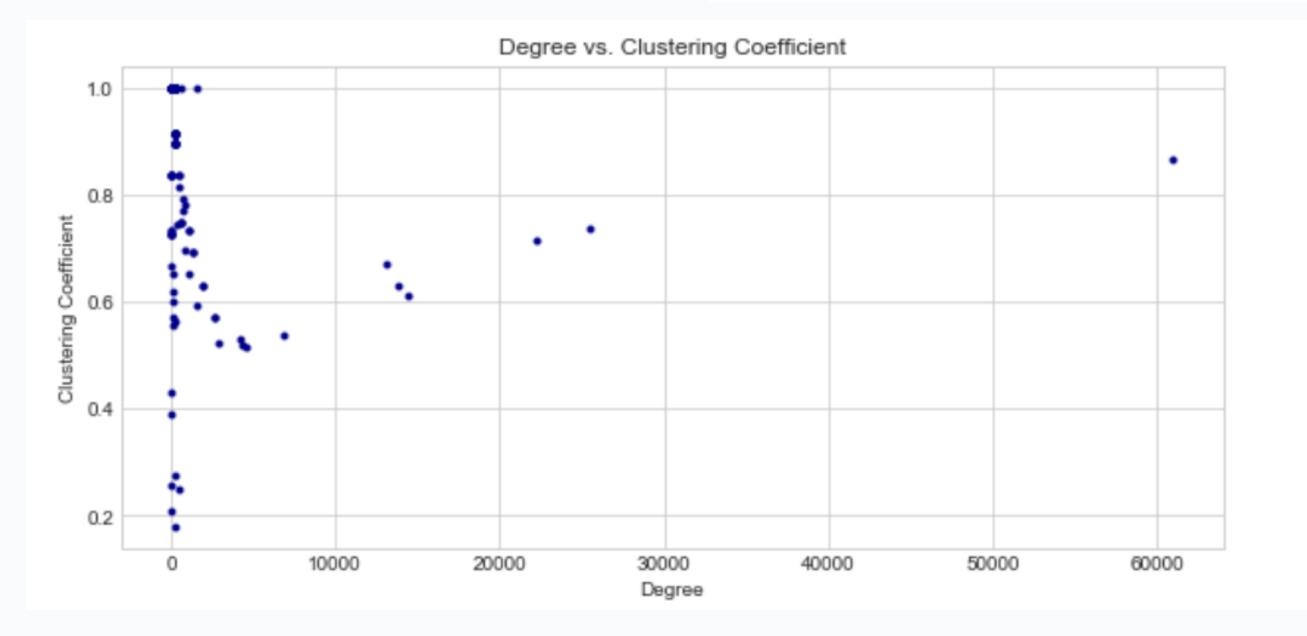
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

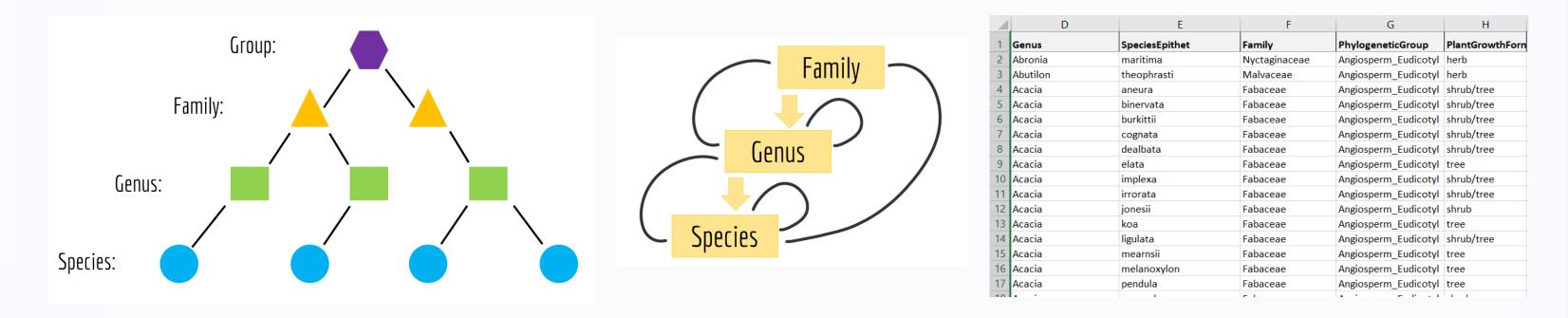
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group onto a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the *TRY Plant Trait Database*. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.



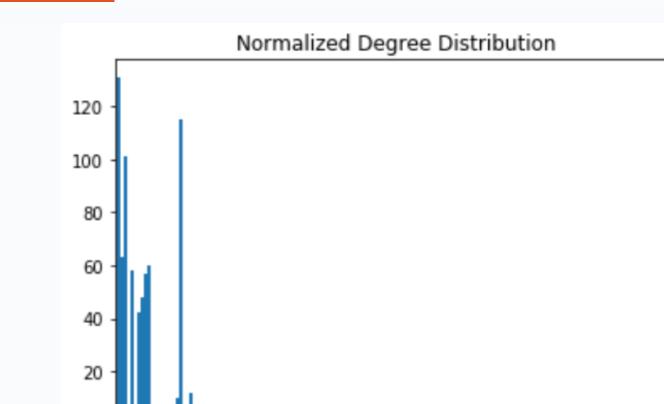
Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network

to a dataset with ground truth data on genetic characteristics.

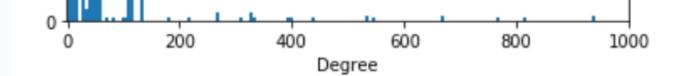
Results

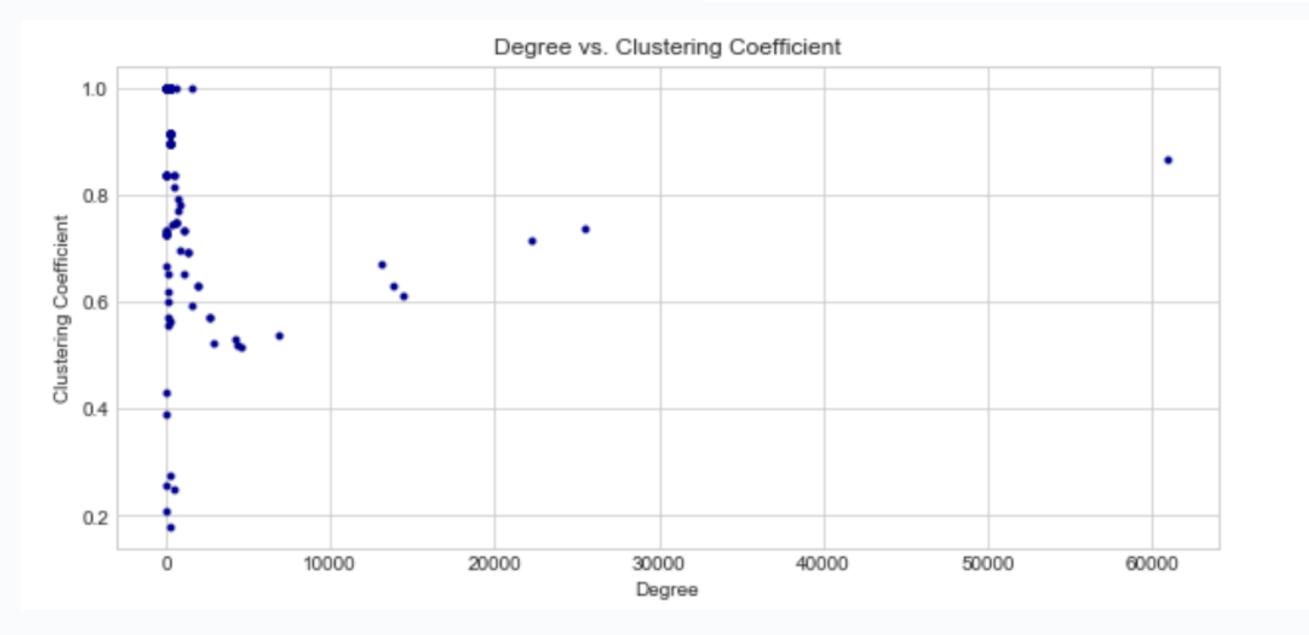
Number of Nodes: 739
Number of Links: 131,321
Connected Components: 15
Clustering Coefficient: 0.986
Smallest Degree: 2
Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.





Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).

Department of Physics and Astronomy - Northwestern University

Abstract

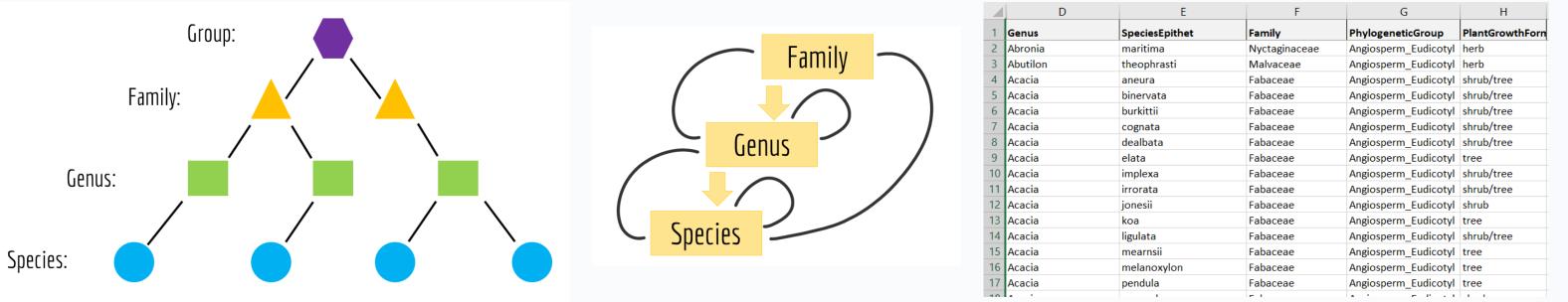
Plant taxonomic classification is based on observable, macroscopic shared characteristics.

What would a classification system based on genetic characteristics (number of genes, number of copies, etc.) look like? How do genetic characteristics relate to our current classification system?

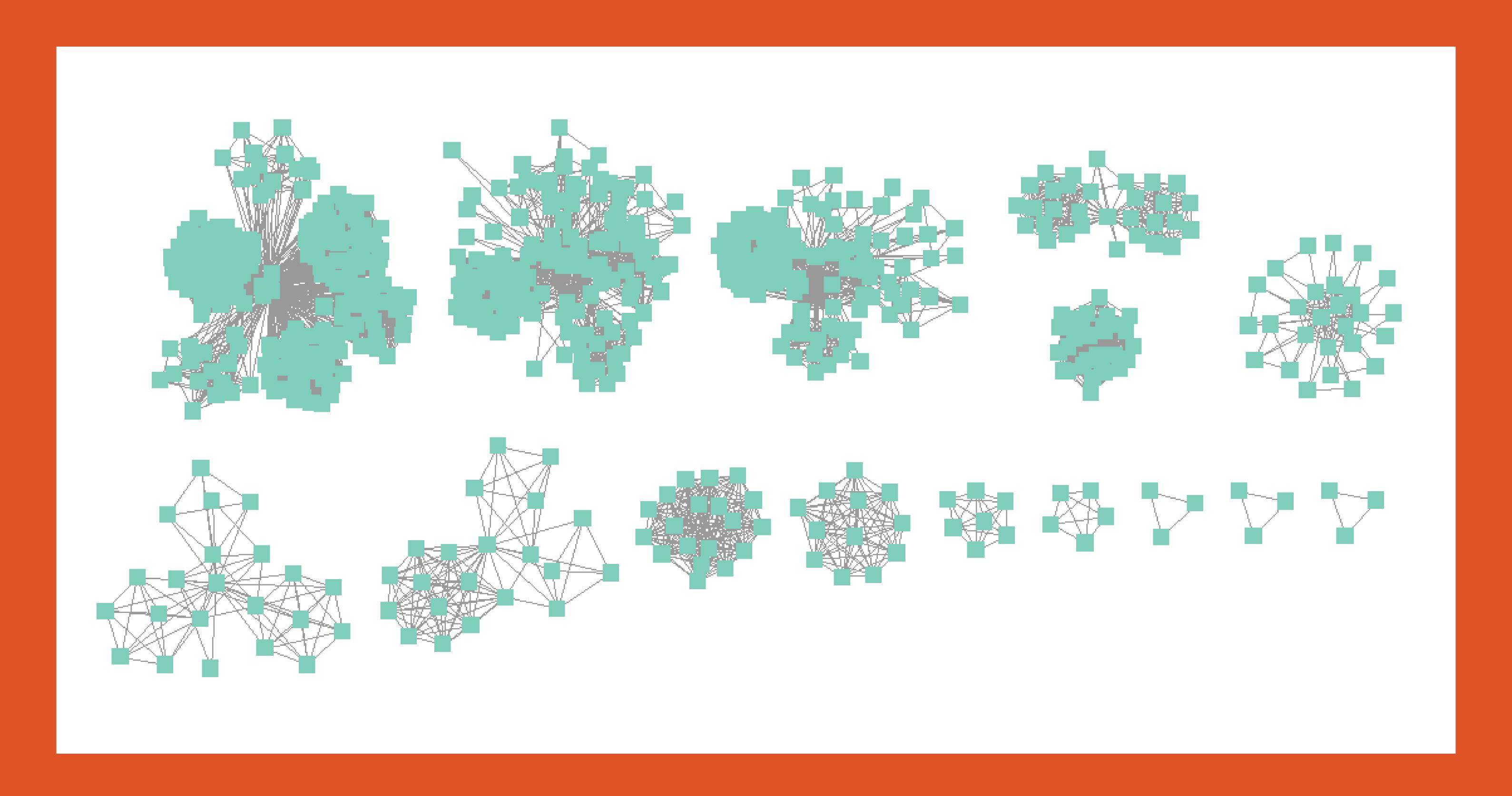
We begin to answer these questions studying the tripartite network for the Gymnosperm taxonomic group as a single network. The original network has a hierarchical structure that is difficult to gain information from, thus we will project this network. The three kinds of nodes for this tripartite network are the taxonomic family, genus, and species.

Method

We began with data from the TRY Plant Trait Database. There were 66,043 species from ~10 groups in the database. Our analysis was narrowed to one group, the Gymnosperms, plants with unprotected seeds including conifers, cycads, and ginkos. In this group, there are 15 families, 77 genera, and 647 species. Links were formed between species in the same genus, genera in the same family, species and its genera, genera and its family, and species and its family. Cytoscape was used to analyze this projection network.

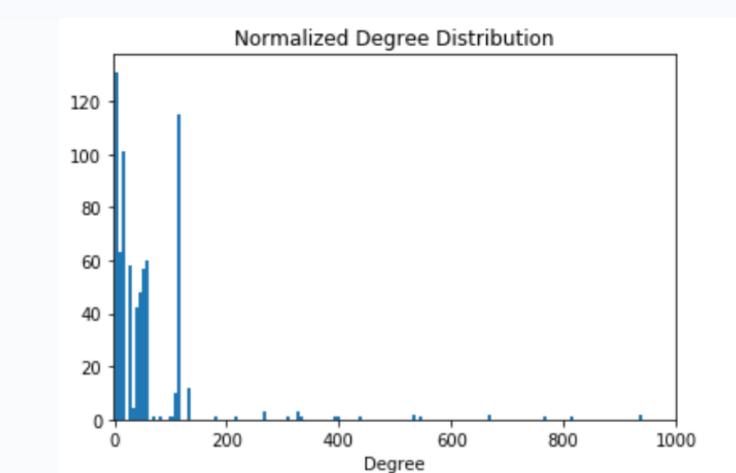


12	Acacia	Jonean	Tabaccac	Angiosperin_Educedy	SHIUD
13	Acacia	koa	Fabaceae	Angiosperm_Eudicotyl	tree
14	Acacia	ligulata	Fabaceae	Angiosperm_Eudicotyl	shrub/tree
15	Acacia	mearnsii	Fabaceae	Angiosperm_Eudicotyl	tree
16	Acacia	melanoxylon	Fabaceae	Angiosperm_Eudicotyl	tree
	Acacia	pendula	Fabaceae	Angiosperm_Eudicotyl	tree
10	· ·		e 1	A 1	



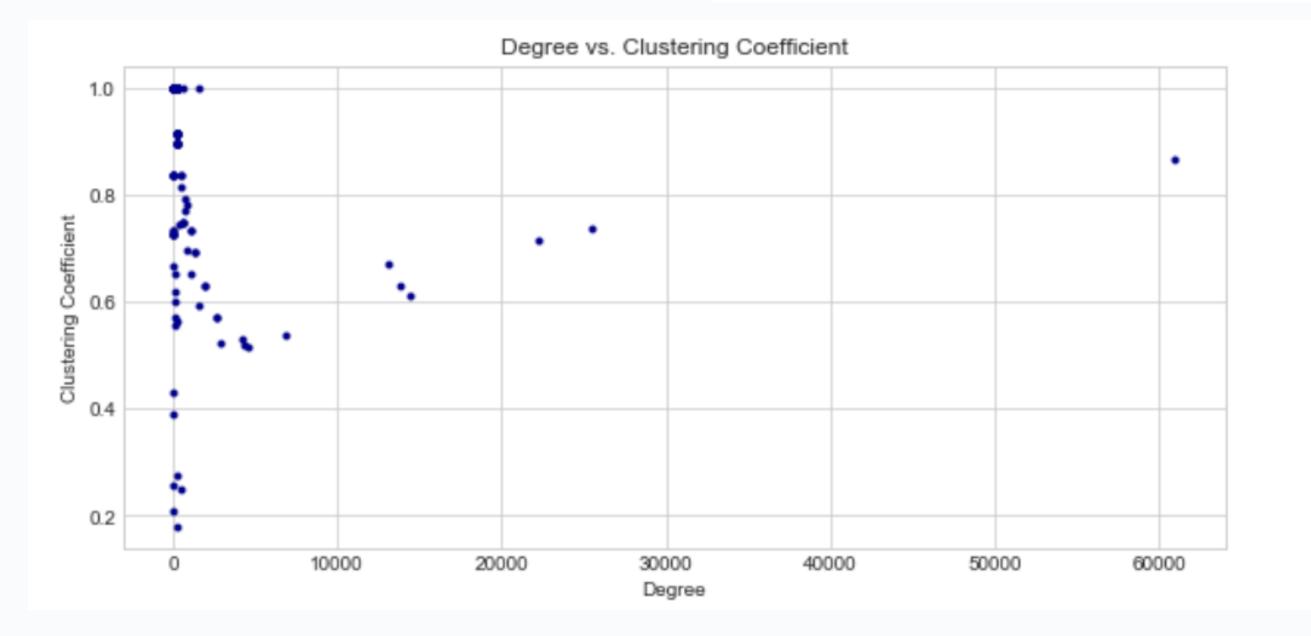
Results

Number of Nodes: 739 Number of Links: 131,321 Connected Components: 15 Clustering Coefficient: 0.986 Smallest Degree: 2 Lowest Degree: 60,950



Discussion

For our plant taxonomic network projection, the number of nodes is the sum of the families, genera, and species in the taxonomic group, Gymnosperms, thus is exactly what was expected. The number of possible links for 739 nodes follows $\frac{N(N-1)}{2} = 272,691$, whereas the number of links is 131,321. This value makes is what one might expect, since the nodes from different families (components) are by definition not able to form a link. There are 15 connected components, just what one might predict since there are 15 families in our dataset. The clustering coefficient is very close to 1. This is what one would expect for each component is very near fully connected. Since the network is unweighted, the degree distribution does not give us the most useful information.



Moving Forward

We should transform this unweighted, projected network to a weighted network. To as the original question, does the taxonomic classification correlate with genetic classifications, we need to compare the results of the analysis of the weighted network to a dataset with ground truth data on genetic characteristics.

Acknowledgments

The *TRY* initiative and data base is hosted, developed and maintained by J. Kattge and G. Bönisch (Max Planck Institute for Biogeochemistry, Jena, Germany).