

The hypermodular structure of tripartite ecological networks

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Contents

README	3
Datasets	4
Dataset 1 : AZORES	4
Dataset 2 : AZORES	9
Dataset 3 : AZORES	14
Dataset 4 : GALAPAGOS	19
Dataset 5 : DORSET	24
Dataset 6 : NORWOOD	29
Dataset 7 : NORWOOD	34
Dataset 8 : NORWOOD	39
Dataset 9 : BORNEO	44
Dataset 10 : COIMBRA	49
Dataset 11 : BEIRA	54
Dataset 12 : PURBECK	59
Dataset 13 : HAWAII	64
Dataset 14 : BRISTOL	69
Dataset 15 : POLAND	74
Dataset 16 : GALAPAGOS	79
Dataset 17 : MOZAMBIQUE	84
Dataset 18 : NEW ZEALAND	89
Dataset 19 : CORDOBA1	94
Dataset 20 : CORDOBA2	99
Dataset 21 : CORDOBA2	104
Dataset 22 : CORDOBA2	109
Dataset 23 : CORDOBA2	114
Dataset 24 : CORDOBA2	119
Dataset 25 : COSTA RICA	124
Dataset 26 : MULLER	127
Dataset 27 : SERENQUETI	130
Dataset 28 : dattilo	133
Dataset 29 : hackett HH	136
Dataset 30 : hackett HH	141
Dataset 31 : SMOKY MOUNTAINS	146
Dataset 32 : SHINOHARA	149
Dataset 33 : Vitali	154
Dataset 34 : Zhang	159
Dataset 35 : ARAUJO	164
Dataset 36 : BASSET BCI	169
Dataset 37 : BASSET BCI	174

Dataset 38 : BASSET KHC	179
Dataset 39 : BASSET WAN	184
Dataset 40 : BASSET WAN	189
Dataset 41 : dattilo -REMOVED-	194
Dataset 42 : hackett HH -REMOVED-	197
Dataset 43 : hackett HH -REMOVED-	202
Dataset 44 : hackett TP -REMOVED-	207
Dataset 45 : hackett TP -REMOVED-	212
Dataset 46 : hackett TP -REMOVED-	217
Dataset 47 : BASSET KHC -REMOVED-	222
Summary of null model analysis	227
Null Model 1	227
Null Model 2	229
Summary of structural analyses	230
Datasets Info	230
Bipartite networks	231
Tripartite networks	232
Forked vs. Stacked	233
Realized Congruence	233
Adjusted Congruence	233
Hypermodularity	233
Mechanism Testing (Mantel tests)	233
DATASET3	233
DATASET14	235
DATASET18	236
DATASET19	237
DATASET20	239
DATASET21	241
DATASET22	242
DATASET23	244
DATASET24	246
DATASET29	247
DATASET30	249
DATASET32	251

README

This document describes step-by-step the results of the study “The hypermodular structure of tripartite ecological networks”.

The PDF was generated by a R Markdown and other files, available at: https://github.com/pinheirorbp/tripartite_hypermodules. Codes to reproduce all analysis are also provided.

Datasets

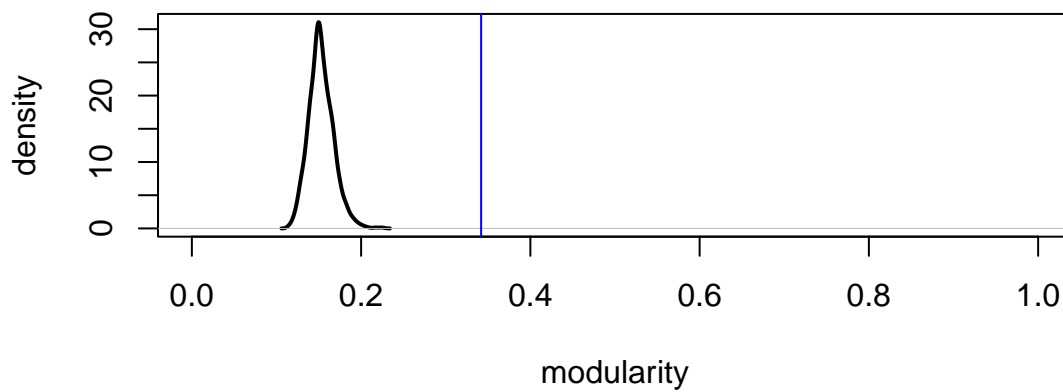
Dataset 1 : AZORES

Topology BN (A-B): Plant - Seed disperser

Modularity

..
Observed Modularity: 0.34
Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

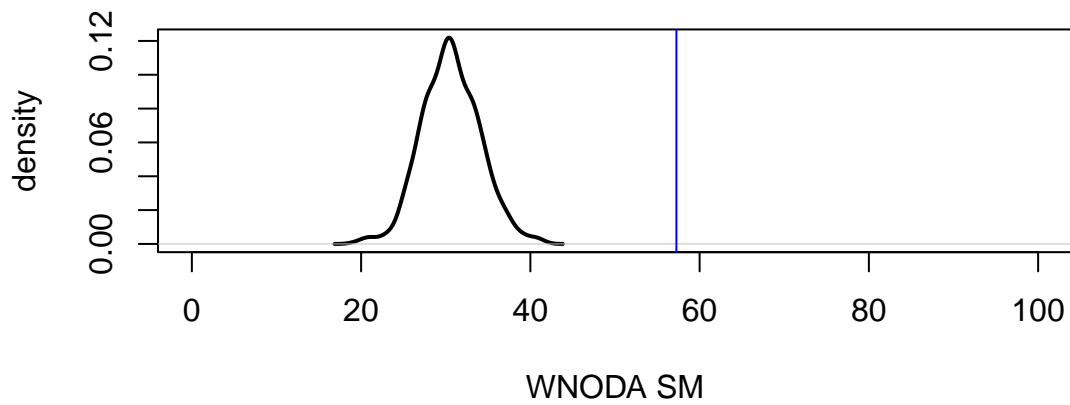


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 30
Nestedness between species in the same module: 57
Nestedness between species in different modules: 19

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

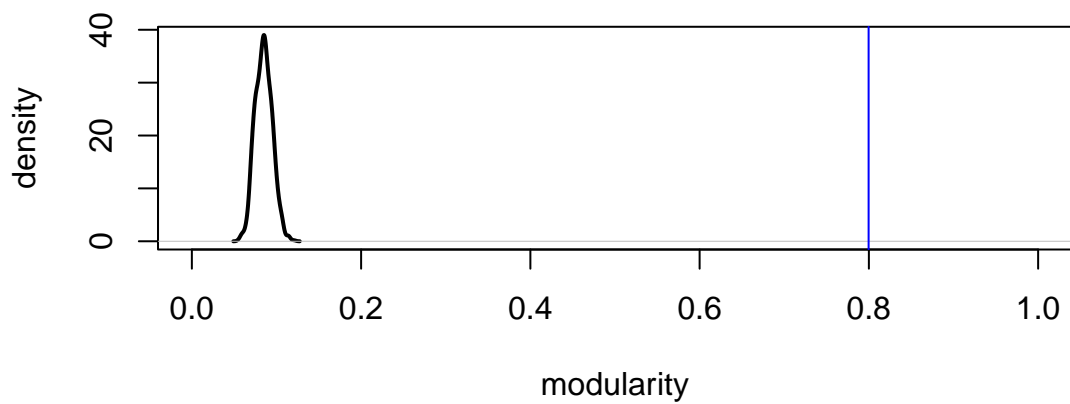
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Seed disperser - Parasite

Modularity

..
 Observed Modularity: 0.8
 Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

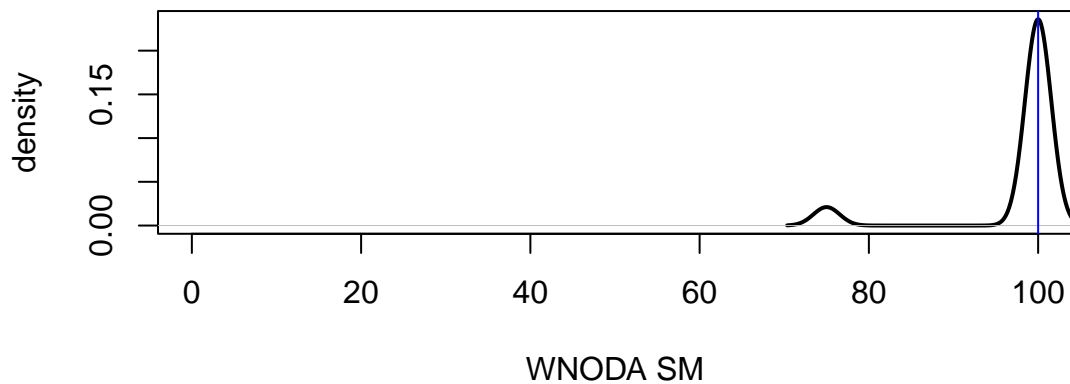


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 3.5
Nestedness between species in the same module 100
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.92

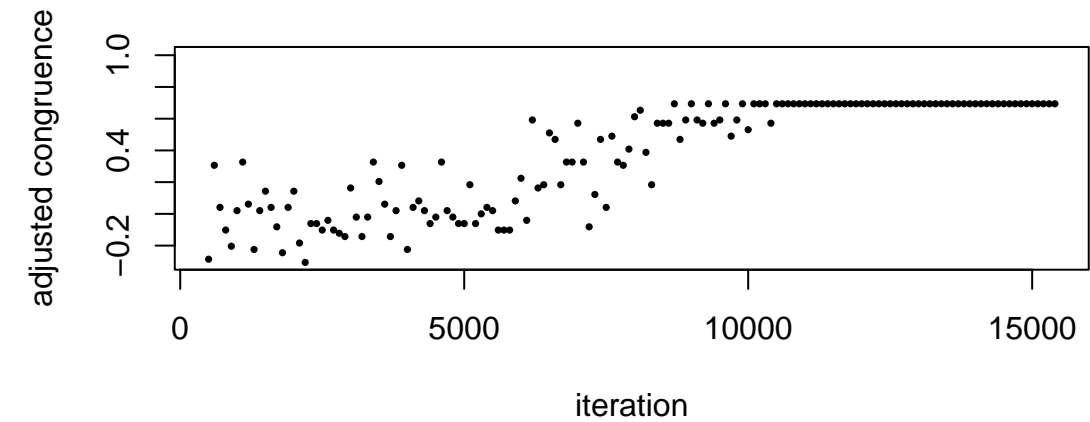
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

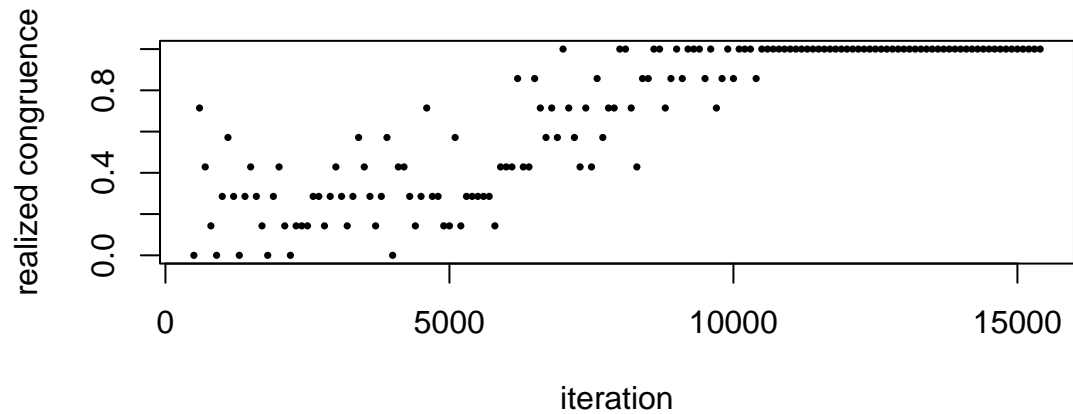
..
BN (A-B) Specialization (H2') 0.38
BN (A-B) Connectance 0.26
BN (B-C) Specialization (H2') 1
BN (B-C) Connectance 0.11
Plant richness in BN (A-B): 41
Seed disperser richness in BN (A-B): 7
Seed disperser richness in BN (B-C): 9
Parasite richness in BN (B-C): 13
Richness of shared Seed dispersers: 9
Number of modules in BN (A-B) 4
Number of modules in BN (B-C) 9

Number of modules in BN (A-B) (only for shared species) 4
Number of modules in BN (B-C) (only for shared species) 7

Hipermodule Congruence
Optimization procedure

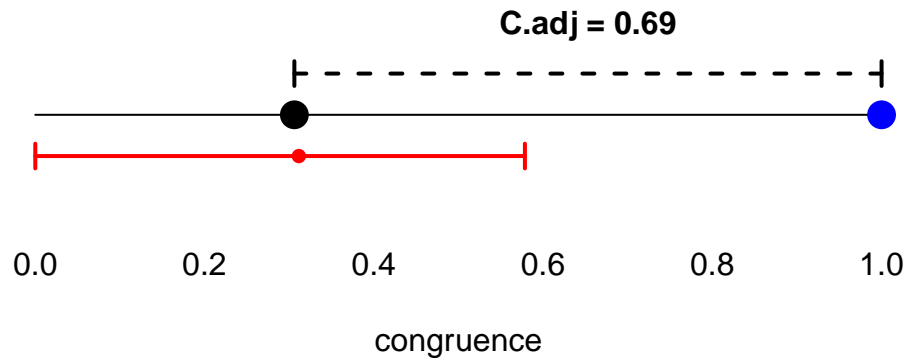


..



Adjusted Congruence: 0.69
Realized Congruence: 1
Hypermodularity: 0.48

Null Model 1

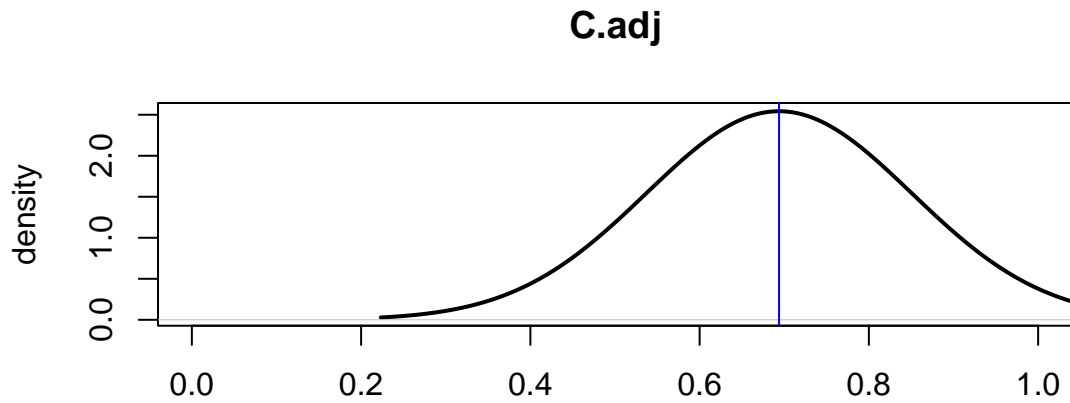


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.005

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

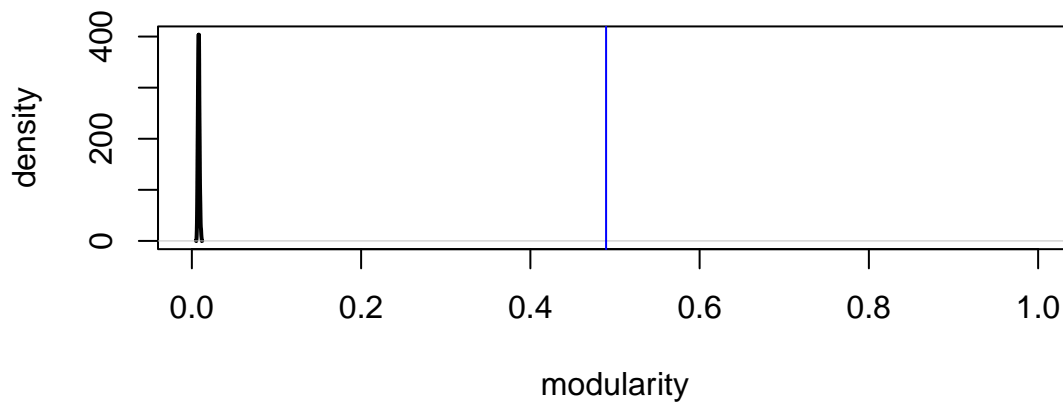
Dataset 2 : AZORES

Topology BN (A-B): Herbivore - Plant

Modularity

..
Observed Modularity: 0.49
Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

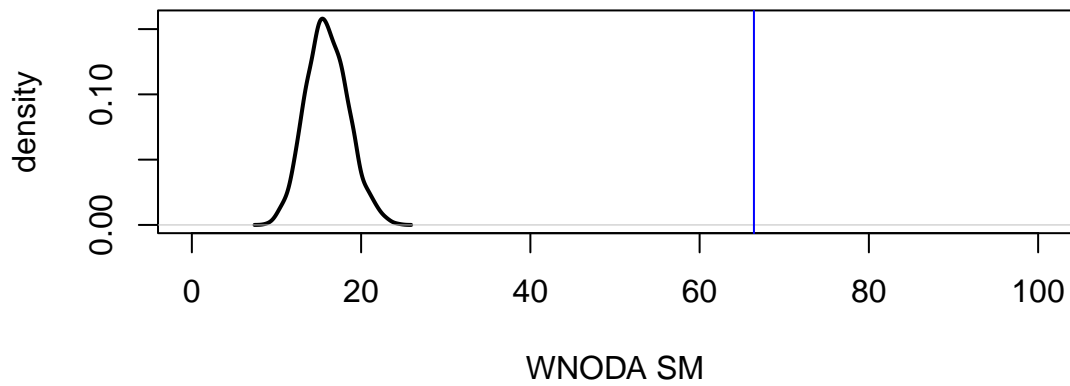


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 28
Nestedness between species in the same module: 66
Nestedness between species in different modules: 19

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

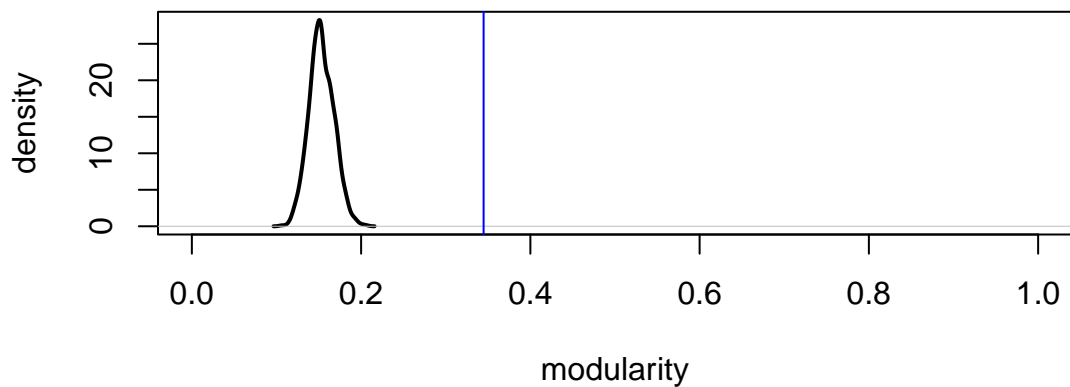
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Seed disperser

Modularity

..
 Observed Modularity: 0.34
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

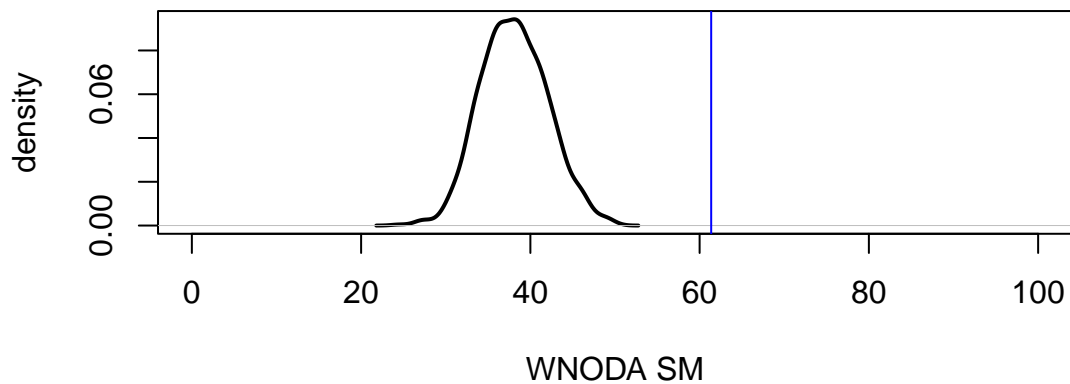


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 30
Nestedness between species in the same module 61
Nestedness between species in different modules 19

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

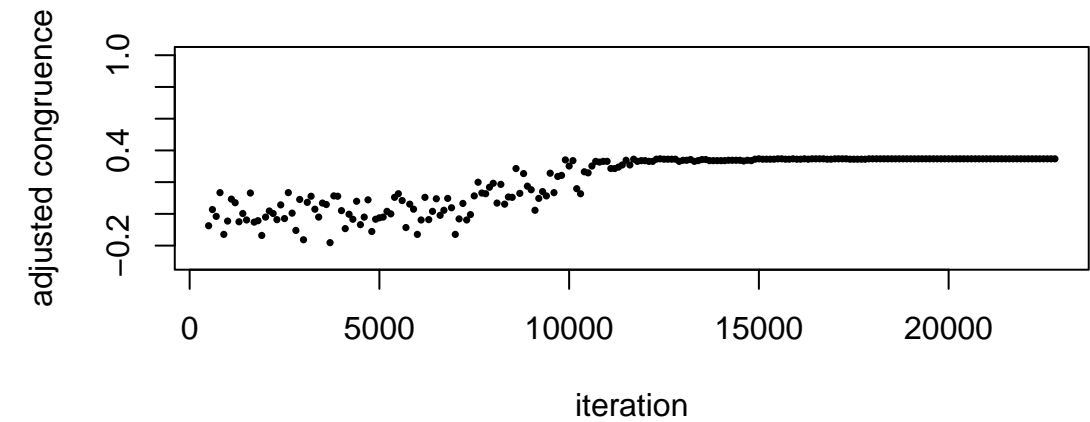
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

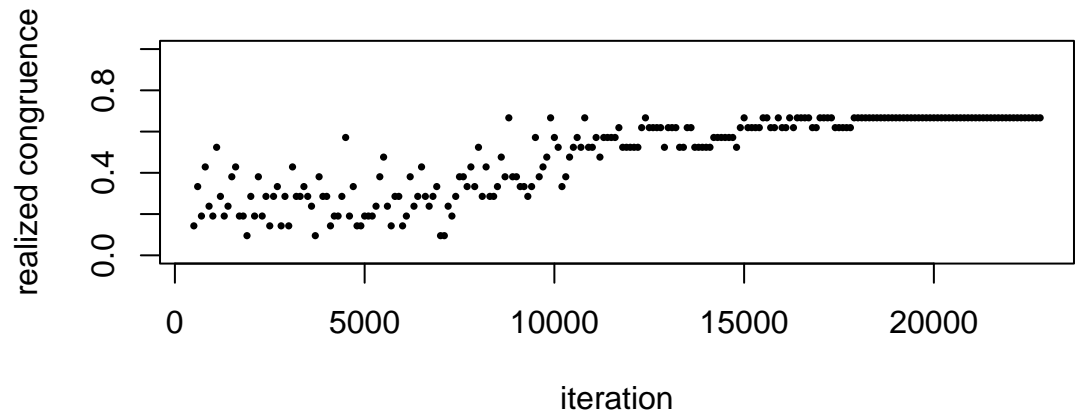
..
BN (A-B) Specialization (H2') 0.54
BN (A-B) Connectance 0.082
BN (B-C) Specialization (H2') 0.38
BN (B-C) Connectance 0.26
Herbivore richness in BN (A-B): 36
Plant richness in BN (A-B): 31
Plant richness in BN (B-C): 41
Seed disperser richness in BN (B-C): 7
Richness of shared Plants:41
Number of modules in BN (A-B) 8
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 8
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

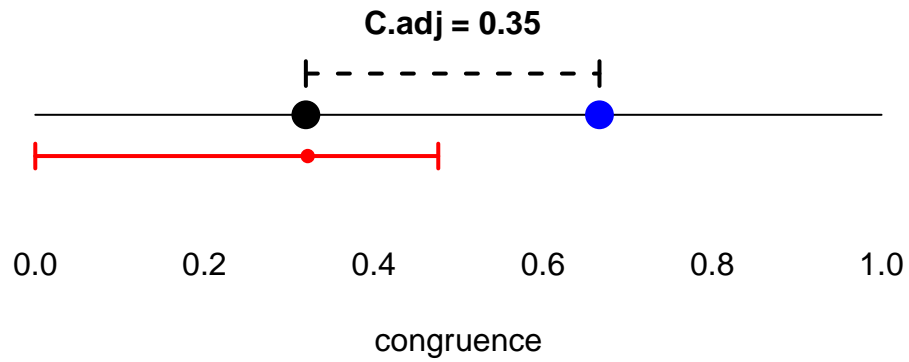


..



..
Adjusted Congruence: 0.35
Realized Congruence: 0.67
Hypermodularity: 0.13

Null Model 1

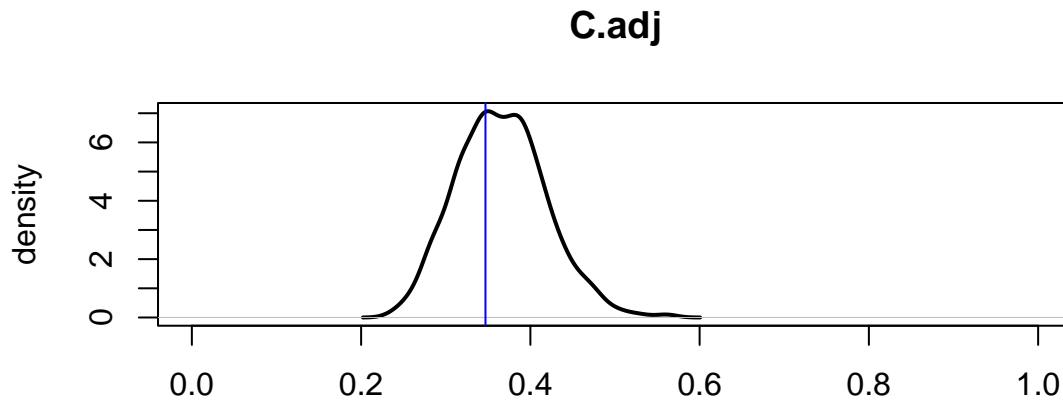


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.001

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.62

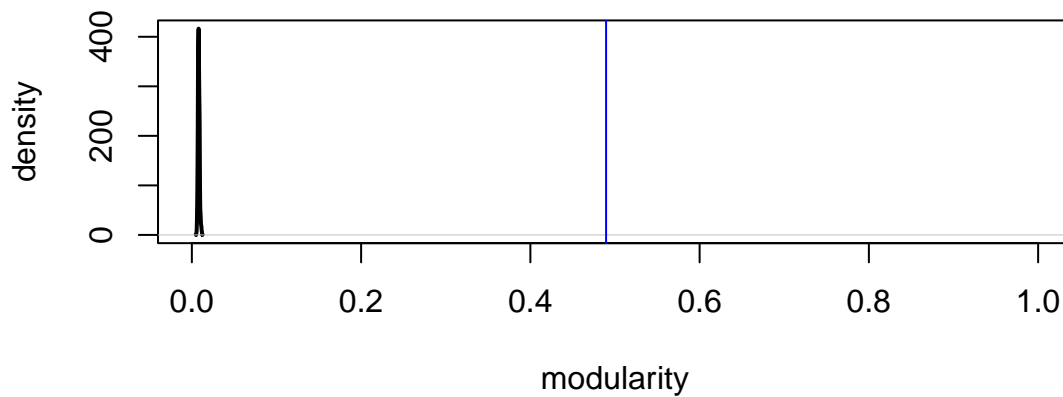
Dataset 3 : AZORES

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.49
Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

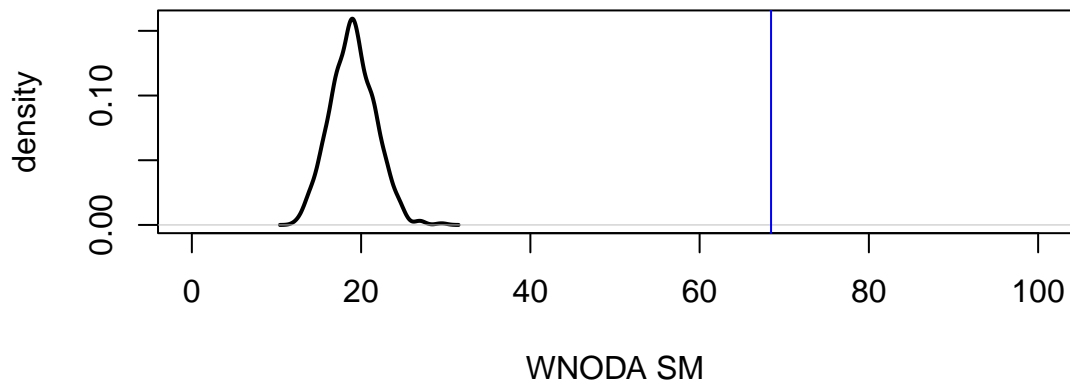


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 28
Nestedness between species in the same module: 68
Nestedness between species in different modules: 19

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

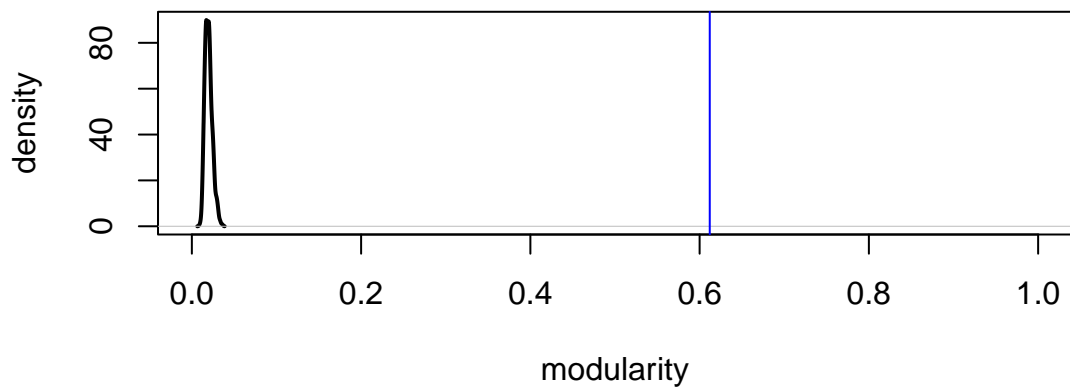
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.61
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

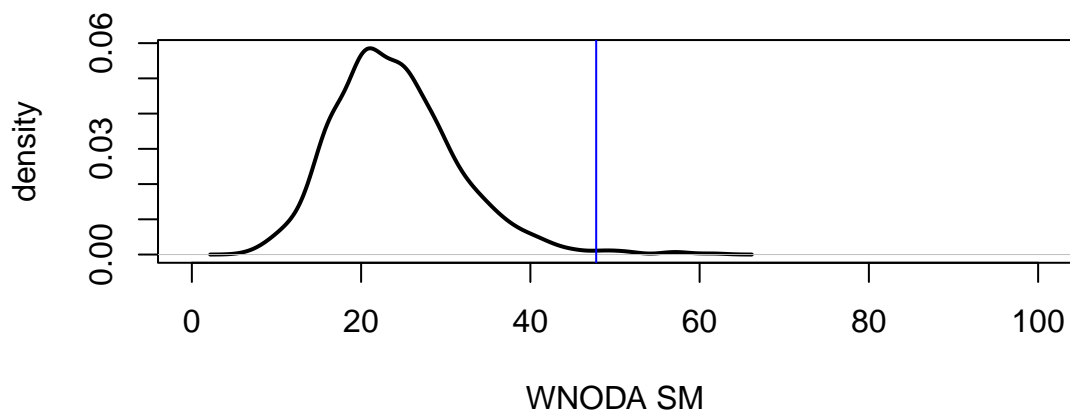


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 11
Nestedness between species in the same module 48
Nestedness between species in different modules 0.73

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.01

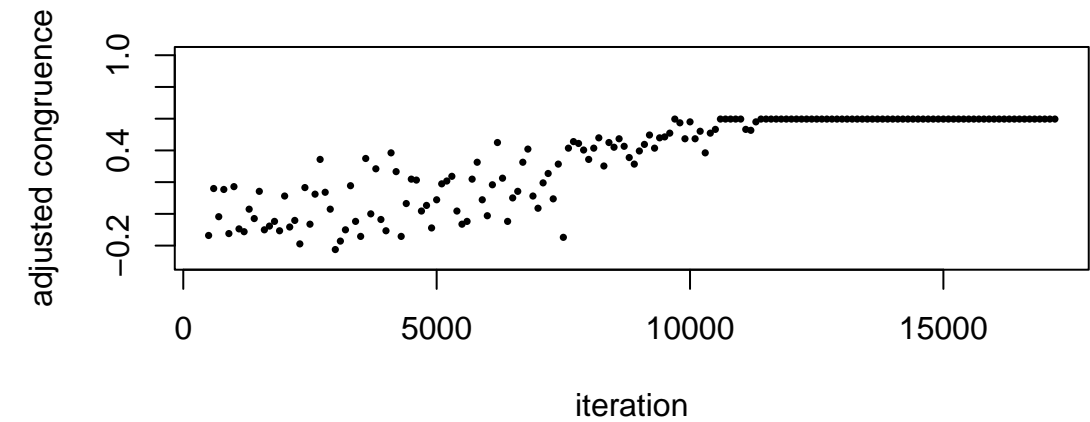
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

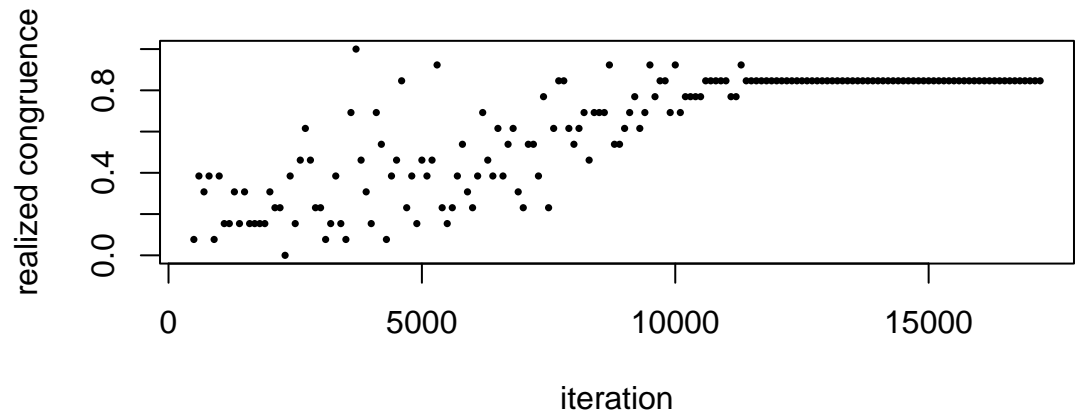
..
BN (A-B) Specialization (H2') 0.54
BN (A-B) Connectance 0.082
BN (B-C) Specialization (H2') 1
BN (B-C) Connectance 0.12
Plant richness in BN (A-B): 31
Herbivore richness in BN (A-B): 36
Herbivore richness in BN (B-C): 13
Parasitoid richness in BN (B-C): 12
Richness of shared Herbivores:13
Number of modules in BN (A-B) 9
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 6
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

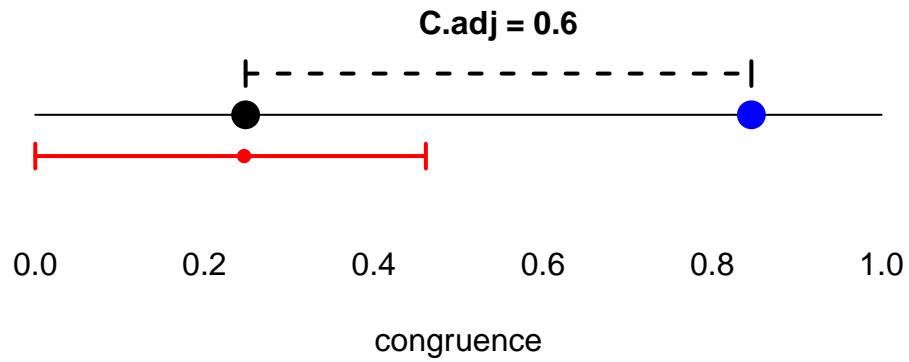


..



Adjusted Congruence: 0.6
Realized Congruence: 0.85
Hypermodularity: 0.48

Null Model 1

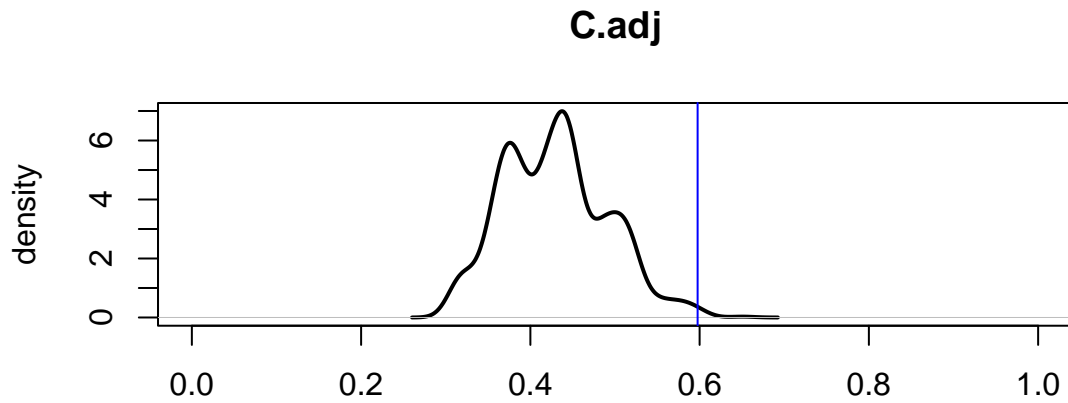


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.006

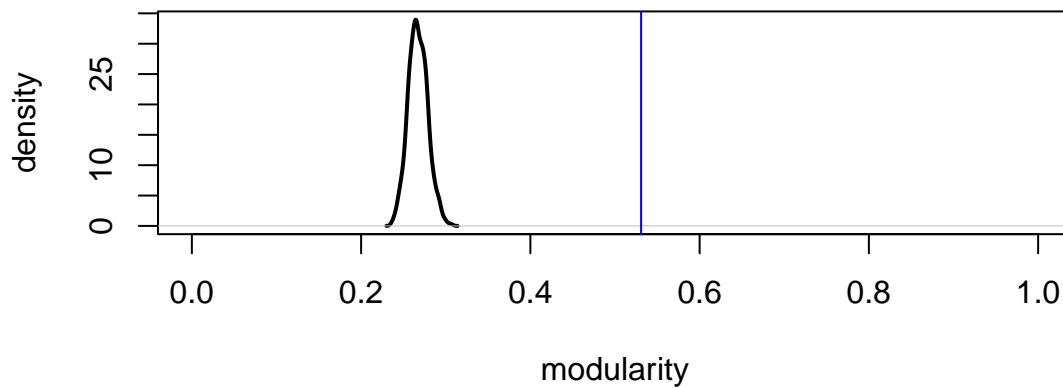
Dataset 4 : GALAPAGOS

Topology BN (A-B): Seed disperser - Plant

Modularity

..
Observed Modularity: 0.53
Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

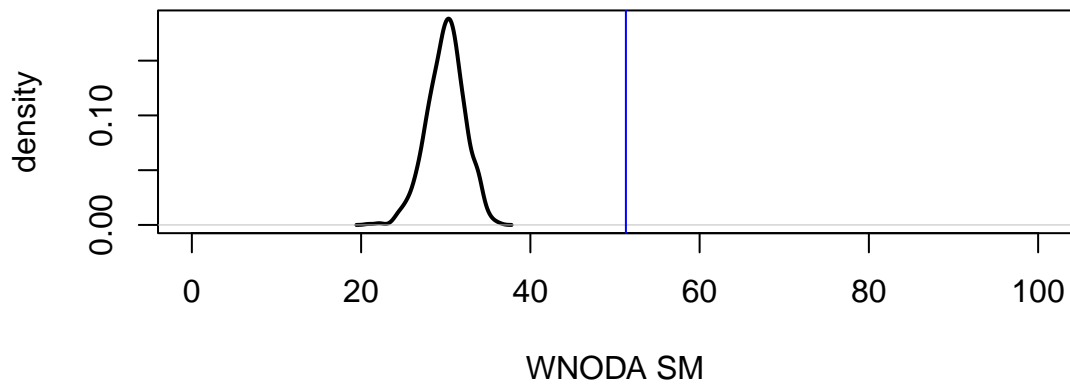


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 16
Nestedness between species in the same module: 51
Nestedness between species in different modules: 6

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

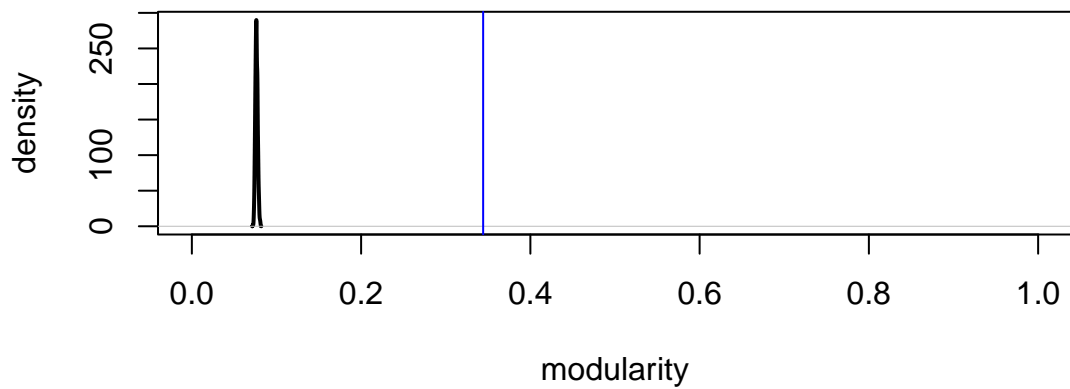
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Pollinator

Modularity

..
 Observed Modularity: 0.34
 Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

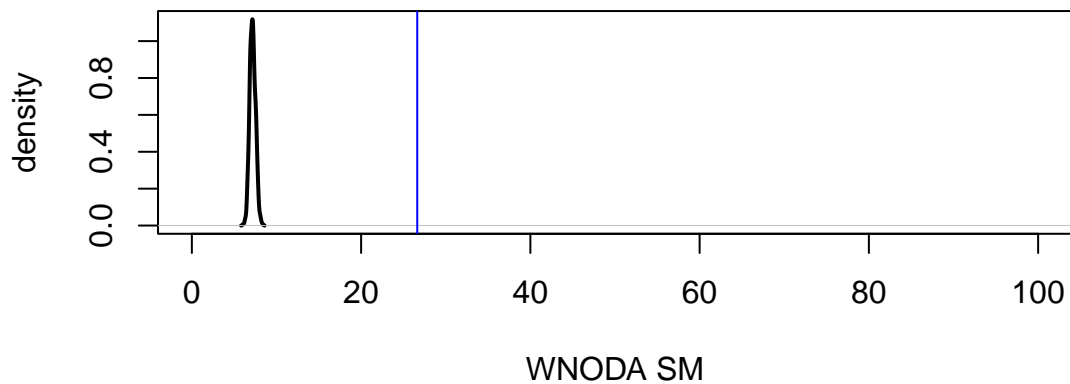


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 13
Nestedness between species in the same module 27
Nestedness between species in different modules 9.8

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

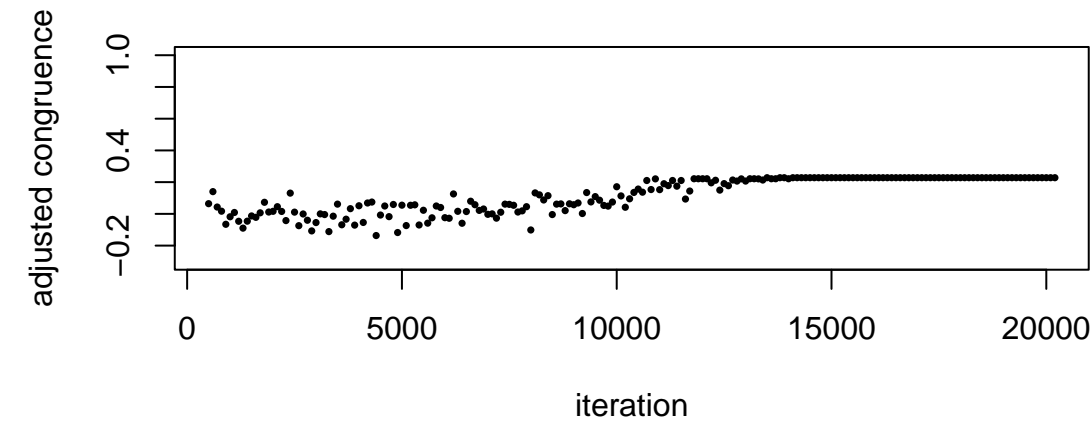
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

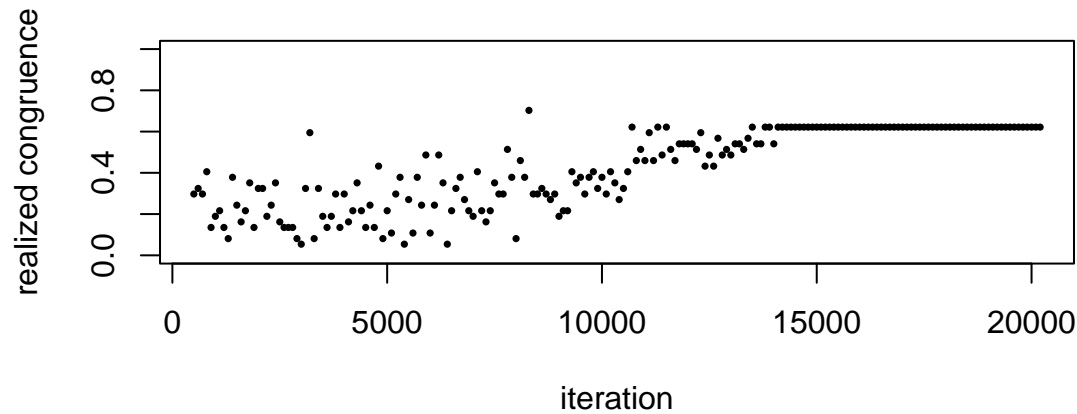
..
BN (A-B) Specialization (H2') 0.39
BN (A-B) Connectance 0.11
BN (B-C) Specialization (H2') 0.37
BN (B-C) Connectance 0.052
Seed disperser richness in BN (A-B): 21
Plant richness in BN (A-B): 84
Plant richness in BN (B-C): 110
Pollinator richness in BN (B-C): 212
Richness of shared Plants: 110
Number of modules in BN (A-B) 5
Number of modules in BN (B-C) 8

Number of modules in BN (A-B) (only for shared species) 5
Number of modules in BN (B-C) (only for shared species) 7

Hipermodule Congruence
Optmization procedure

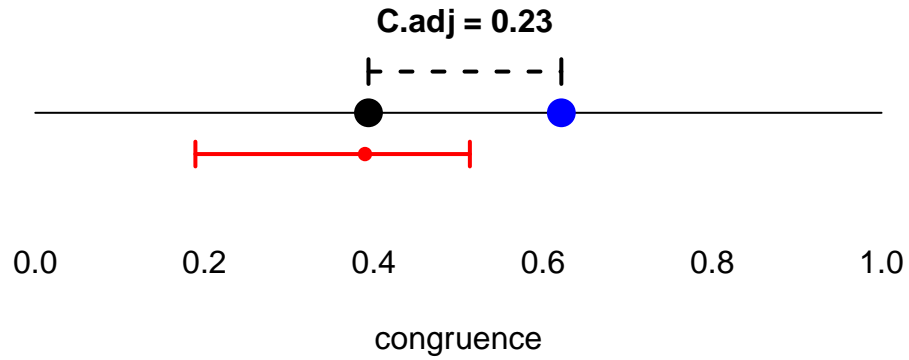


..



..
Adjusted Congruence: 0.23
Realized Congruence: 0.62
Hypermodularity: 0.19

Null Model 1

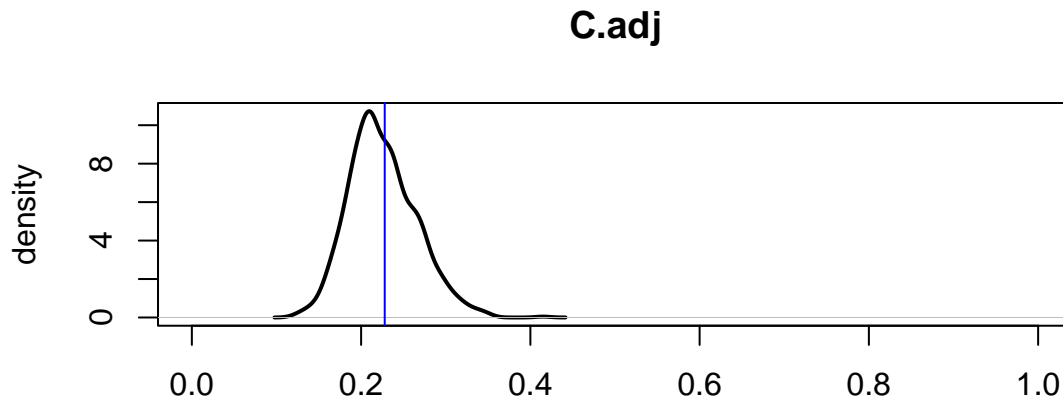


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.004

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.44

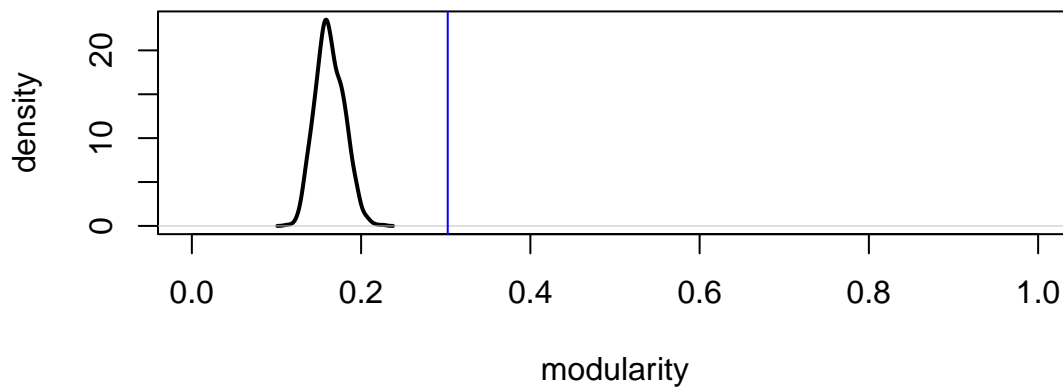
Dataset 5 : DORSET

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.3
Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

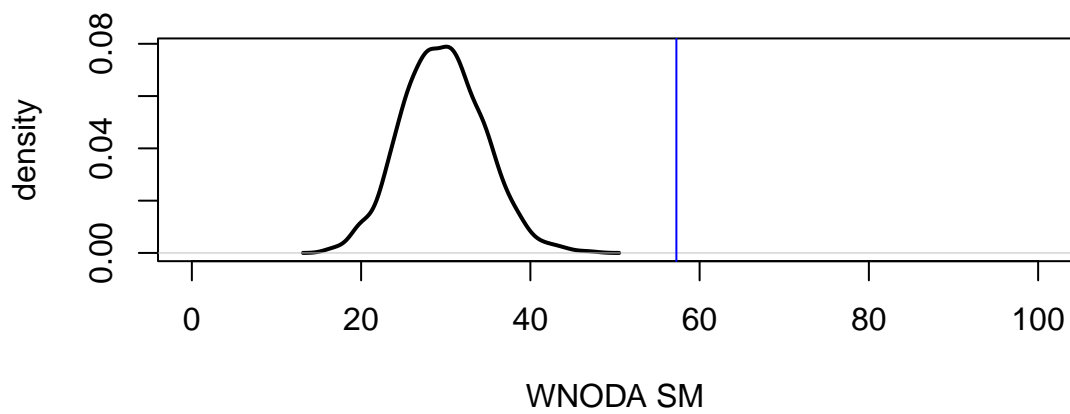


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 34
Nestedness between species in the same module: 57
Nestedness between species in different modules: 23

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

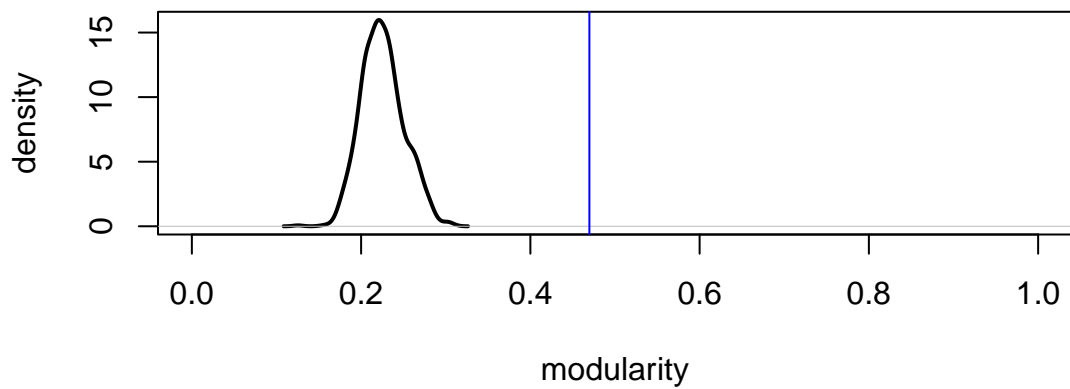
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.47
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

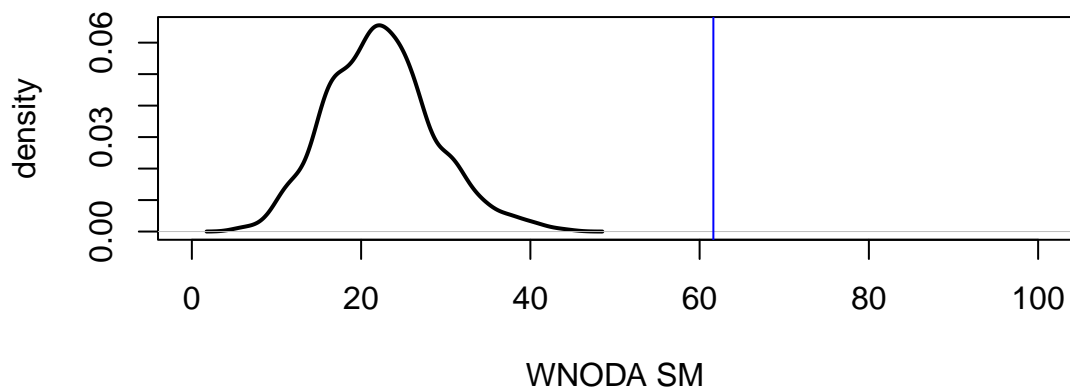


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 21
Nestedness between species in the same module 62
Nestedness between species in different modules 11

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

CONCLUSION: BN (B-C) has a compound topology

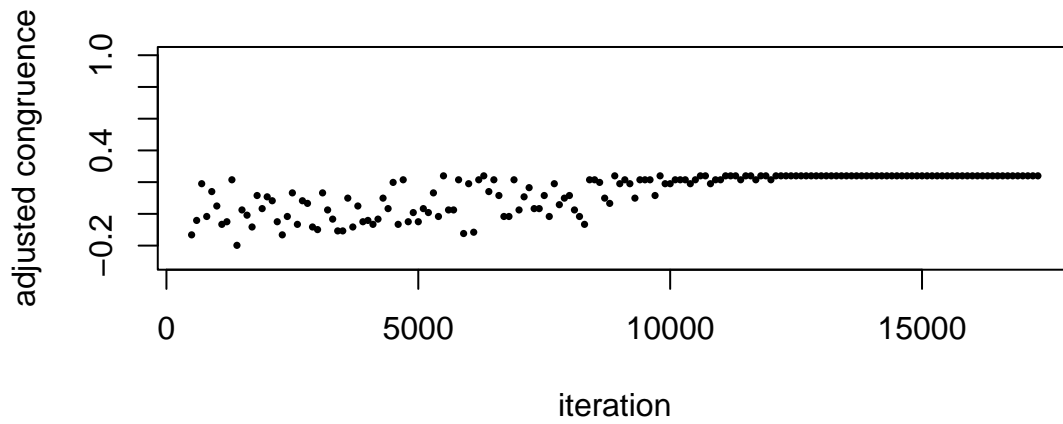
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 0.32
BN (A-B) Connectance 0.2
BN (B-C) Specialization (H2') 0.48
BN (B-C) Connectance 0.19
Plant richness in BN (A-B): 11
Herbivore richness in BN (A-B): 25
Herbivore richness in BN (B-C): 11
Parasitoid richness in BN (B-C): 15
Richness of shared Herbivores: 11
Number of modules in BN (A-B) 4
Number of modules in BN (B-C) 5

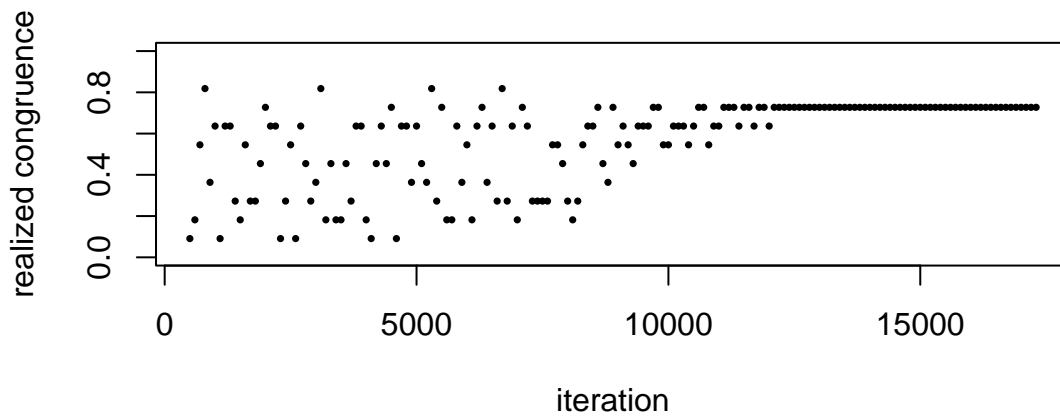
Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence

Optmization procedure



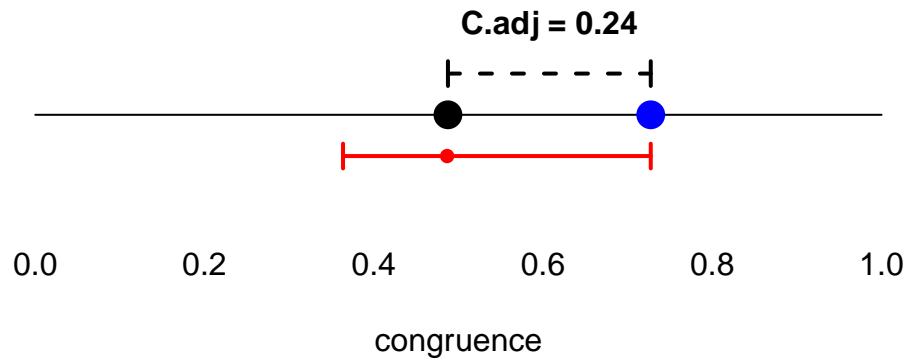
..



..

Adjusted Congruence: 0.24
Realized Congruence: 0.73
Hypermodularity: 0.14

Null Model 1

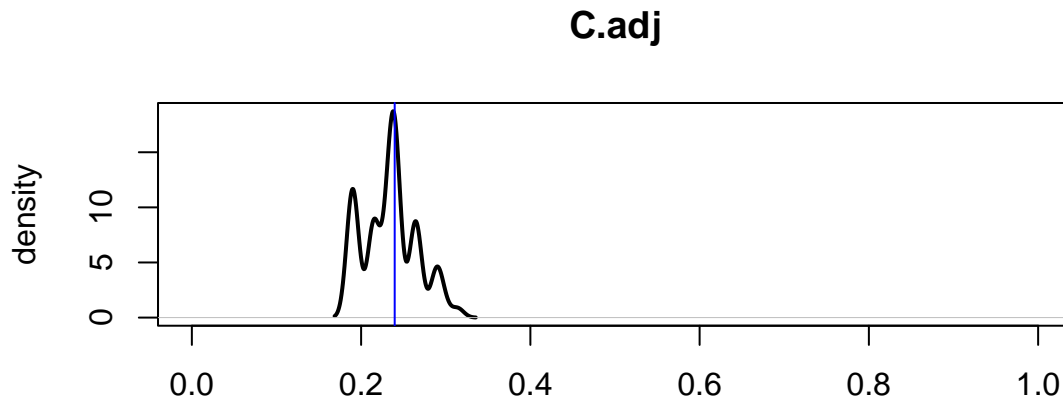


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.052

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.39

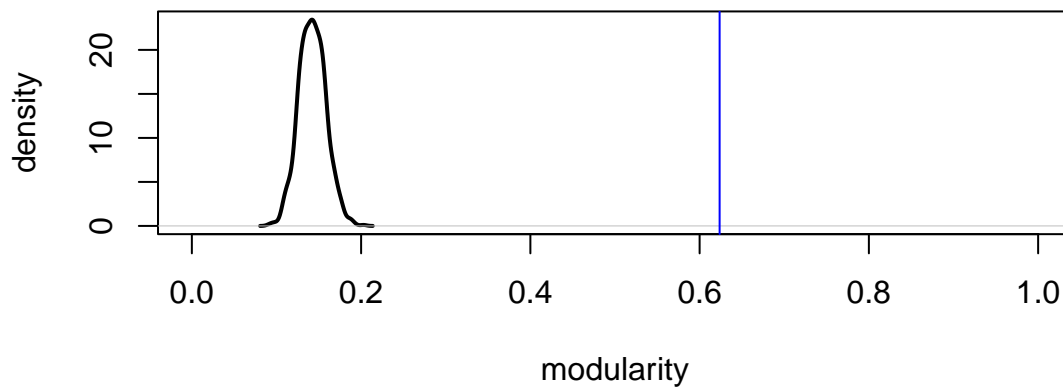
Dataset 6 : NORWOOD

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.62
Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

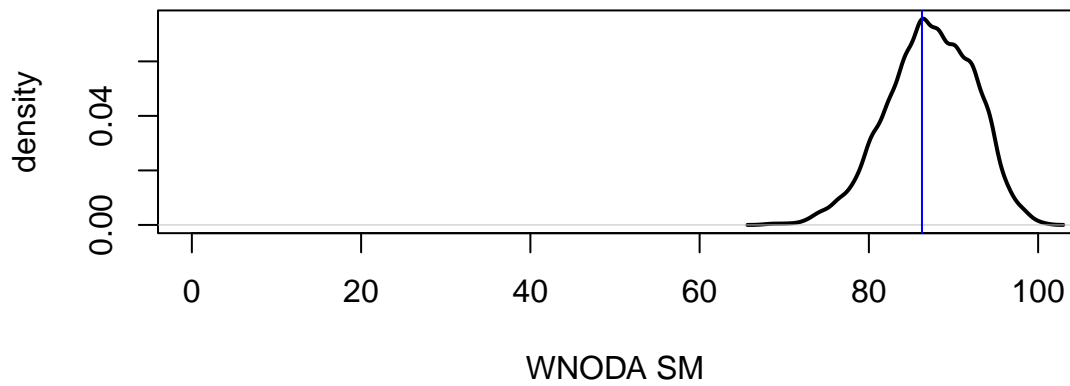


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 24
Nestedness between species in the same module: 86
Nestedness between species in different modules: 0.37

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.66

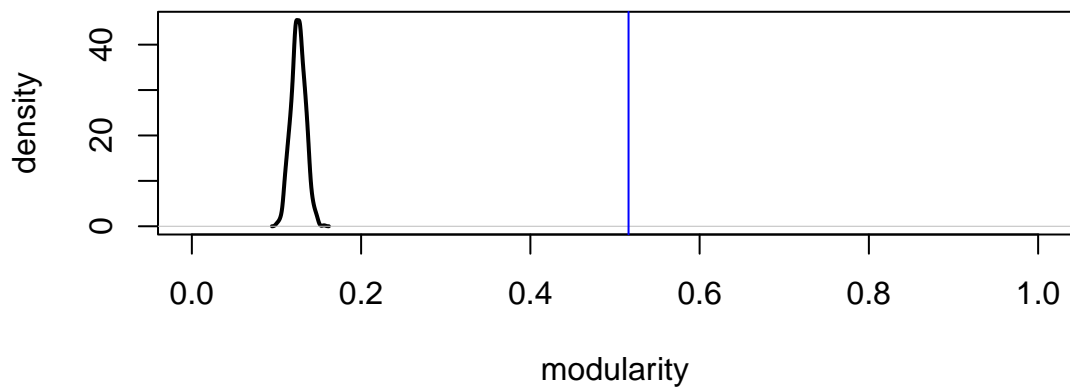
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.52
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

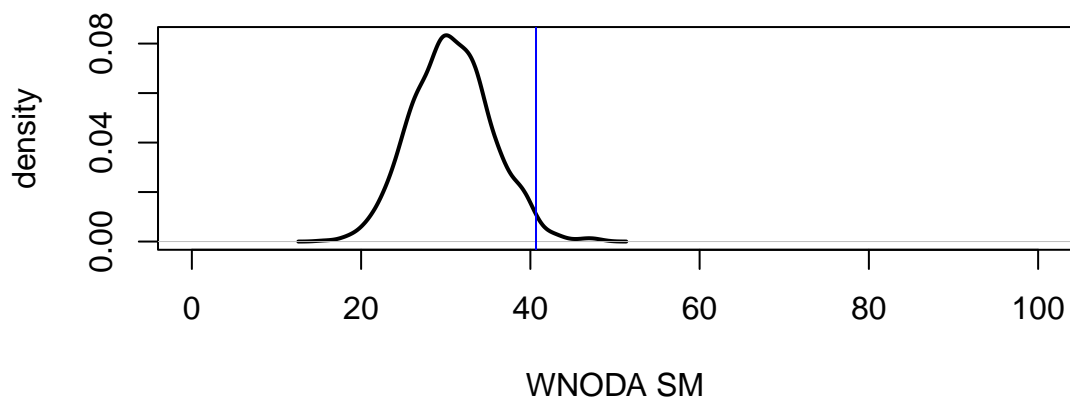


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 17
Nestedness between species in the same module 41
Nestedness between species in different modules 8.8

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.018

CONCLUSION: BN (B-C) has a compound topology

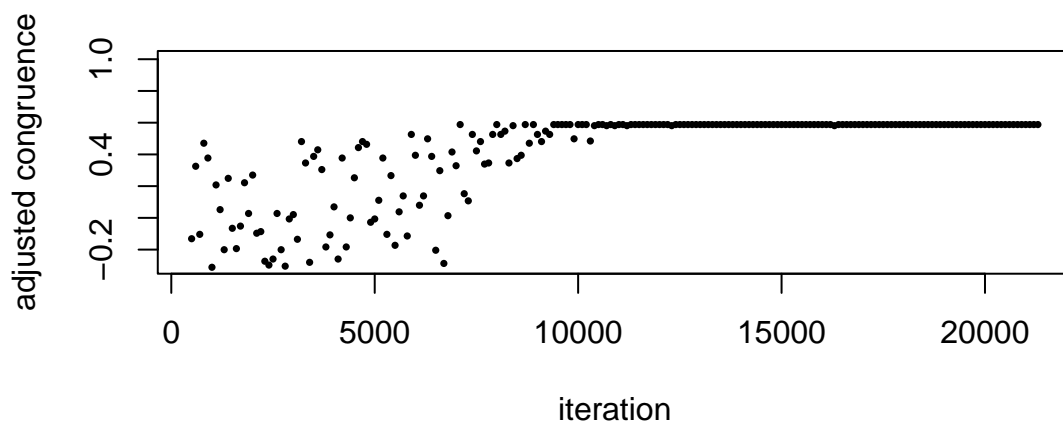
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 0.99
BN (A-B) Connectance 0.18
BN (B-C) Specialization (H2') 0.45
BN (B-C) Connectance 0.25
Plant richness in BN (A-B): 6
Herbivore richness in BN (A-B): 19
Herbivore richness in BN (B-C): 17
Parasitoid richness in BN (B-C): 17
Richness of shared Herbivores: 17
Number of modules in BN (A-B) 6
Number of modules in BN (B-C) 5

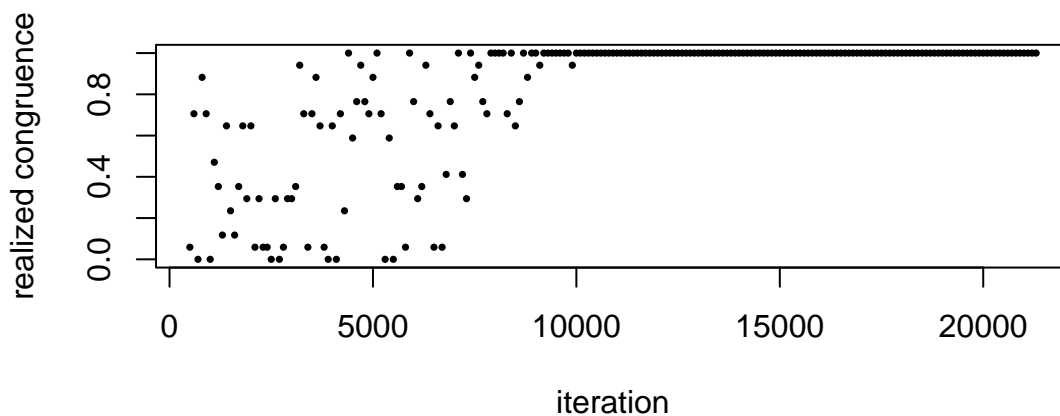
Number of modules in BN (A-B) (only for shared species) 4
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence

Optimization procedure



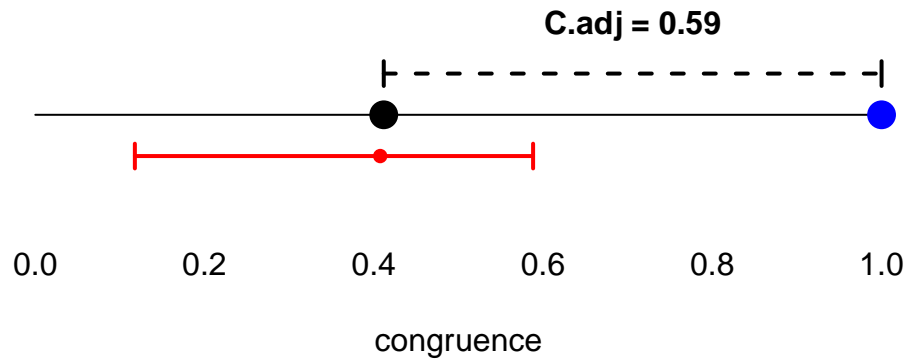
..



..

Adjusted Congruence: 0.59
Realized Congruence: 1
Hypermodularity: 0.52

Null Model 1

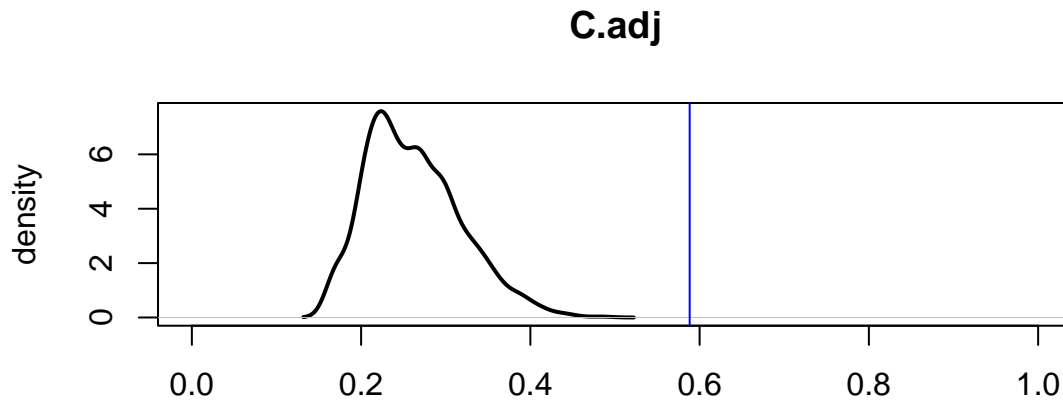


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0

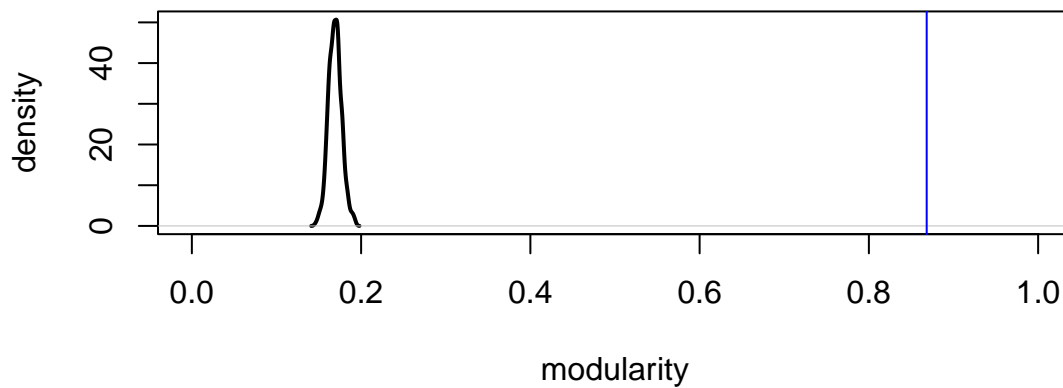
Dataset 7 : NORWOOD

Topology BN (A-B): Herbivore - Plant

Modularity

..
Observed Modularity: 0.87
Number of Modules: 13

Comparison between observed modularity (blue line) and proportional null model (density in black)

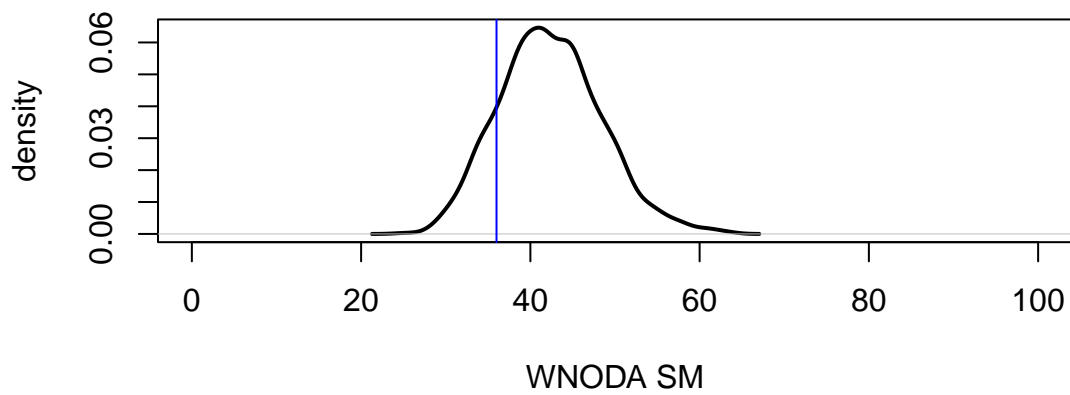


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 2.3
Nestedness between species in the same module: 36
Nestedness between species in different modules: 0.13

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.87

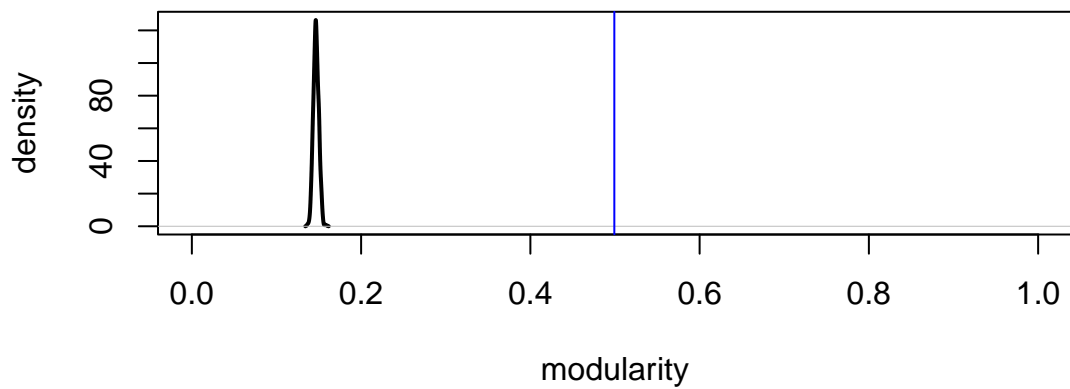
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Plant - Pollinator

Modularity

..
 Observed Modularity: 0.5
 Number of Modules: 17

Comparison between observed modularity (blue line) and proportional null model (density in black)

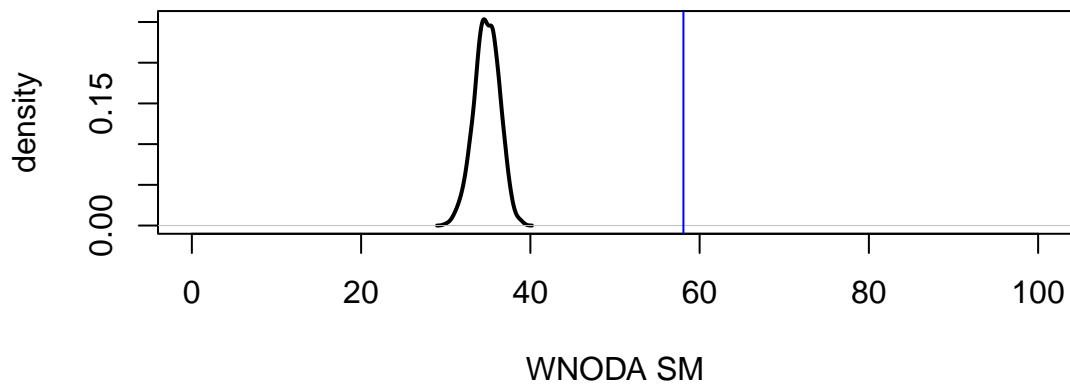


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 12
Nestedness between species in the same module 58
Nestedness between species in different modules 7.6

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

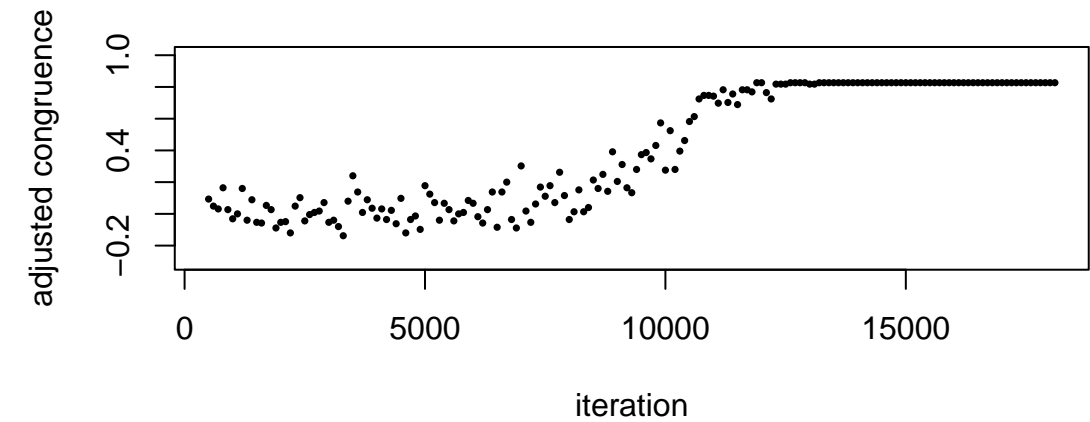
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

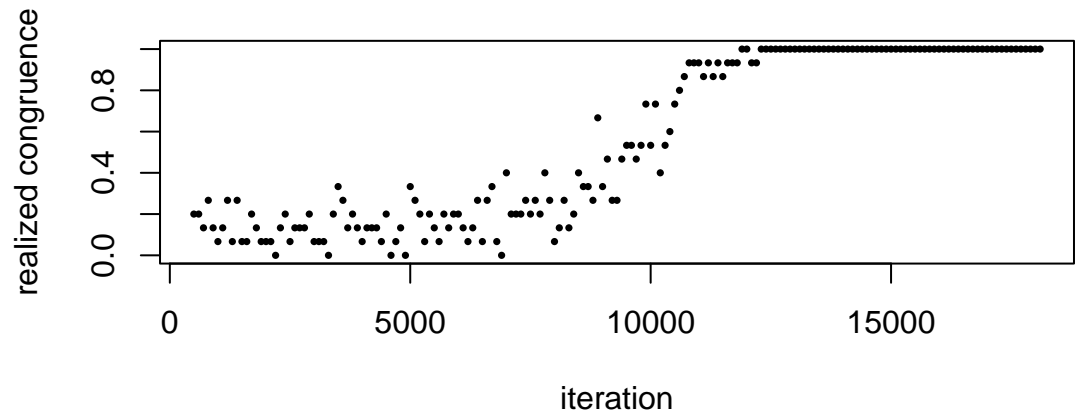
..
BN (A-B) Specialization (H2') 0.89
BN (A-B) Connectance 0.046
BN (B-C) Specialization (H2') 0.57
BN (B-C) Connectance 0.044
Herbivore richness in BN (A-B): 28
Plant richness in BN (A-B): 30
Plant richness in BN (B-C): 47
Pollinator richness in BN (B-C): 241
Richness of shared Plants: 47
Number of modules in BN (A-B) 13
Number of modules in BN (B-C) 17

Number of modules in BN (A-B) (only for shared species) 12
Number of modules in BN (B-C) (only for shared species) 11

Hipermodule Congruence
Optmization procedure

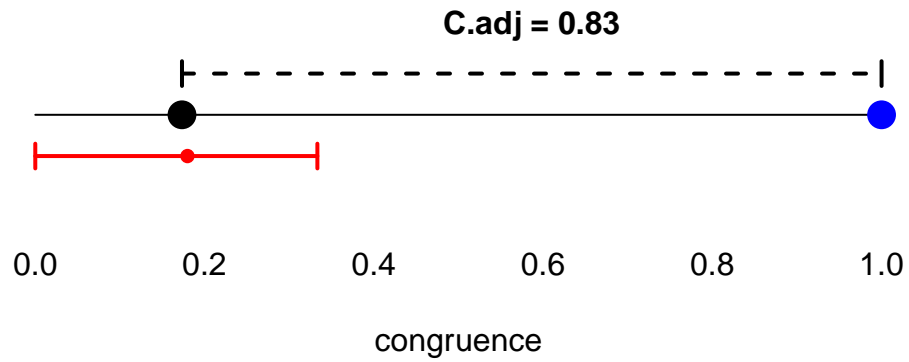


..



Adjusted Congruence: 0.83
Realized Congruence: 1
Hypermodularity: 0.6

Null Model 1

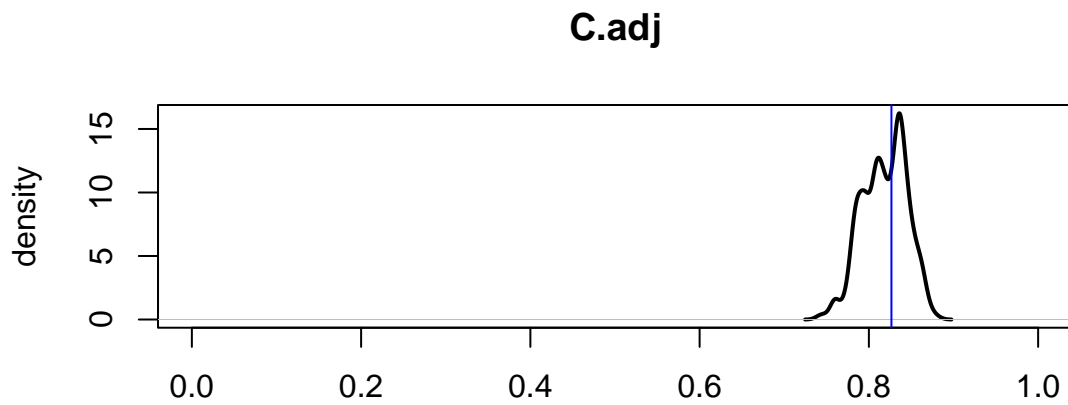


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.47

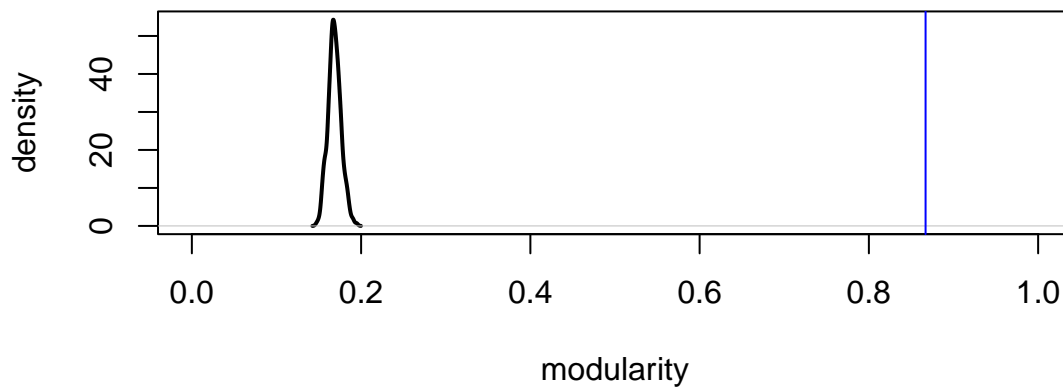
Dataset 8 : NORWOOD

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.87
Number of Modules: 15

Comparison between observed modularity (blue line) and proportional null model (density in black)

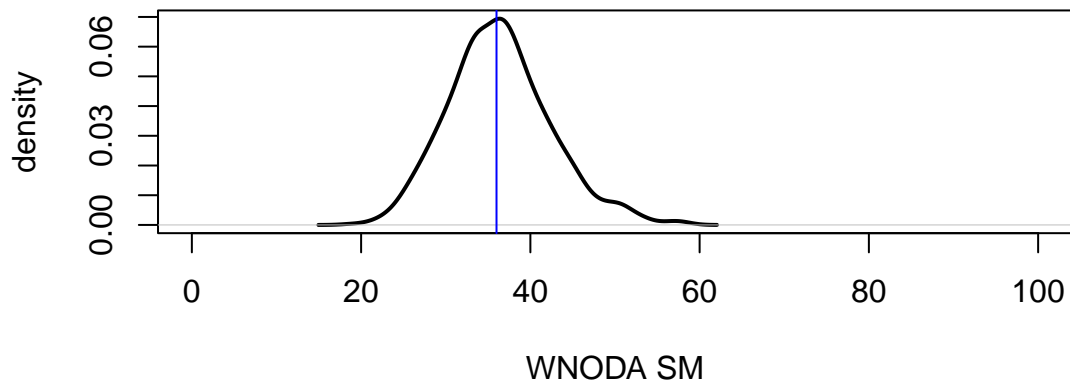


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 2.3
Nestedness between species in the same module: 36
Nestedness between species in different modules: 0.13

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.54

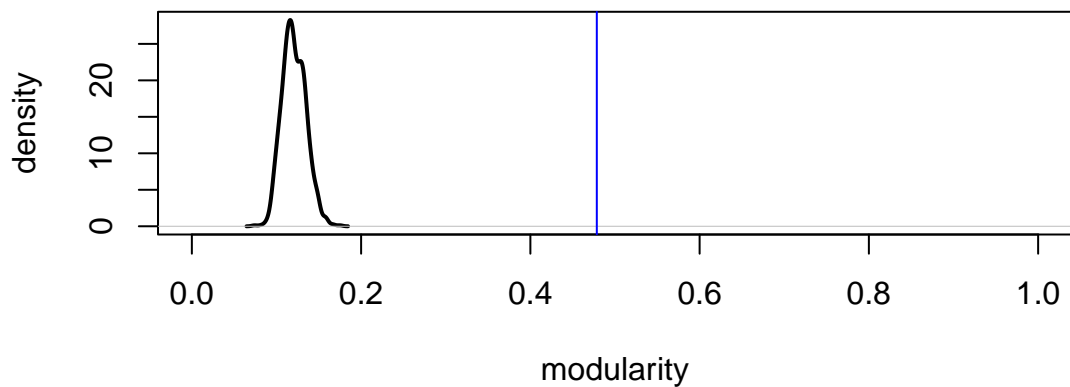
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.48
 Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

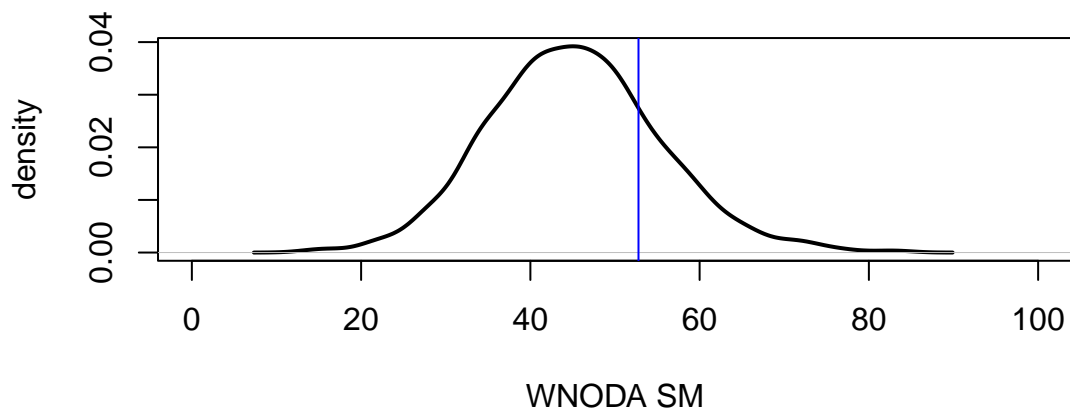


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 30
Nestedness between species in the same module 53
Nestedness between species in different modules 24

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.24

CONCLUSION: BN (B-C) has a purely modular topology

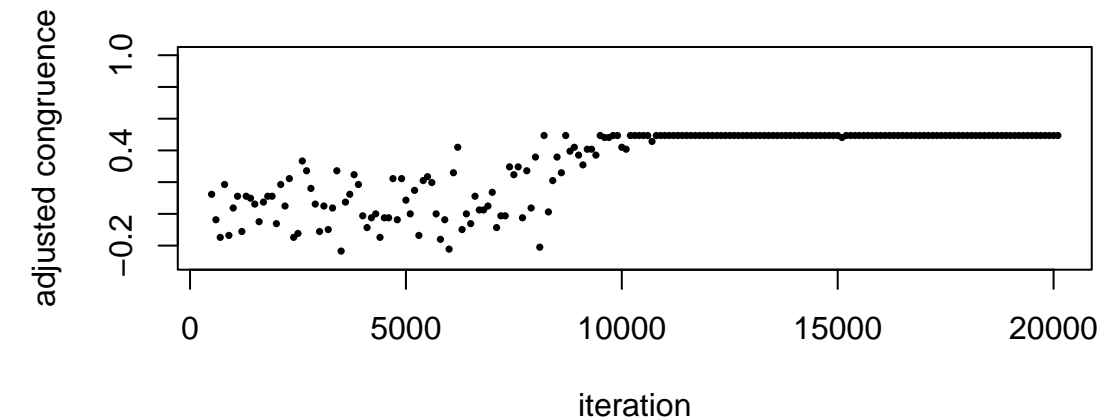
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 0.89
BN (A-B) Connectance 0.046
BN (B-C) Specialization (H2') 0.57
BN (B-C) Connectance 0.21
Plant richness in BN (A-B): 30
Herbivore richness in BN (A-B): 28
Herbivore richness in BN (B-C): 9
Parasitoid richness in BN (B-C): 11
Richness of shared Herbivores: 9
Number of modules in BN (A-B) 15
Number of modules in BN (B-C) 4

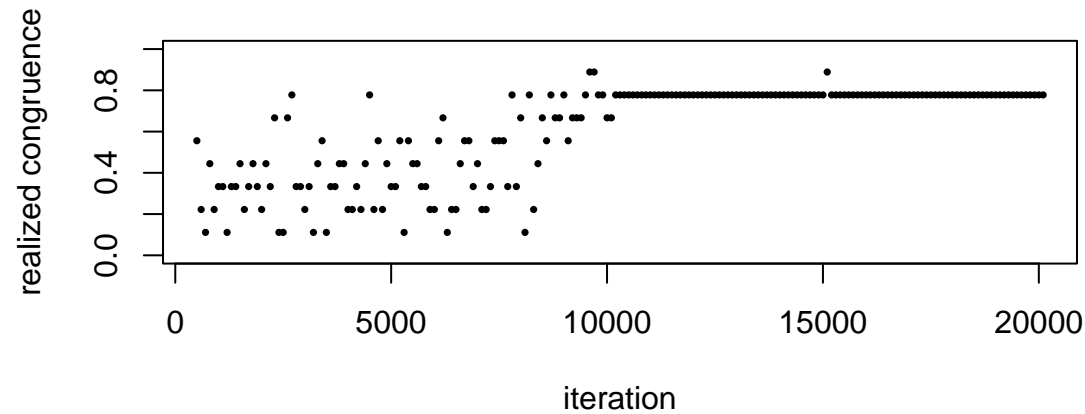
Number of modules in BN (A-B) (only for shared species) 7
Number of modules in BN (B-C) (only for shared species) 4

Hipermodule Congruence

Optimization procedure

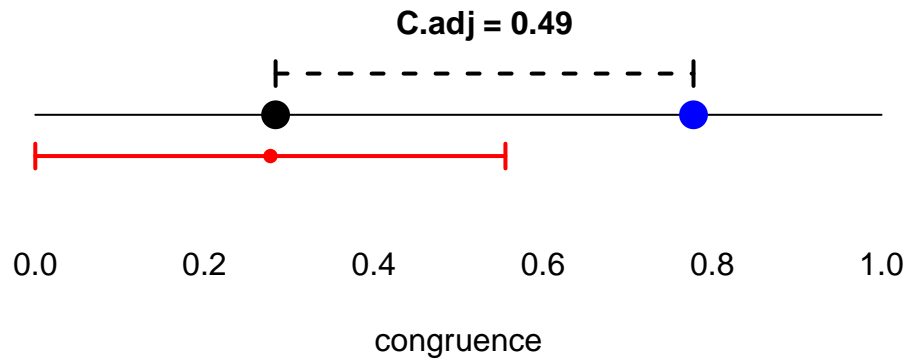


..



Adjusted Congruence: 0.49
Realized Congruence: 0.78
Hypermodularity: 0.48

Null Model 1

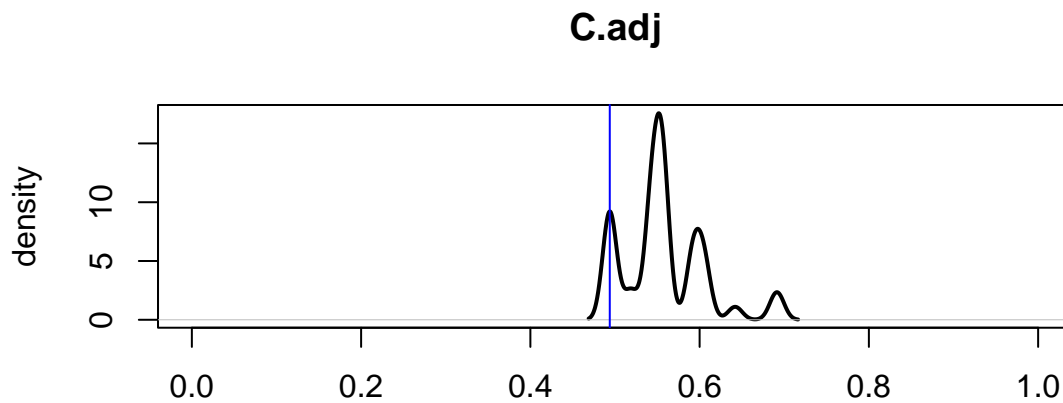


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.003

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

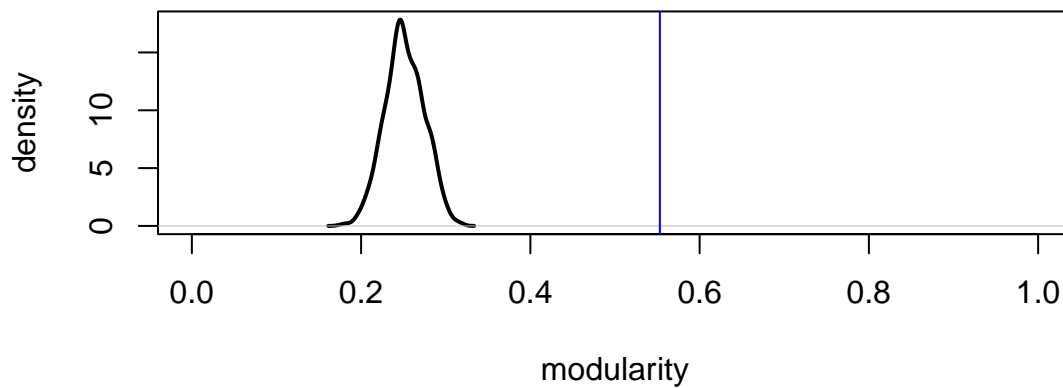
Dataset 9 : BORNEO

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.55
Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

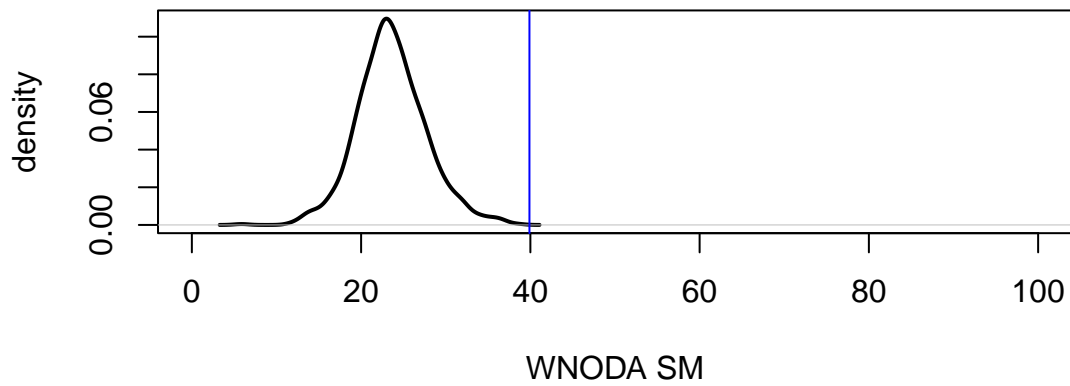


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 17
Nestedness between species in the same module: 40
Nestedness between species in different modules: 11

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

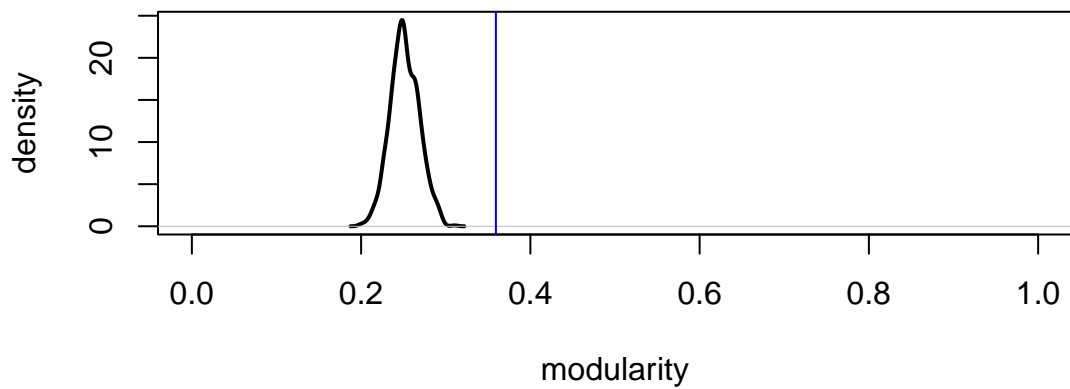
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Defender

Modularity

..
 Observed Modularity: 0.36
 Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

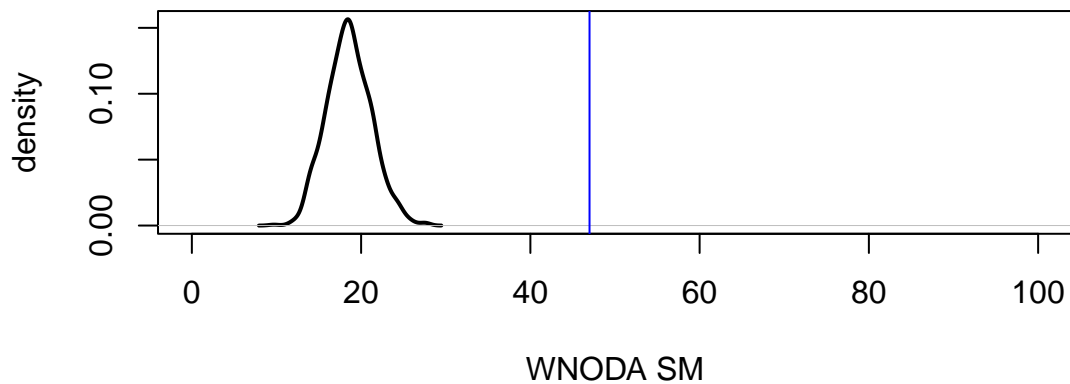


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 21
Nestedness between species in the same module 47
Nestedness between species in different modules 14

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

CONCLUSION: BN (B-C) has a compound topology

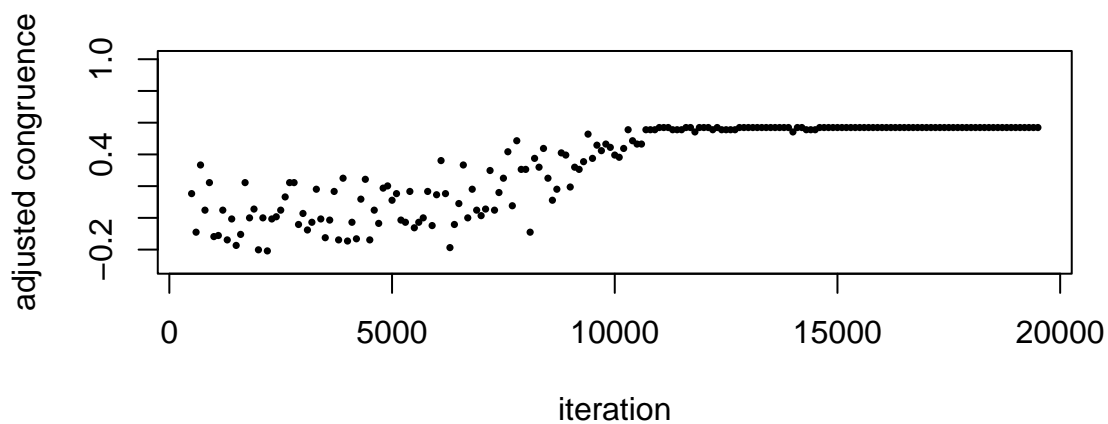
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 0.43
BN (A-B) Connectance 0.15
BN (B-C) Specialization (H2') 0.3
BN (B-C) Connectance 0.21
Plant richness in BN (A-B): 32
Herbivore richness in BN (A-B): 13
Herbivore richness in BN (B-C): 13
Defender richness in BN (B-C): 43
Richness of shared Herbivores:13
Number of modules in BN (A-B) 6
Number of modules in BN (B-C) 6

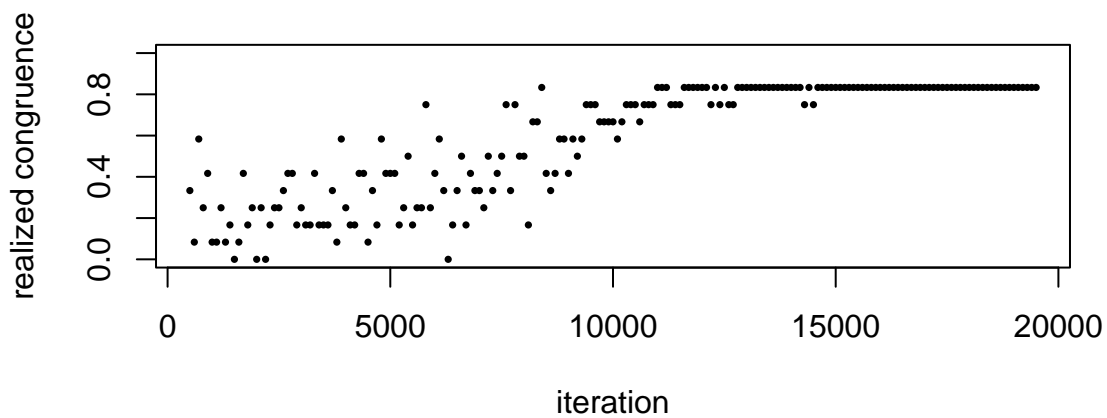
Number of modules in BN (A-B) (only for shared species) 6
Number of modules in BN (B-C) (only for shared species) 6

Hipermodule Congruence

Optimization procedure



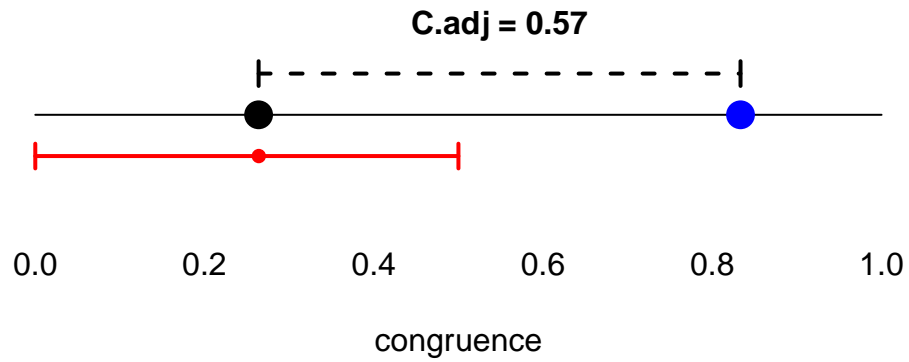
..



..

Adjusted Congruence: 0.57
Realized Congruence: 0.83
Hypermodularity: 0.32

Null Model 1

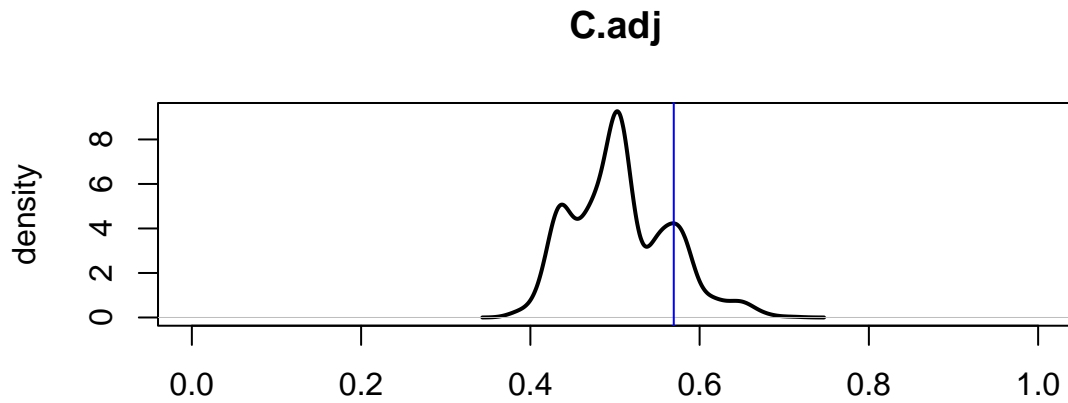


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.18

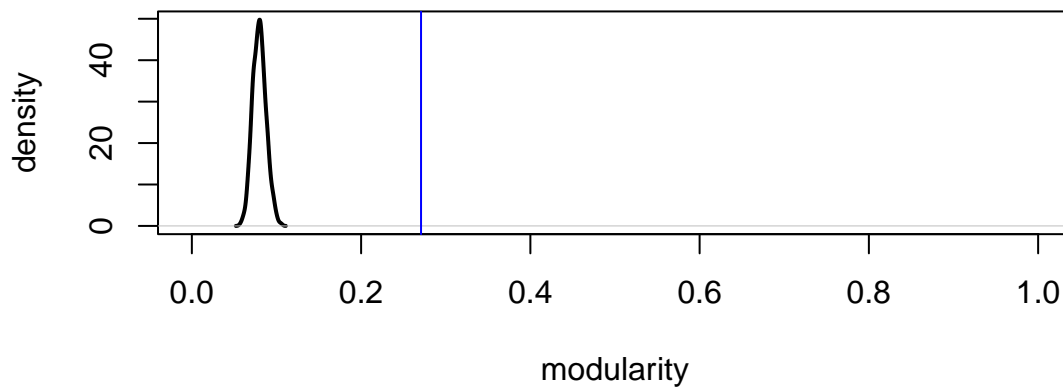
Dataset 10 : COIMBRA

Topology BN (A-B): Plant - Seed disperser

Modularity

..
Observed Modularity: 0.27
Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

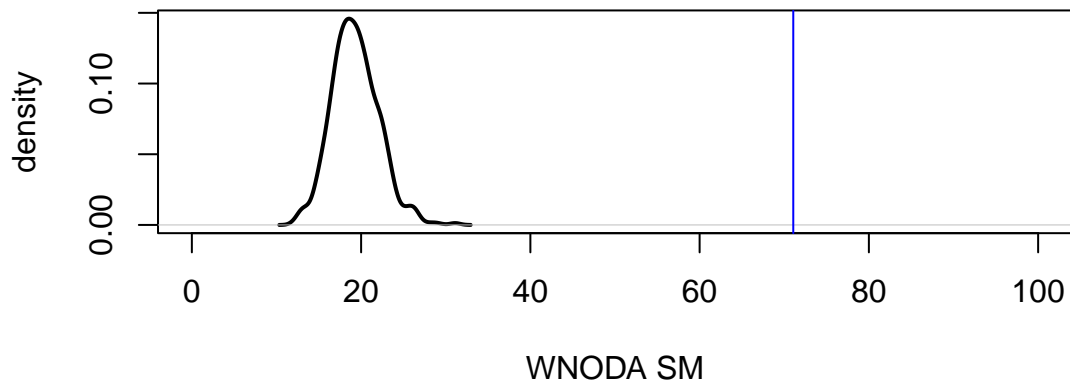


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 55
Nestedness between species in the same module: 71
Nestedness between species in different modules: 46

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

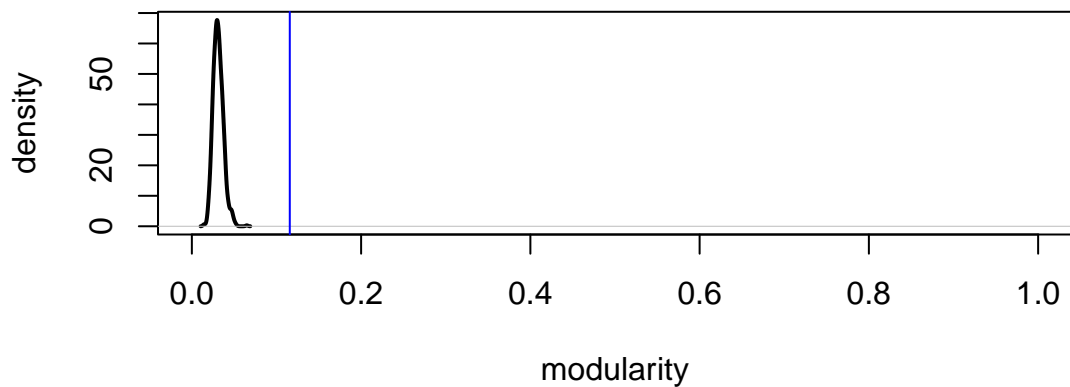
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Seed disperser - Parasite

Modularity

..
 Observed Modularity: 0.12
 Number of Modules: 3

Comparison between observed modularity (blue line) and proportional null model (density in black)

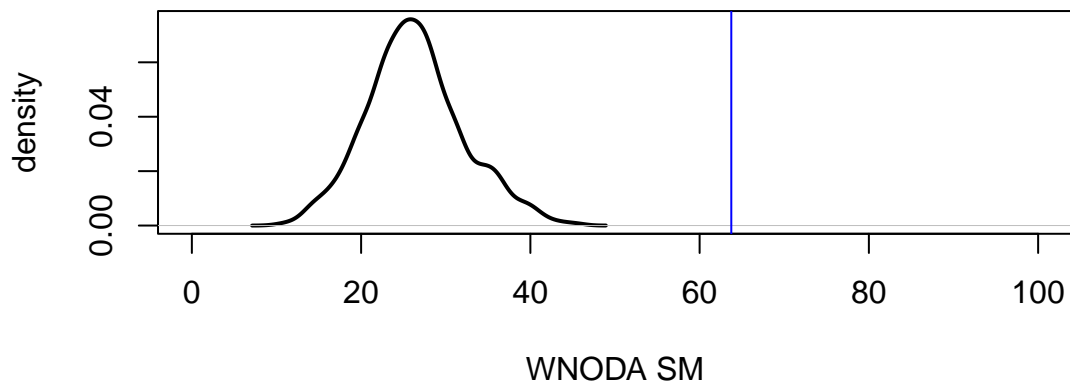


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 59
Nestedness between species in the same module 64
Nestedness between species in different modules 57

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

CONCLUSION: BN (B-C) has a compound topology

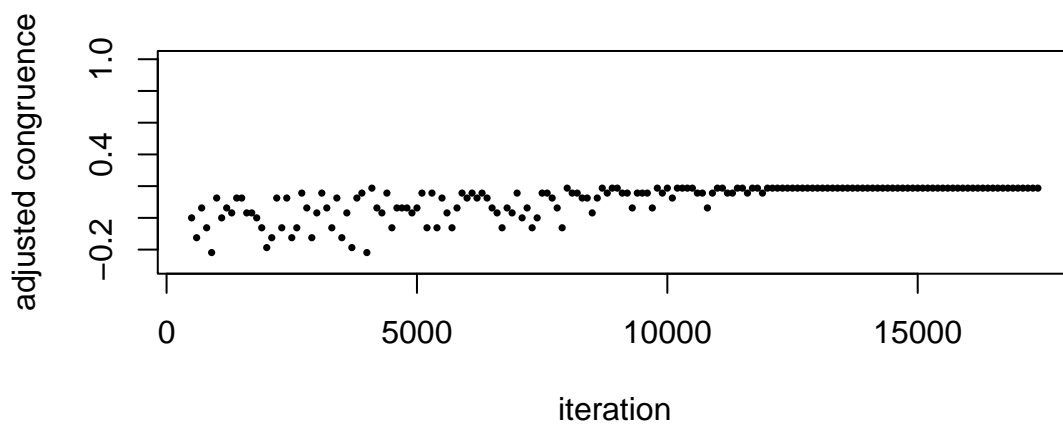
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 0.22
BN (A-B) Connectance 0.25
BN (B-C) Specialization (H2') 0.17
BN (B-C) Connectance 0.43
Plant richness in BN (A-B): 29
Seed disperser richness in BN (A-B): 15
Seed disperser richness in BN (B-C): 18
Parasite richness in BN (B-C): 6
Richness of shared Seed dispersers: 18
Number of modules in BN (A-B) 4
Number of modules in BN (B-C) 3

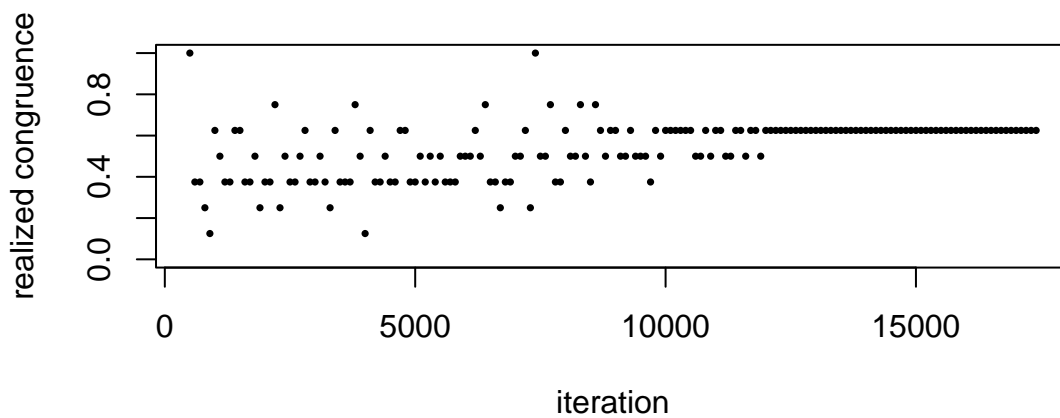
Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 3

Hipermodule Congruence

Optmization procedure



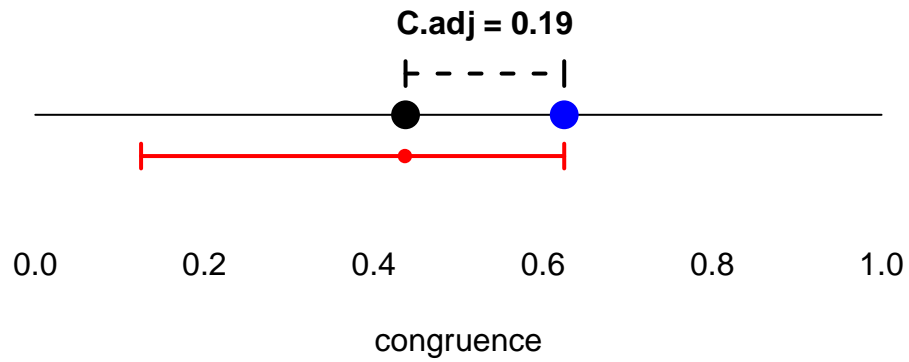
..



..

Adjusted Congruence: 0.19
Realized Congruence: 0.62
Hypermodularity: 0.072

Null Model 1

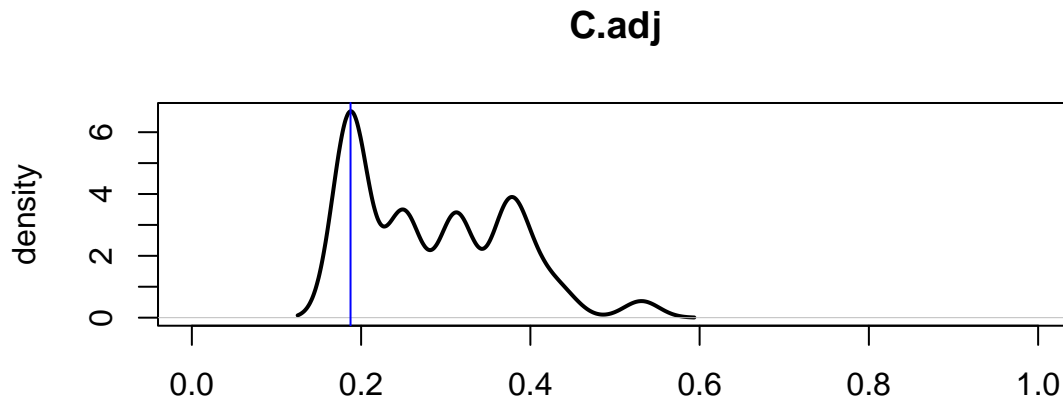


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.35

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

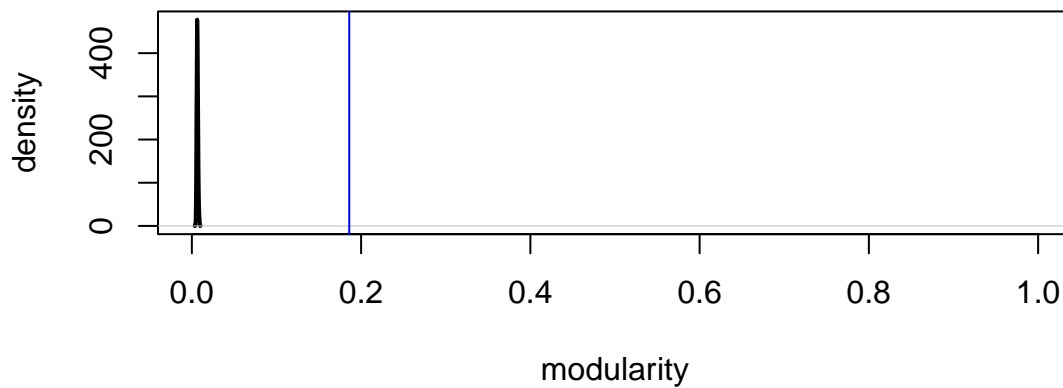
Dataset 11 : BEIRA

Topology BN (A-B): Plant - herbivore

Modularity

..
Observed Modularity: 0.19
Number of Modules: 14

Comparison between observed modularity (blue line) and proportional null model (density in black)

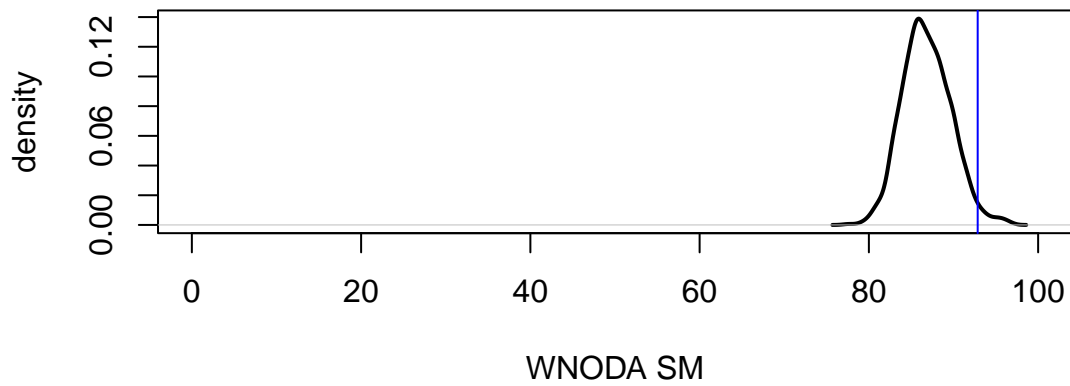


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 9.3
Nestedness between species in the same module: 93
Nestedness between species in different modules: 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.027

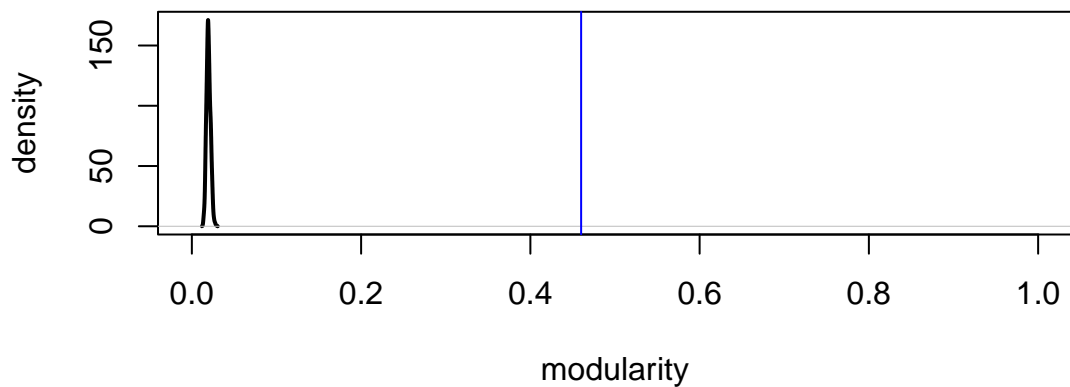
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.46
 Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

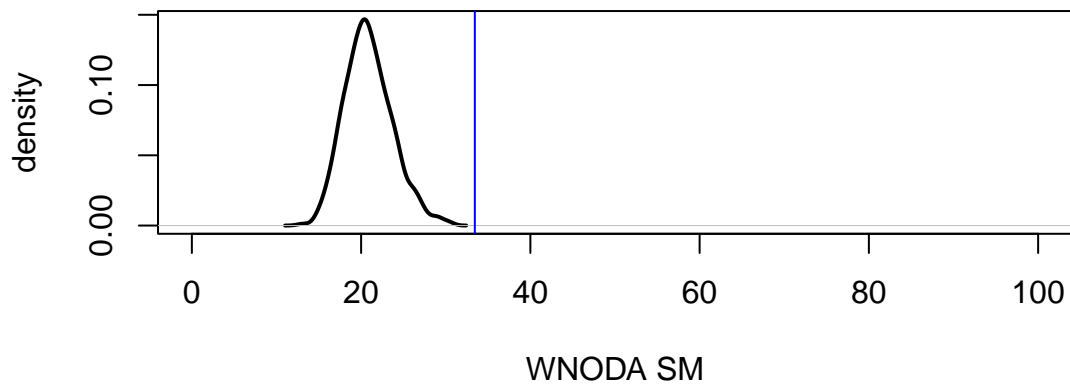


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 10
Nestedness between species in the same module 33
Nestedness between species in different modules 3.3

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

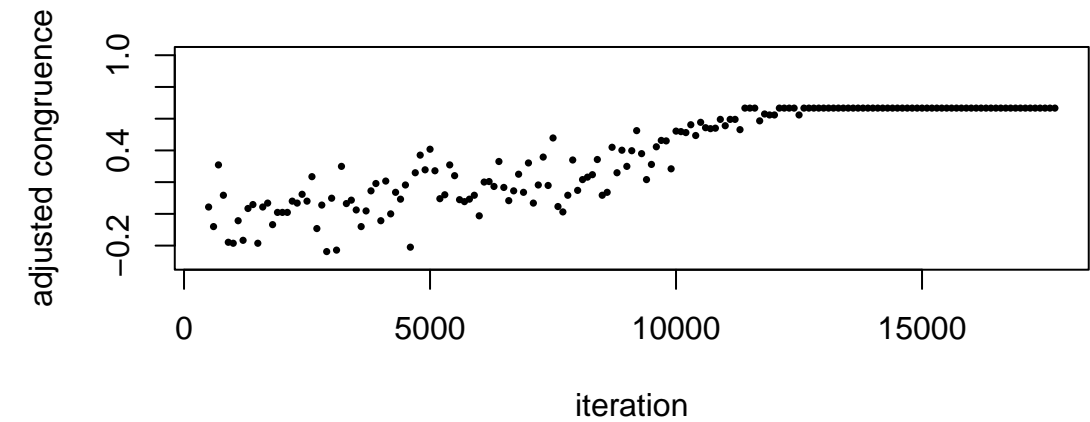
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

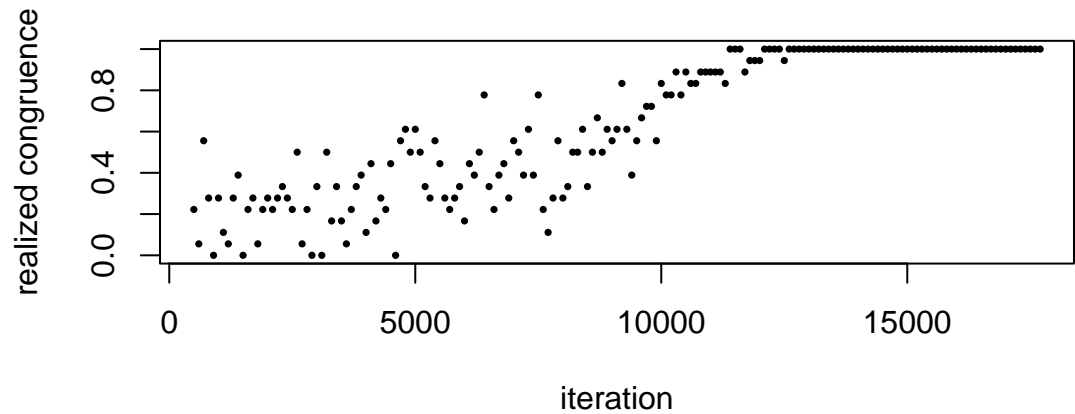
..
BN (A-B) Specialization (H2') 0.97
BN (A-B) Connectance 0.062
BN (B-C) Specialization (H2') 0.69
BN (B-C) Connectance 0.1
Plant richness in BN (A-B): 22
herbivore richness in BN (A-B): 31
herbivore richness in BN (B-C): 18
Parasitoid richness in BN (B-C): 40
Richness of shared herbivores: 18
Number of modules in BN (A-B) 14
Number of modules in BN (B-C) 6

Number of modules in BN (A-B) (only for shared species) 9
Number of modules in BN (B-C) (only for shared species) 6

Hipermodule Congruence
Optmization procedure

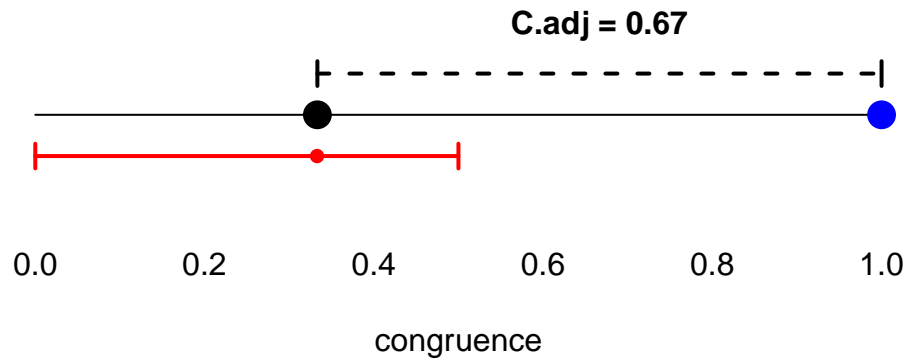


..



..
Adjusted Congruence: 0.67
Realized Congruence: 1
Hypermodularity: 0.39

Null Model 1

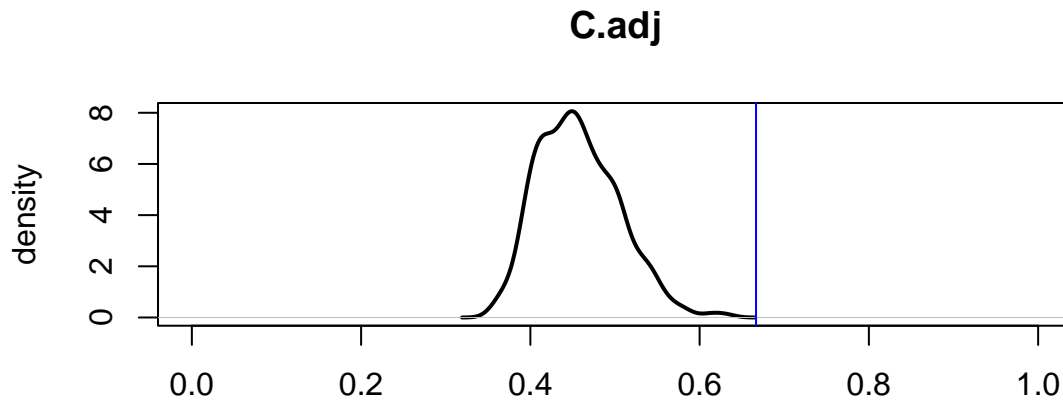


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0

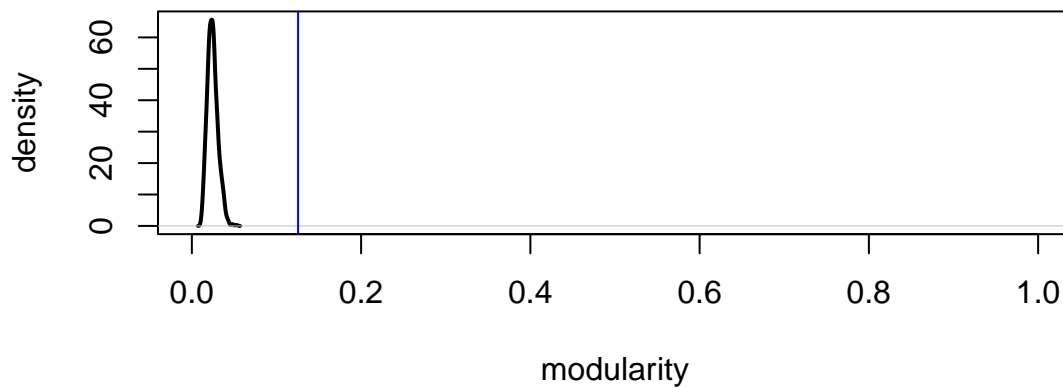
Dataset 12 : PURBECK

Topology BN (A-B): Plant - Pollinator

Modularity

..
Observed Modularity: 0.13
Number of Modules: 3

Comparison between observed modularity (blue line) and proportional null model (density in black)

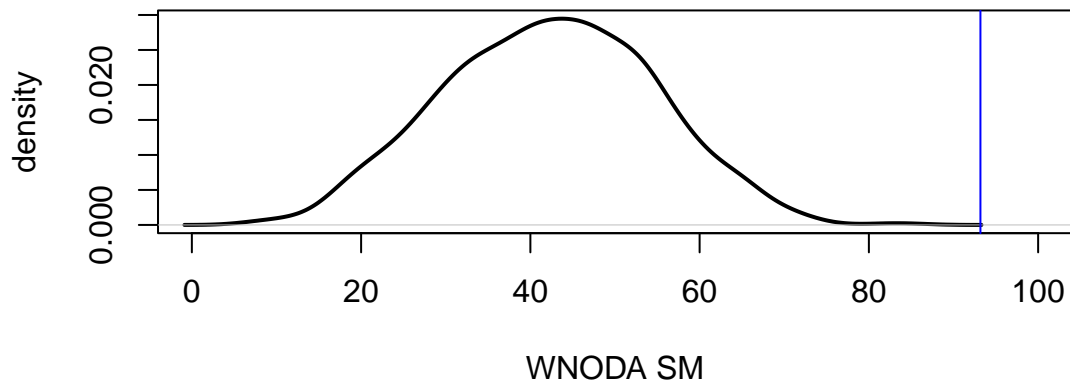


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 88
Nestedness between species in the same module: 93
Nestedness between species in different modules: 87

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

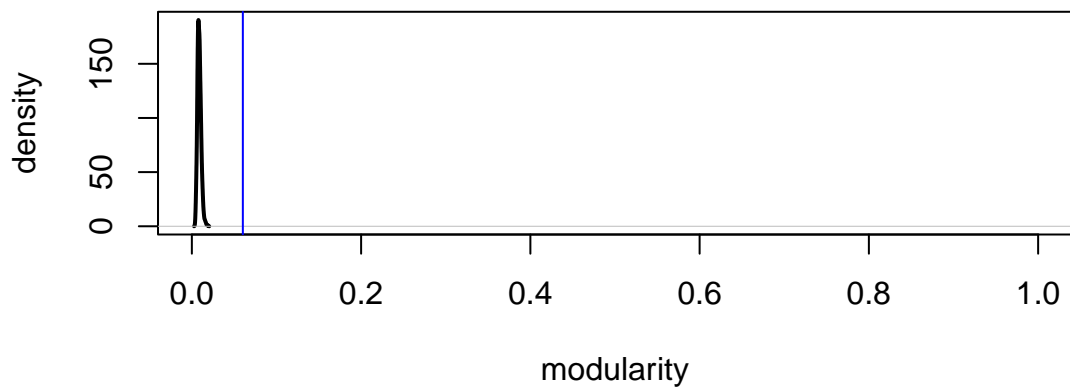
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Pollinator - Parasitoid

Modularity

..
 Observed Modularity: 0.06
 Number of Modules: 2

Comparison between observed modularity (blue line) and proportional null model (density in black)

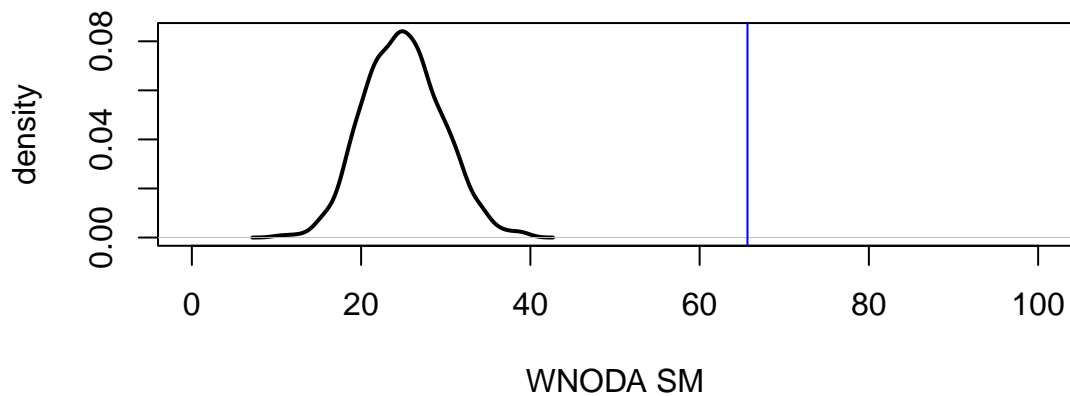


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 70
Nestedness between species in the same module 66
Nestedness between species in different modules 74

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

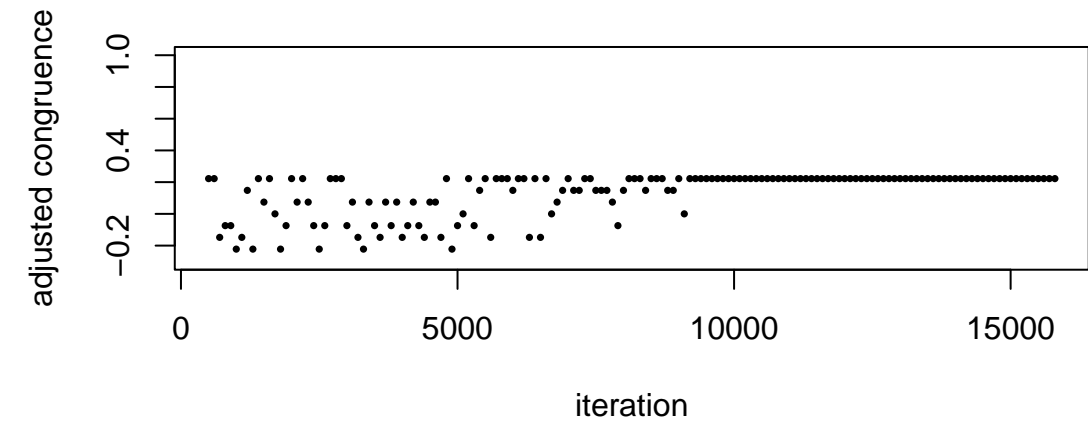
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

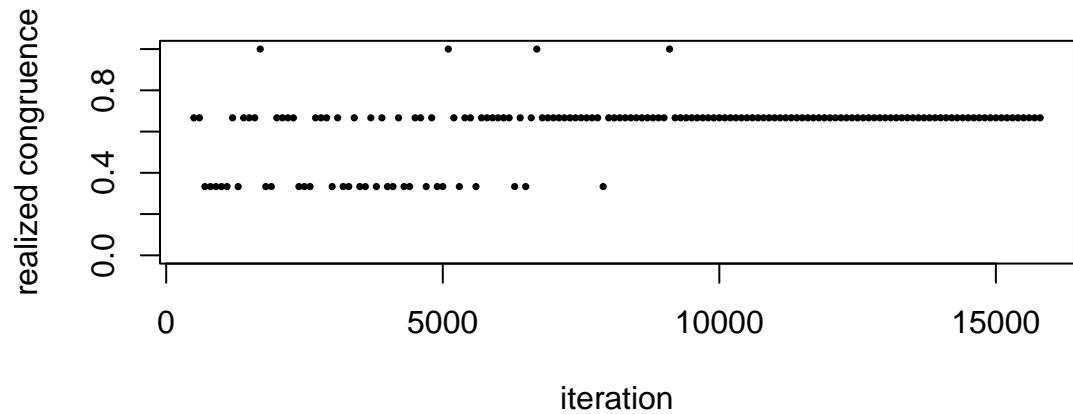
..
BN (A-B) Specialization (H2') 0.085
BN (A-B) Connectance 0.78
BN (B-C) Specialization (H2') 0.15
BN (B-C) Connectance 0.53
Plant richness in BN (A-B): 4
Pollinator richness in BN (A-B): 9
Pollinator richness in BN (B-C): 9
Parasitoid richness in BN (B-C): 11
Richness of shared Pollinators: 9
Number of modules in BN (A-B) 3
Number of modules in BN (B-C) 2

Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 2

Hipermodule Congruence
Optmization procedure

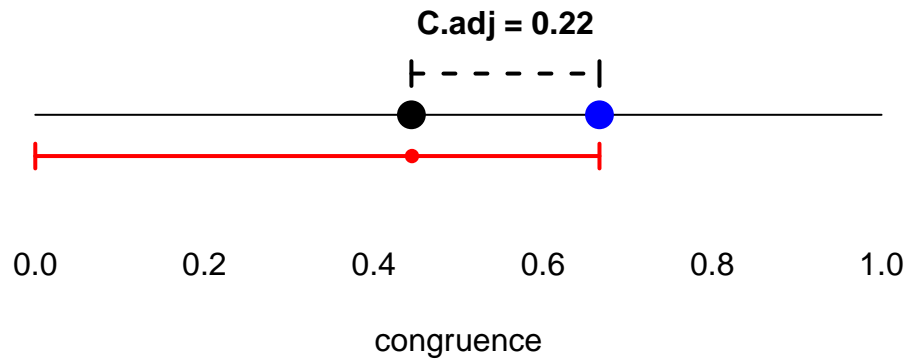


..



..
Adjusted Congruence: 0.22
Realized Congruence: 0.67
Hypermodularity: 0.062

Null Model 1

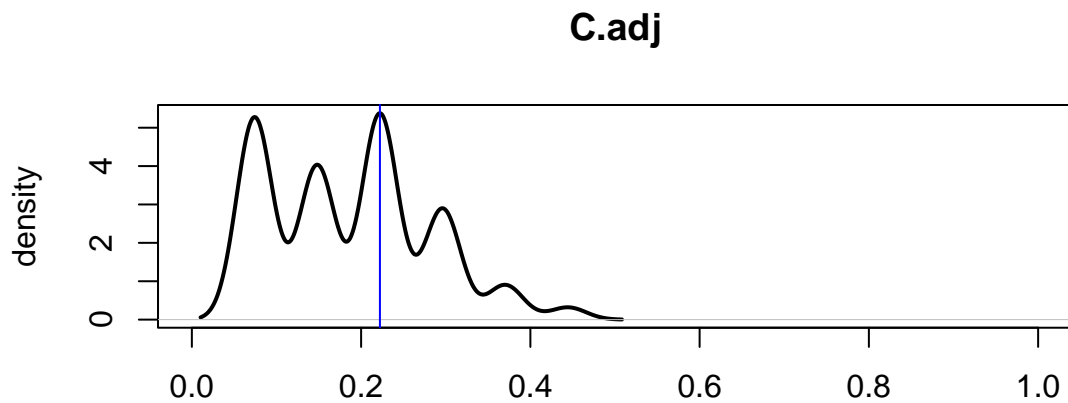


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.24

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.50

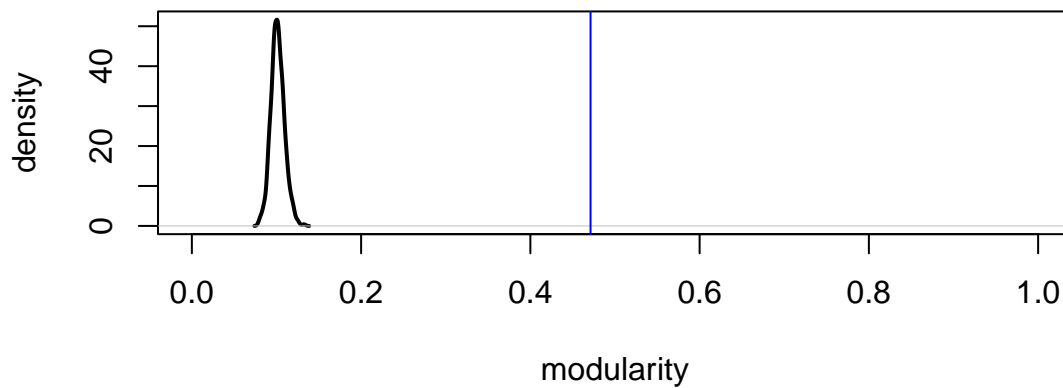
Dataset 13 : HAWAII

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.47
Number of Modules: 10

Comparison between observed modularity (blue line) and proportional null model (density in black)

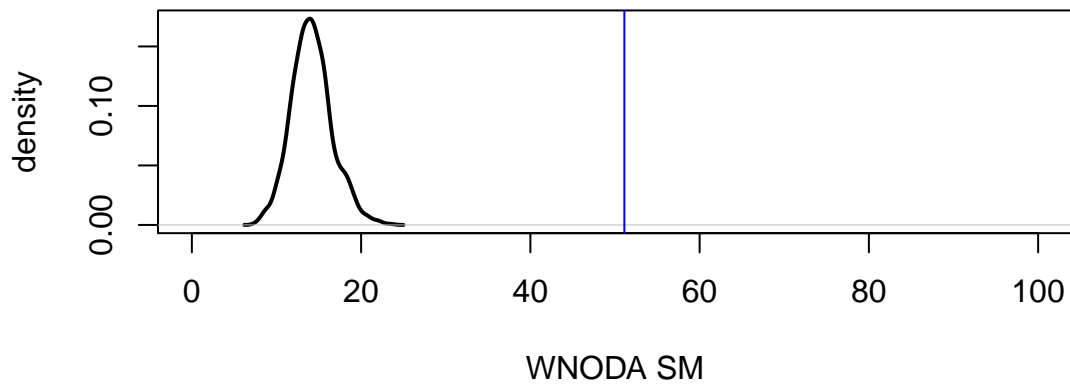


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 19
Nestedness between species in the same module: 51
Nestedness between species in different modules: 12

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

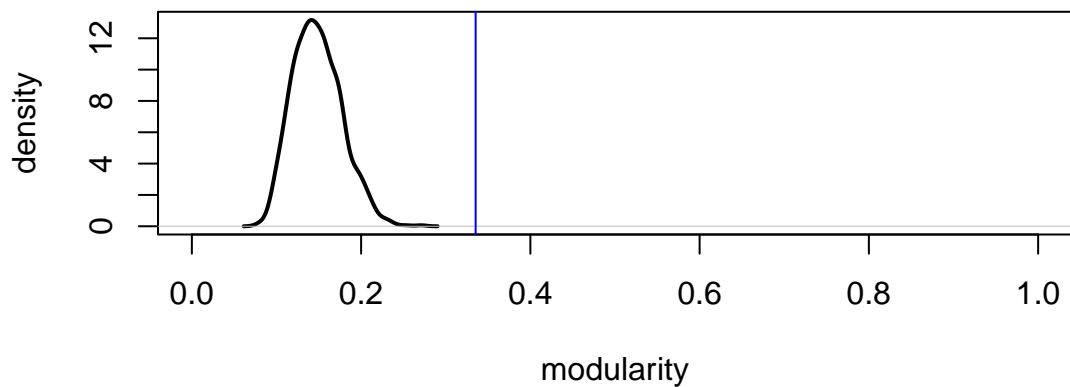
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.34
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

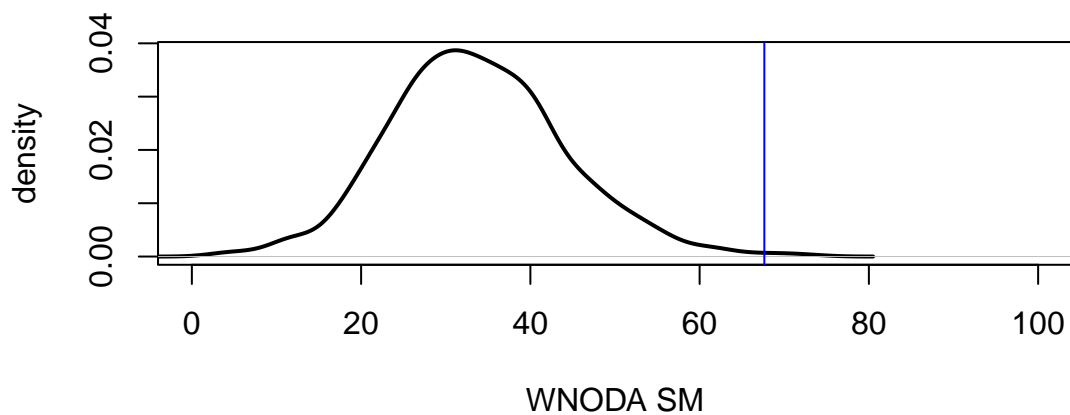


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 19
Nestedness between species in the same module 68
Nestedness between species in different modules 8.8

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.005

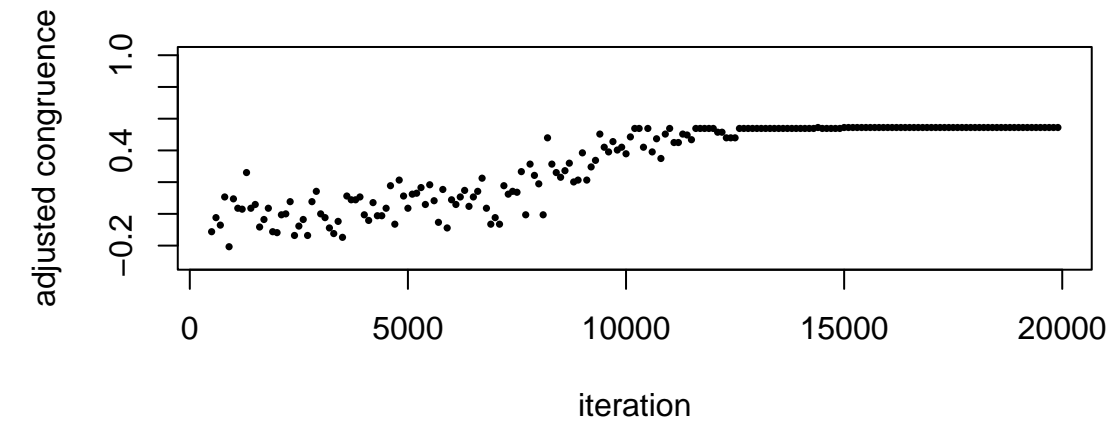
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

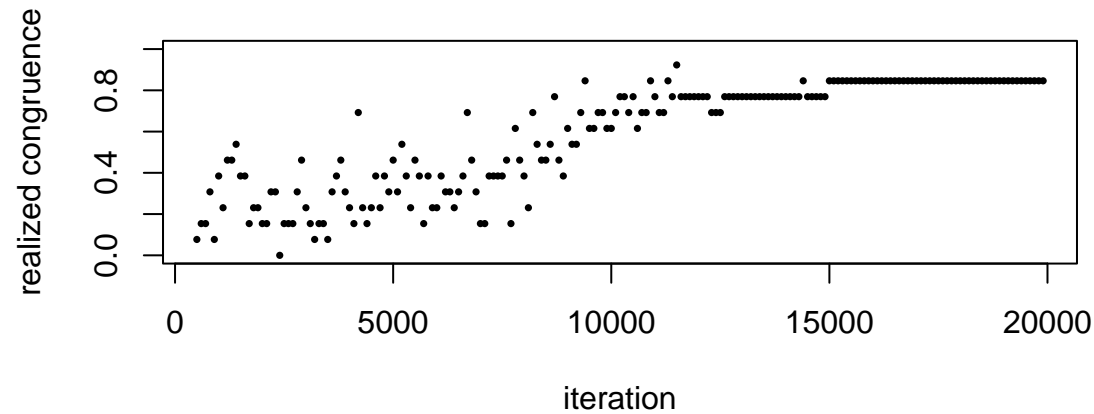
..
BN (A-B) Specialization (H2') 0.64
BN (A-B) Connectance 0.084
BN (B-C) Specialization (H2') 0.67
BN (B-C) Connectance 0.21
Plant richness in BN (A-B): 32
Herbivore richness in BN (A-B): 28
Herbivore richness in BN (B-C): 13
Parasitoid richness in BN (B-C): 7
Richness of shared Herbivores:13
Number of modules in BN (A-B) 10
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 9
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

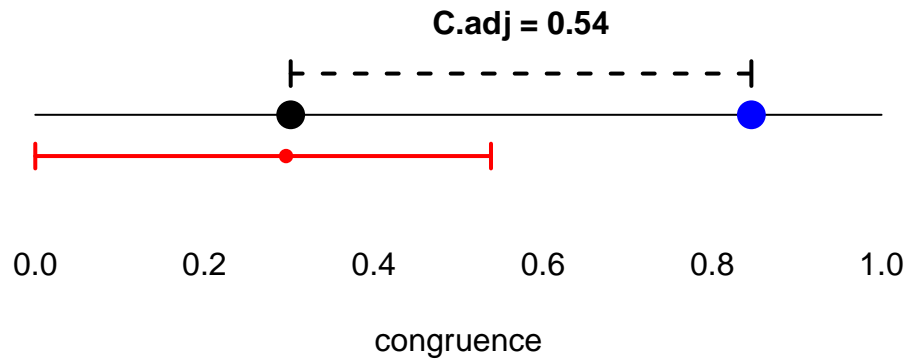


..



Adjusted Congruence: 0.54
Realized Congruence: 0.85
Hypermodularity: 0.12

Null Model 1

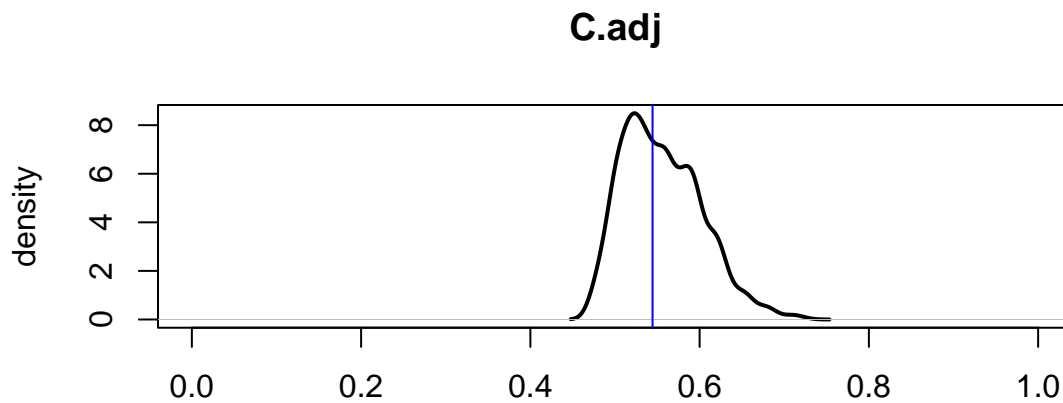


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.55

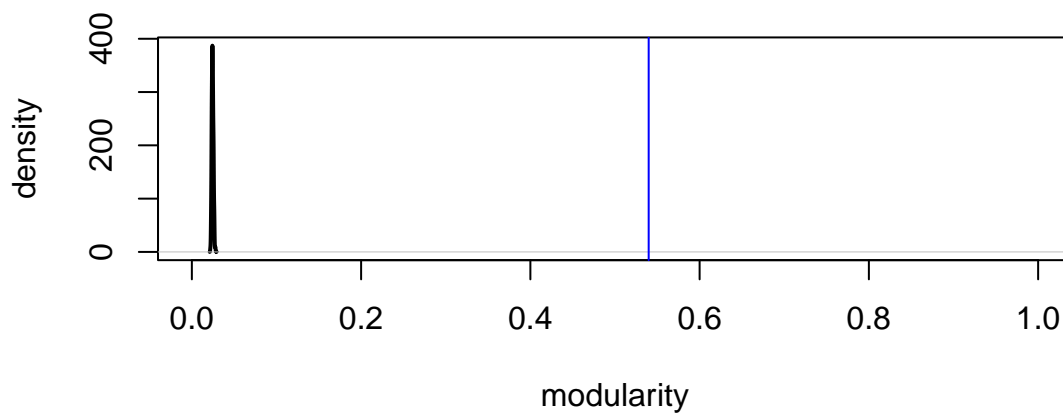
Dataset 14 : BRISTOL

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.54
Number of Modules: 23

Comparison between observed modularity (blue line) and proportional null model (density in black)

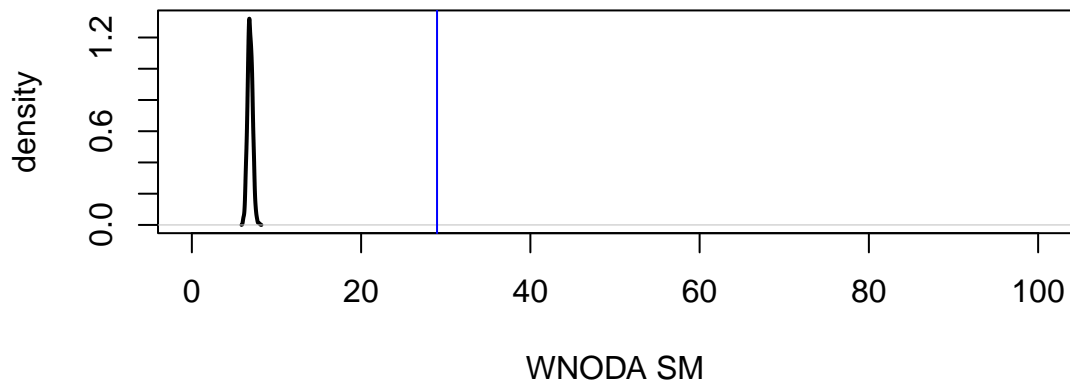


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 4.8
Nestedness between species in the same module: 29
Nestedness between species in different modules: 1.2

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

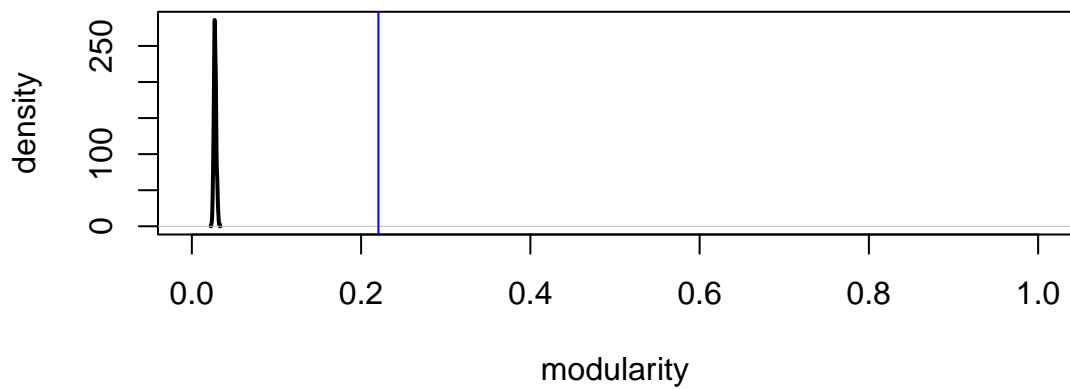
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.22
 Number of Modules: 7

Comparison between observed modularity (blue line) and proportional null model (density in black)

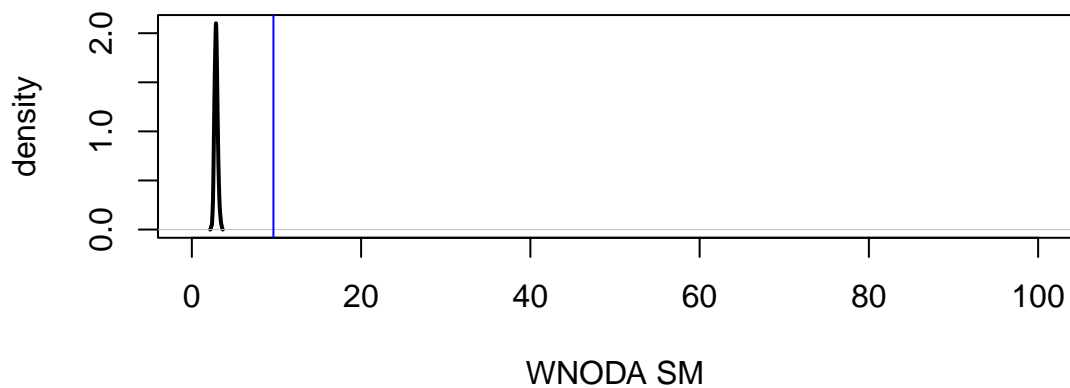


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 3
Nestedness between species in the same module 9.6
Nestedness between species in different modules 1.7

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

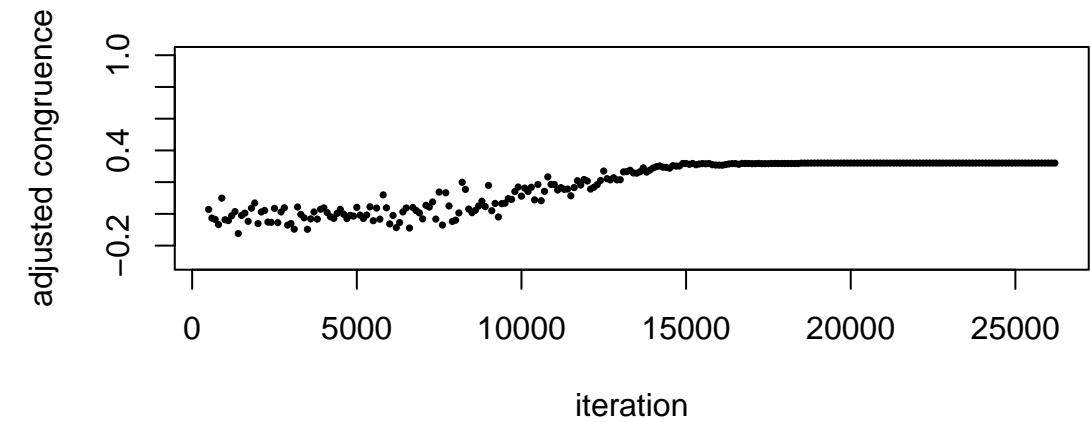
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

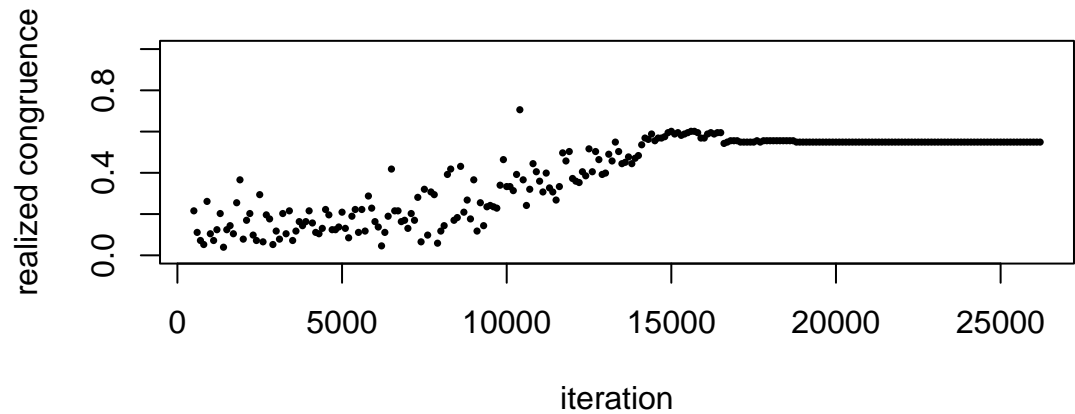
..
BN (A-B) Specialization (H2') 0.86
BN (A-B) Connectance 0.015
BN (B-C) Specialization (H2') 0.49
BN (B-C) Connectance 0.019
Plant richness in BN (A-B): 139
Herbivore richness in BN (A-B): 357
Herbivore richness in BN (B-C): 157
Parasitoid richness in BN (B-C): 192
Richness of shared Herbivores: 157
Number of modules in BN (A-B) 23
Number of modules in BN (B-C) 7

Number of modules in BN (A-B) (only for shared species) 21
Number of modules in BN (B-C) (only for shared species) 7

Hipermodule Congruence
Optmization procedure

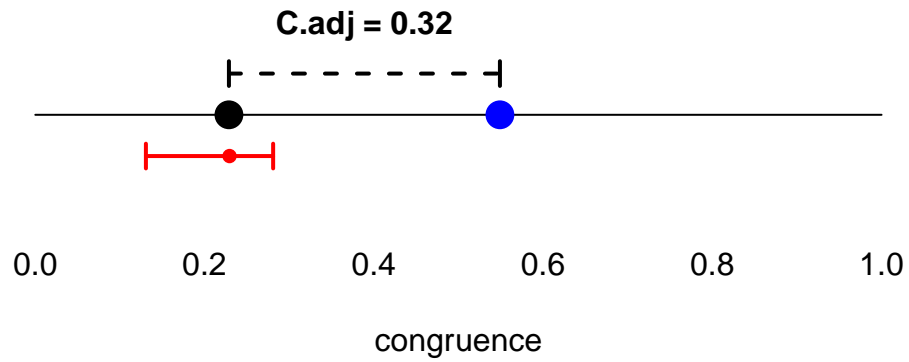


..



..
Adjusted Congruence: 0.32
Realized Congruence: 0.55
Hypermodularity: 0.27

Null Model 1

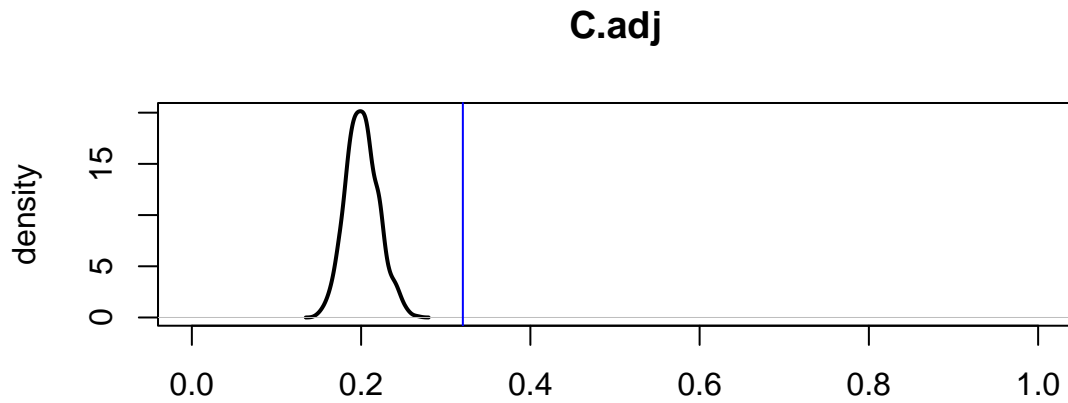


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0

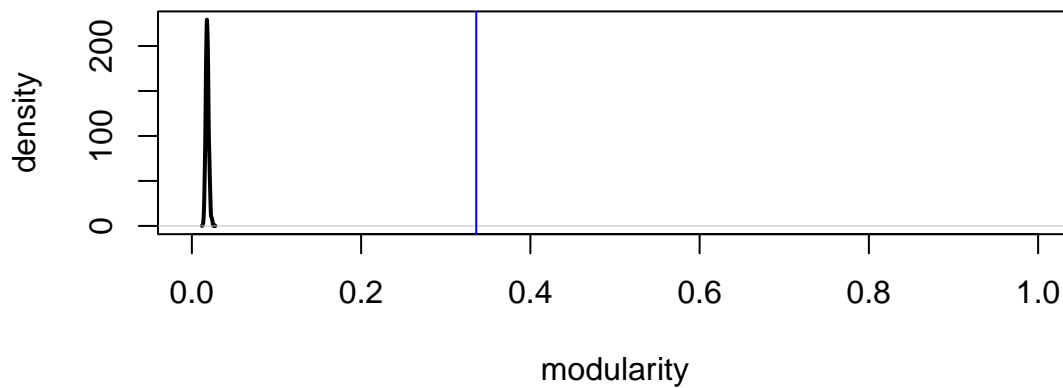
Dataset 15 : POLAND

Topology BN (A-B): Seed disperser - Plant

Modularity

..
Observed Modularity: 0.34
Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

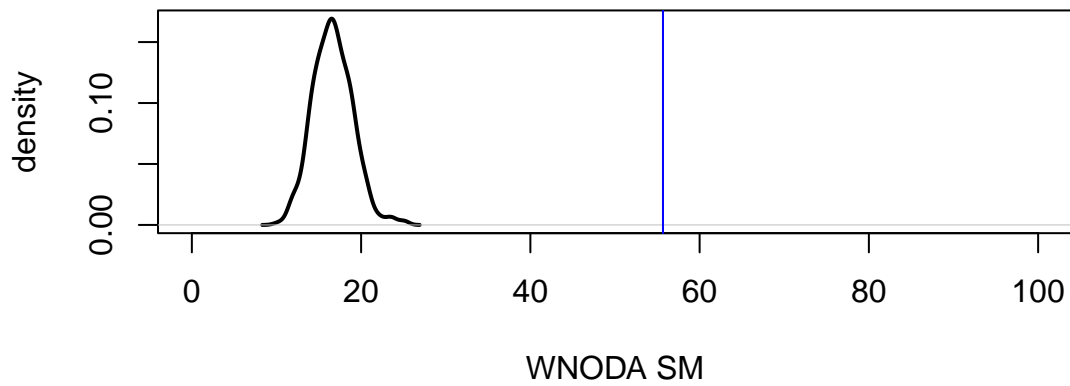


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 54
Nestedness between species in the same module: 56
Nestedness between species in different modules: 53

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

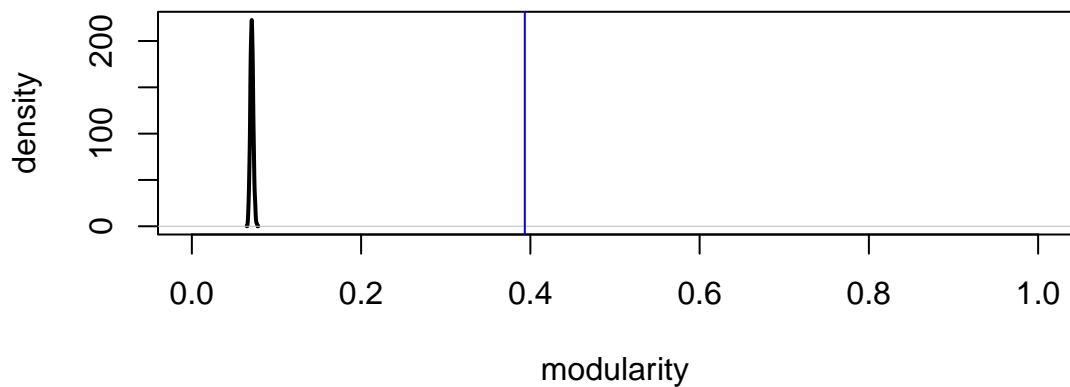
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Pollinator

Modularity

..
 Observed Modularity: 0.39
 Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

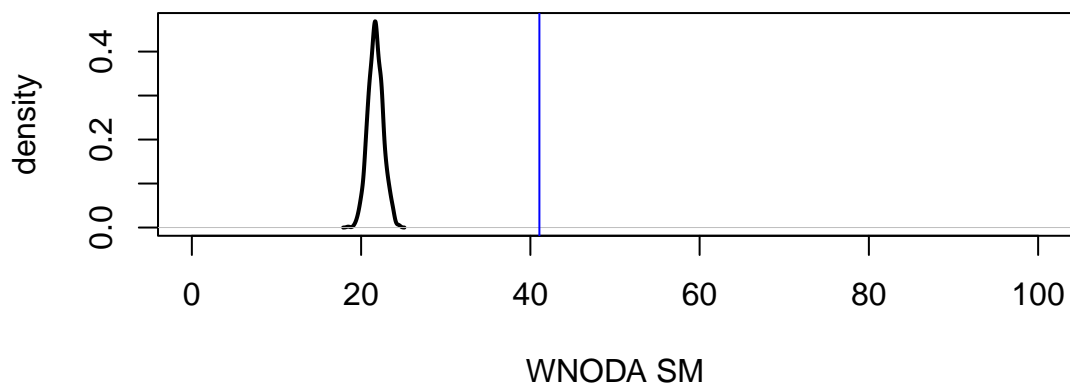


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 23
Nestedness between species in the same module 41
Nestedness between species in different modules 19

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

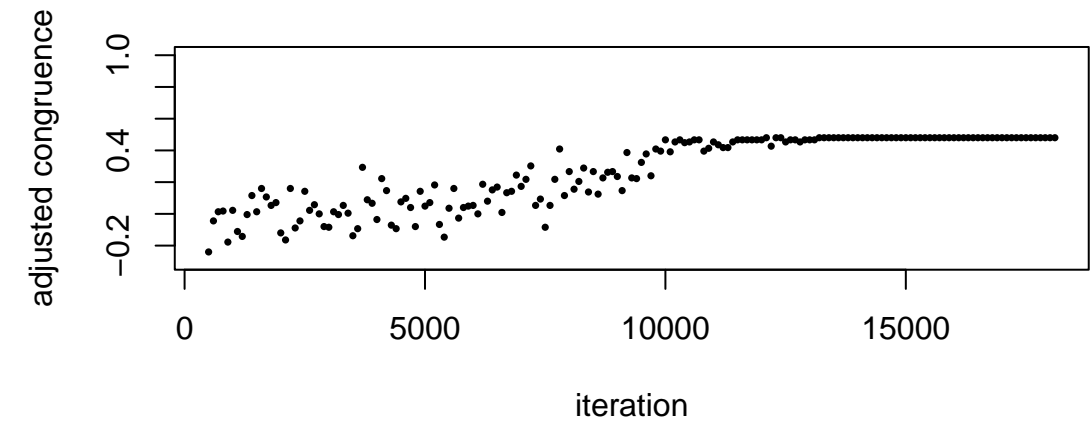
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

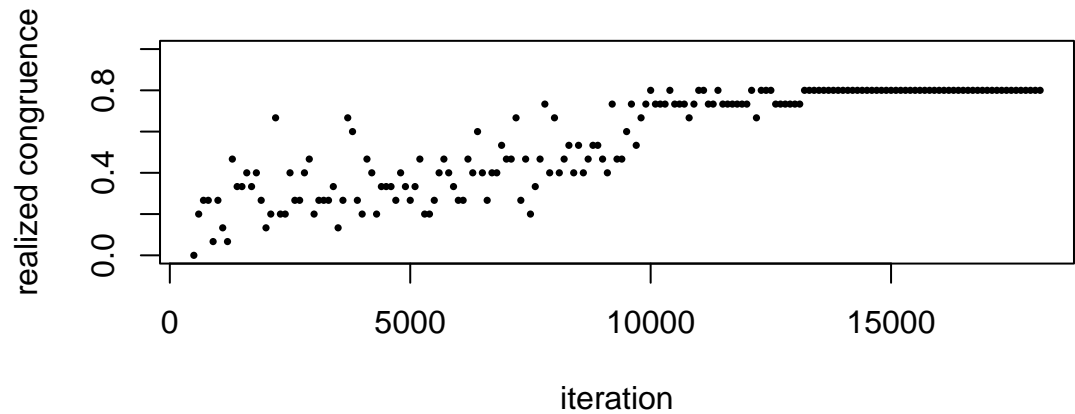
..
BN (A-B) Specialization (H2') 0.27
BN (A-B) Connectance 0.26
BN (B-C) Specialization (H2') 0.43
BN (B-C) Connectance 0.23
Seed disperser richness in BN (A-B): 34
Plant richness in BN (A-B): 15
Plant richness in BN (B-C): 15
Pollinator richness in BN (B-C): 308
Richness of shared Plants:15
Number of modules in BN (A-B) 4
Number of modules in BN (B-C) 9

Number of modules in BN (A-B) (only for shared species) 4
Number of modules in BN (B-C) (only for shared species) 9

Hipermodule Congruence
Optmization procedure

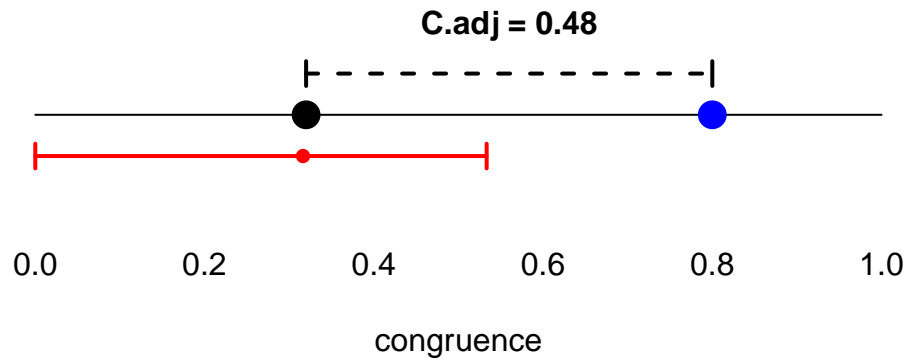


..



Adjusted Congruence: 0.48
Realized Congruence: 0.8
Hypermodularity: 0.27

Null Model 1

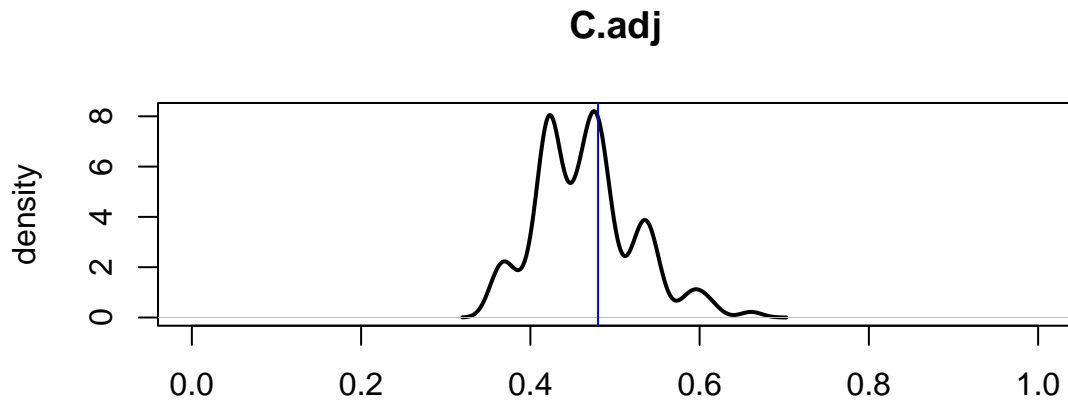


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.35

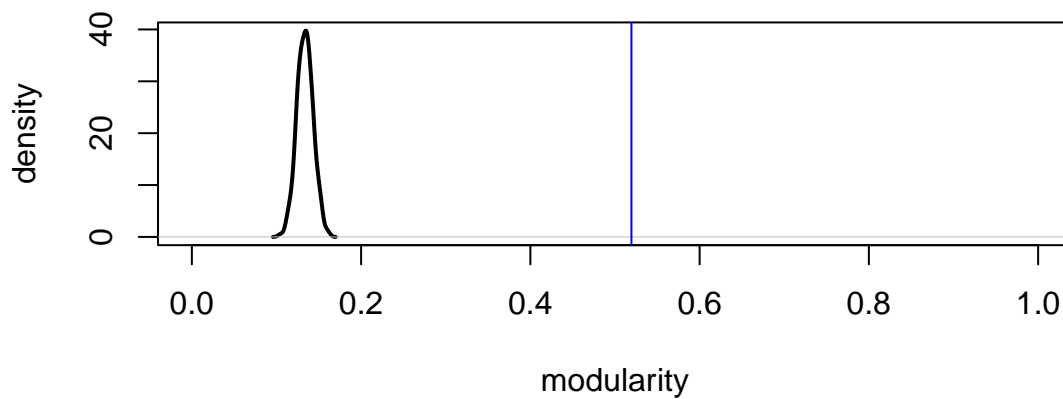
Dataset 16 : GALAPAGOS

Topology BN (A-B): Plant - Seed disperser

Modularity

..
Observed Modularity: 0.52
Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

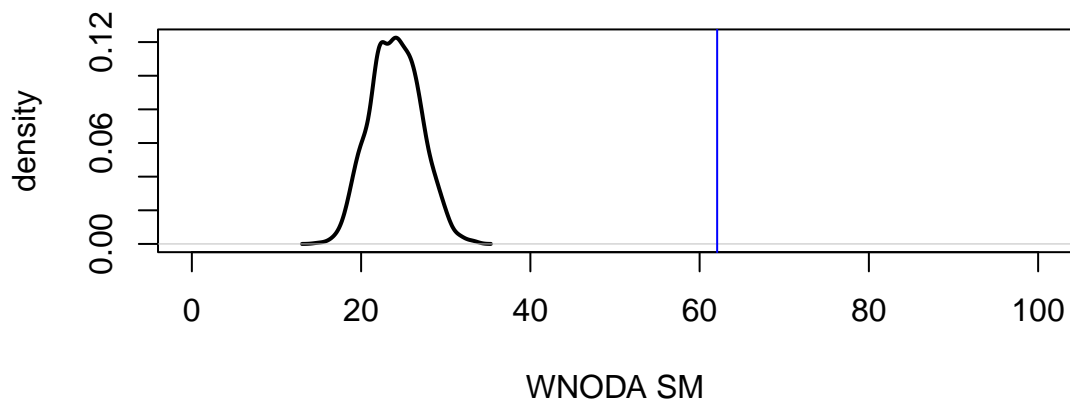


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 23
Nestedness between species in the same module: 62
Nestedness between species in different modules: 12

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

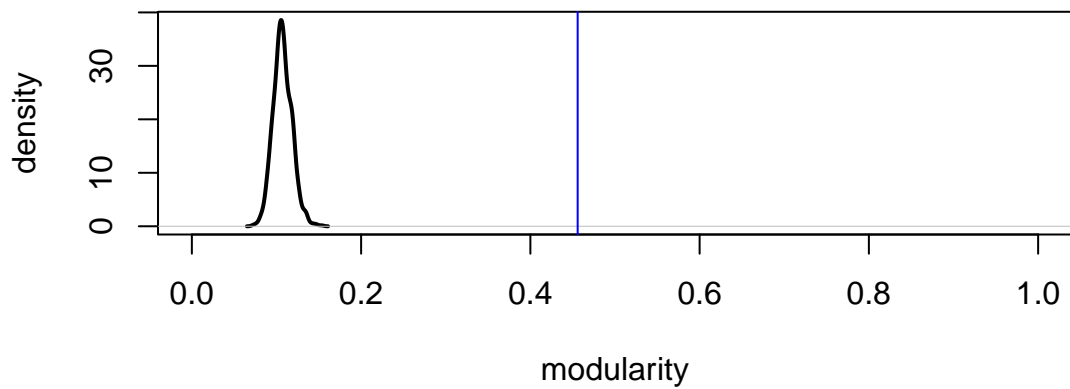
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Seed disperser - Parasite

Modularity

..
 Observed Modularity: 0.46
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

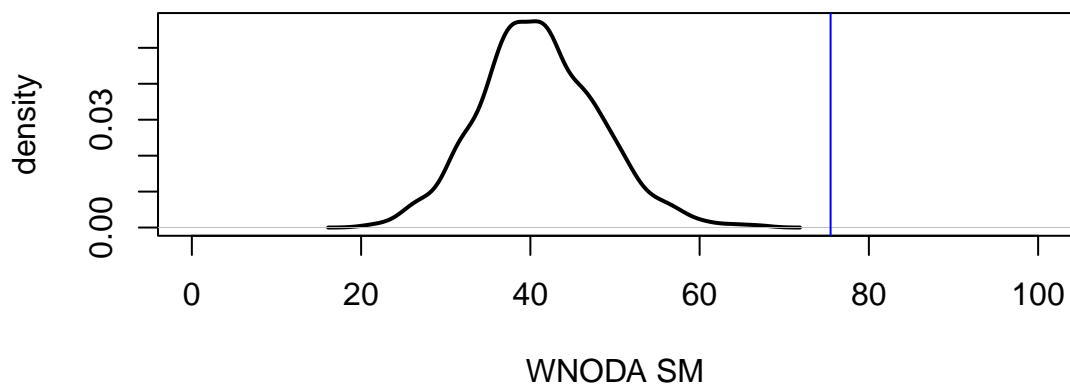


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 26
Nestedness between species in the same module 75
Nestedness between species in different modules 15

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

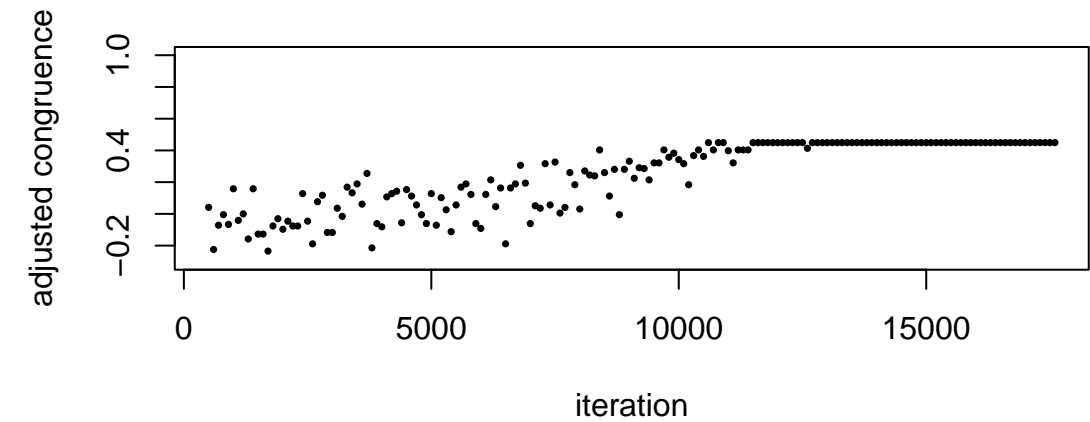
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

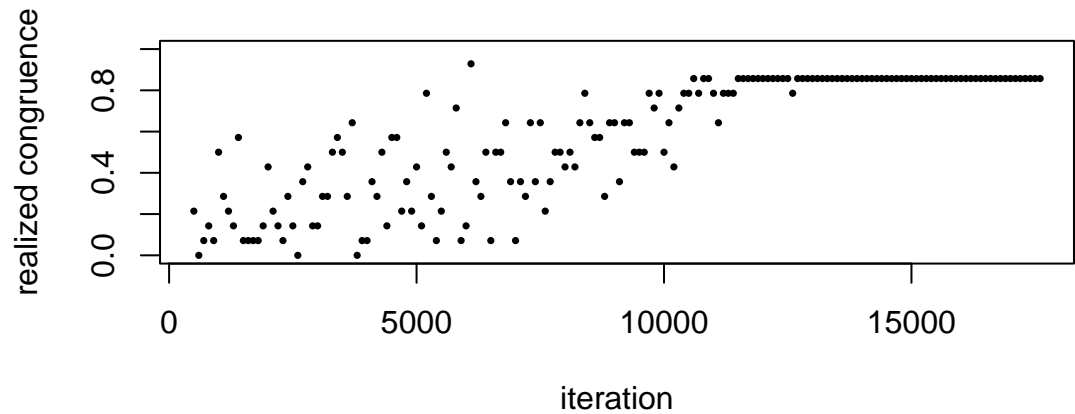
..
BN (A-B) Specialization (H2') 0.5
BN (A-B) Connectance 0.15
BN (B-C) Specialization (H2') 0.55
BN (B-C) Connectance 0.21
Plant richness in BN (A-B): 46
Seed disperser richness in BN (A-B): 16
Seed disperser richness in BN (B-C): 15
Parasite richness in BN (B-C): 13
Richness of shared Seed dispersers: 15
Number of modules in BN (A-B) 6
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 6
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

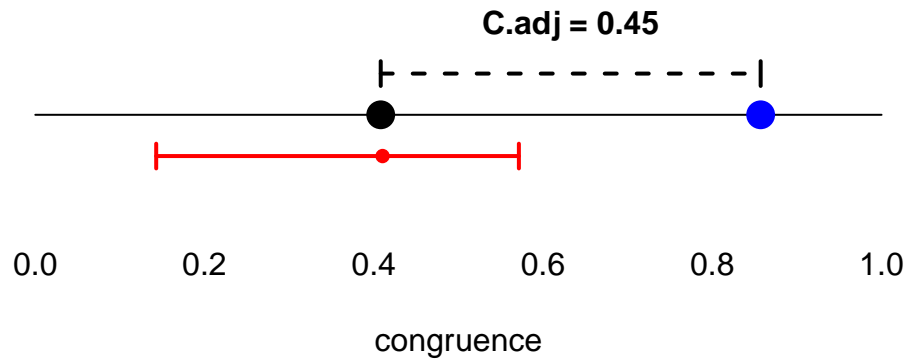


..



Adjusted Congruence: 0.45
Realized Congruence: 0.86
Hypermodularity: 0.34

Null Model 1

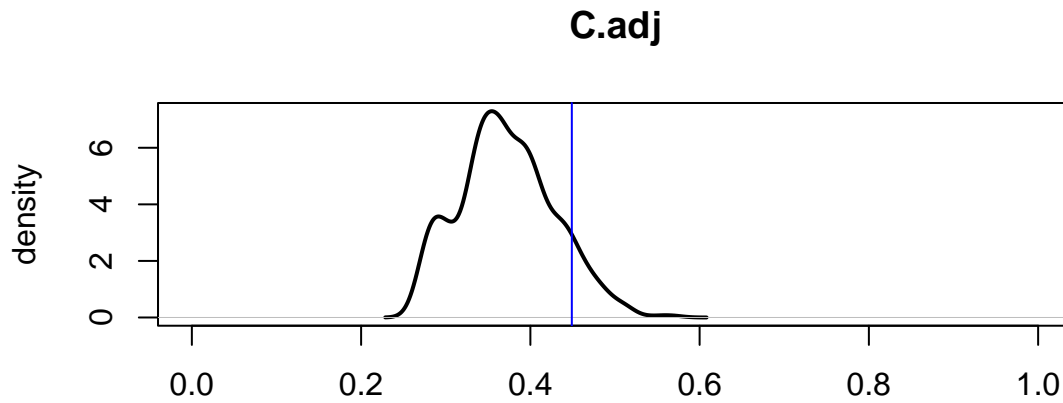


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.002

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.11

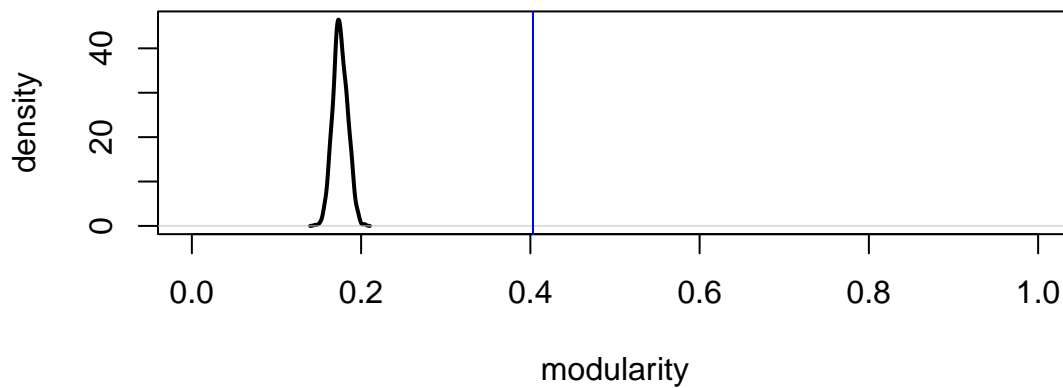
Dataset 17 : MOZAMBIQUE

Topology BN (A-B): Mycorrhiza - Plant

Modularity

..
Observed Modularity: 0.4
Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

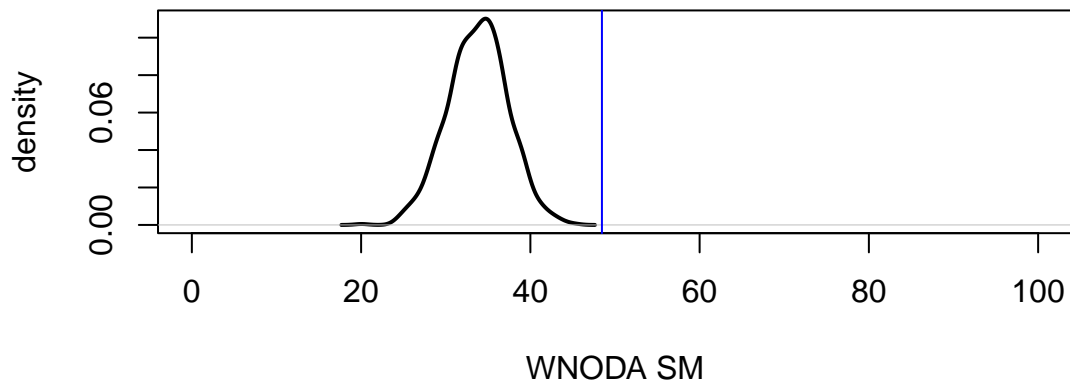


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 20
Nestedness between species in the same module: 48
Nestedness between species in different modules: 12

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

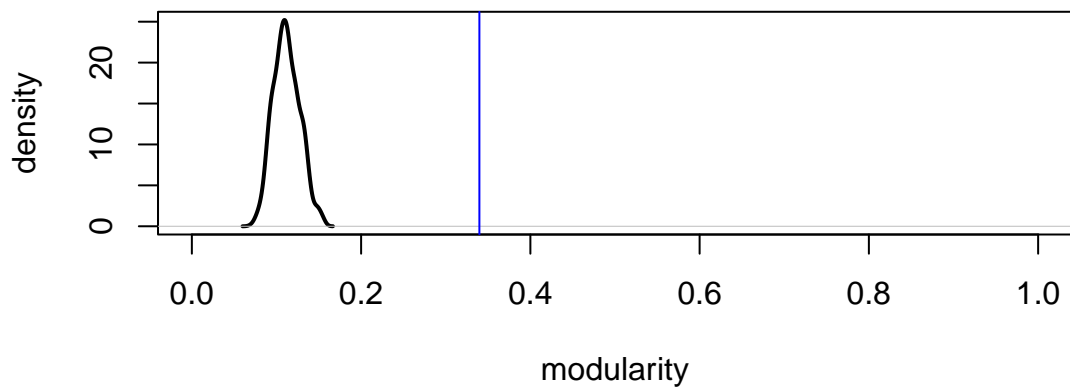
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Seed disperser

Modularity

..
 Observed Modularity: 0.34
 Number of Modules: 7

Comparison between observed modularity (blue line) and proportional null model (density in black)

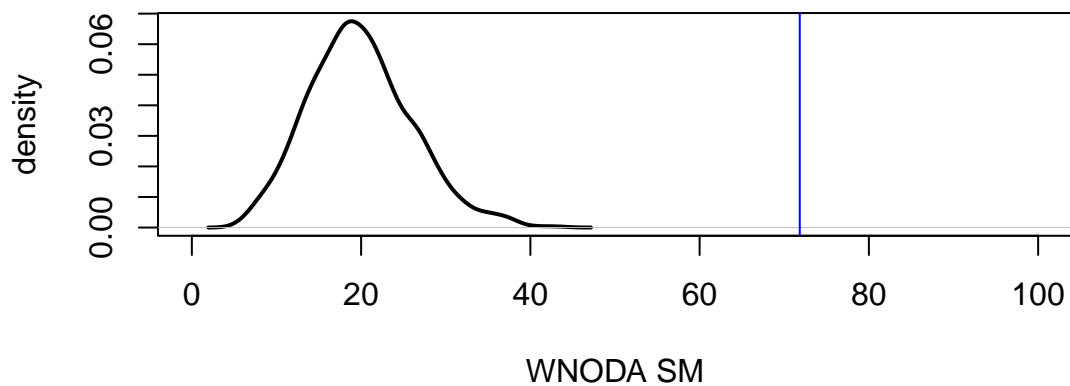


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 23
Nestedness between species in the same module 72
Nestedness between species in different modules 16

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

CONCLUSION: BN (B-C) has a compound topology

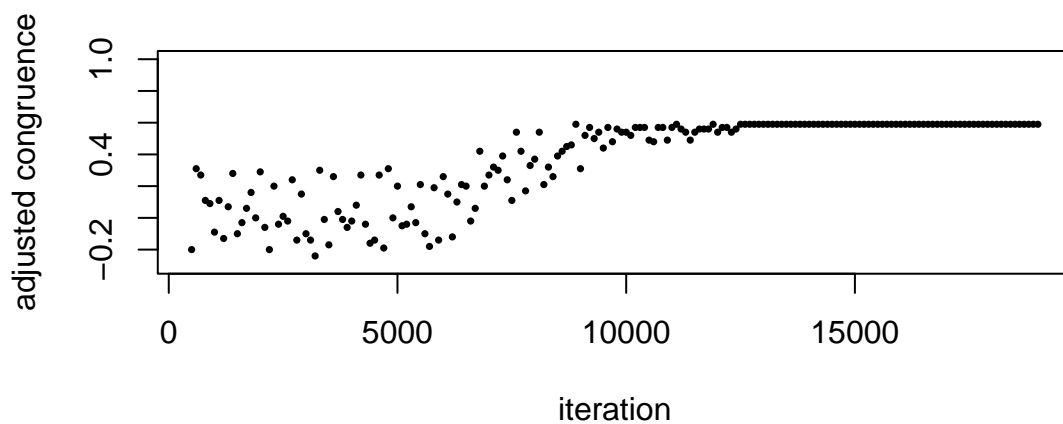
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 0.38
BN (A-B) Connectance 0.18
BN (B-C) Specialization (H2') 0.42
BN (B-C) Connectance 0.16
Mycorrhiza richness in BN (A-B): 55
Plant richness in BN (A-B): 16
Plant richness in BN (B-C): 16
Seed disperser richness in BN (B-C): 16
Richness of shared Plants: 16
Number of modules in BN (A-B) 8
Number of modules in BN (B-C) 7

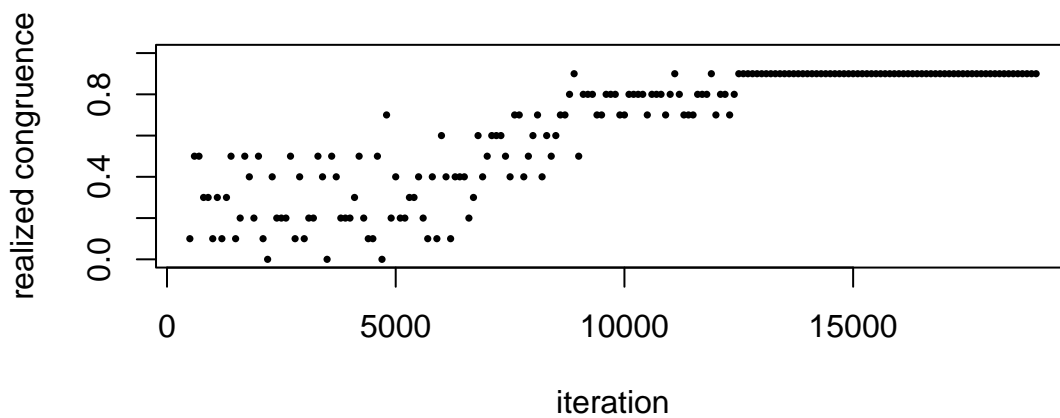
Number of modules in BN (A-B) (only for shared species) 6
Number of modules in BN (B-C) (only for shared species) 6

Hipermodule Congruence

Optimization procedure



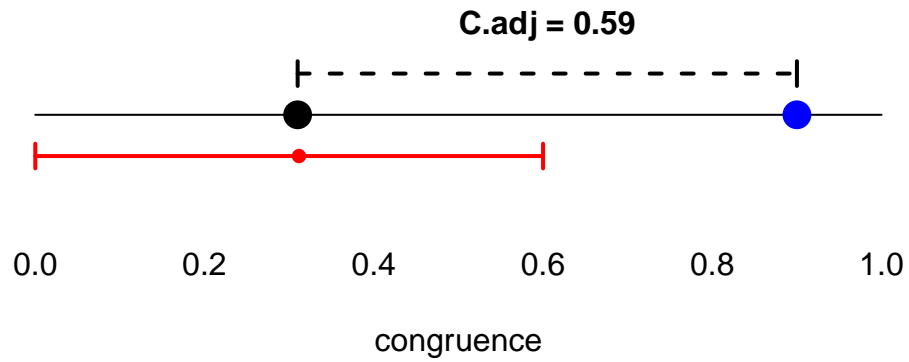
..



..

Adjusted Congruence: 0.59
Realized Congruence: 0.9
Hypermodularity: 0.44

Null Model 1

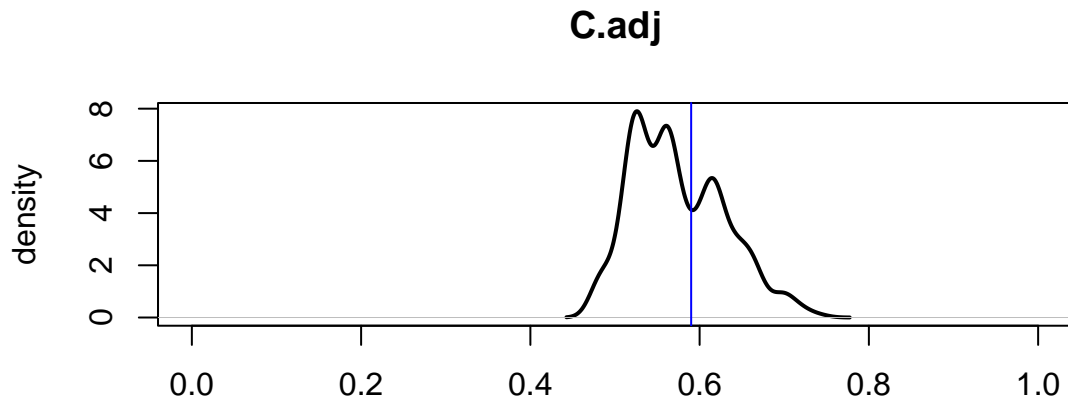


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.38

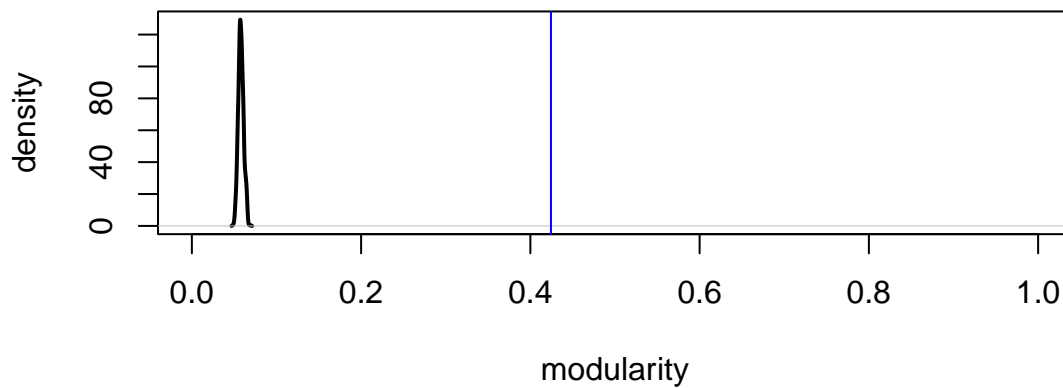
Dataset 18 : NEW ZEALAND

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.42
Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

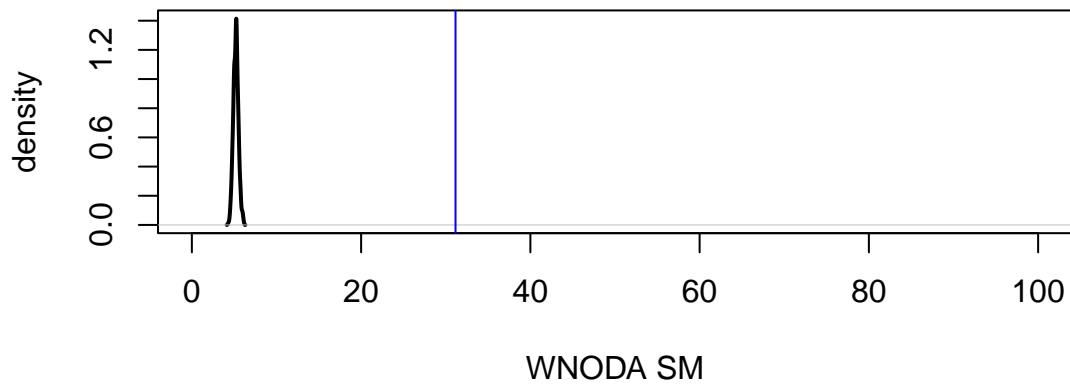


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 22
Nestedness between species in the same module: 31
Nestedness between species in different modules: 18

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

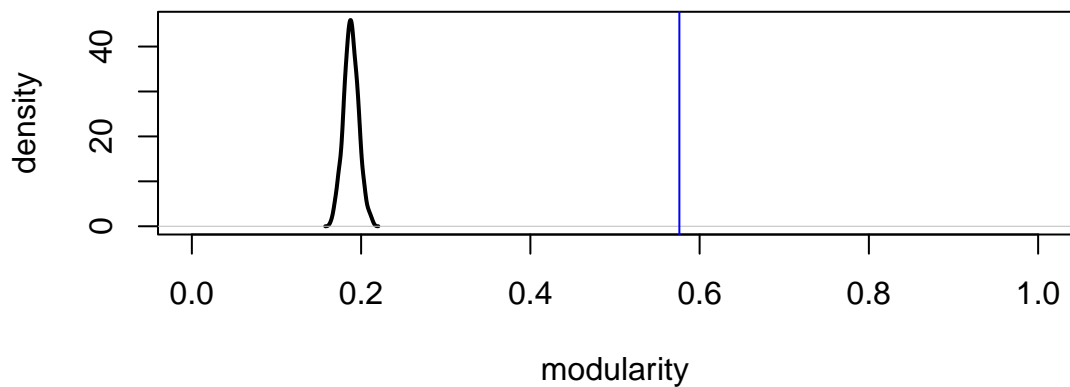
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.58
 Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

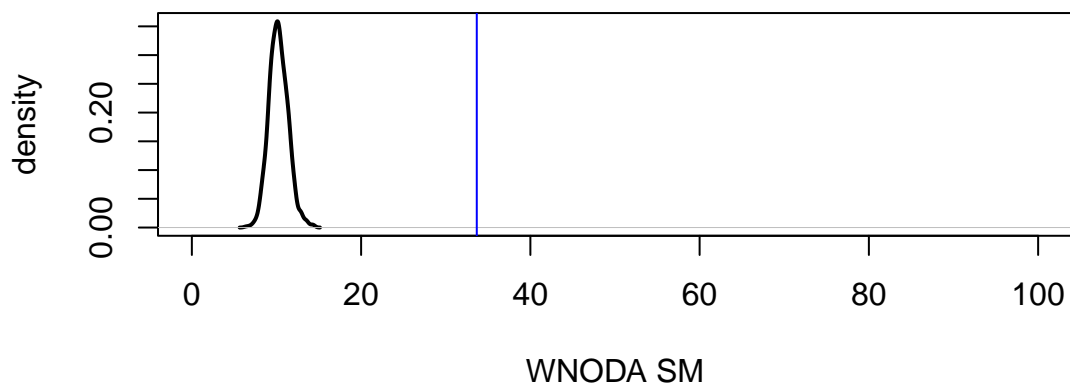


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 9.2
Nestedness between species in the same module 34
Nestedness between species in different modules 4.7

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

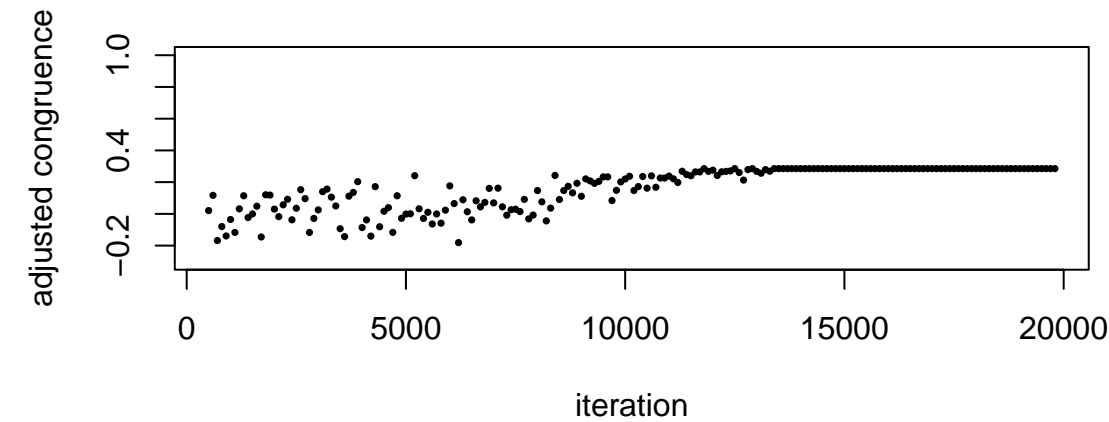
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

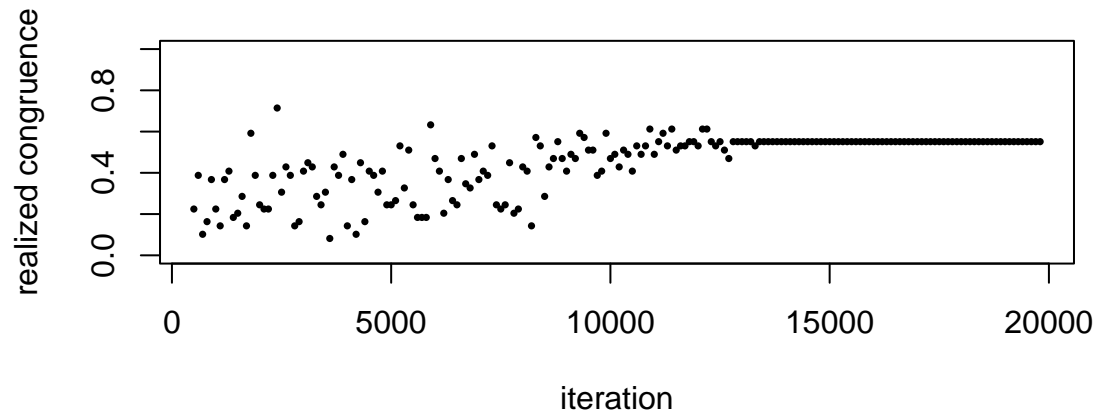
..
BN (A-B) Specialization (H2') 0.33
BN (A-B) Connectance 0.08
BN (B-C) Specialization (H2') 0.5
BN (B-C) Connectance 0.074
Plant richness in BN (A-B): 75
Herbivore richness in BN (A-B): 90
Herbivore richness in BN (B-C): 49
Parasitoid richness in BN (B-C): 60
Richness of shared Herbivores: 49
Number of modules in BN (A-B) 5
Number of modules in BN (B-C) 8

Number of modules in BN (A-B) (only for shared species) 4
Number of modules in BN (B-C) (only for shared species) 8

Hipermodule Congruence
Optmization procedure

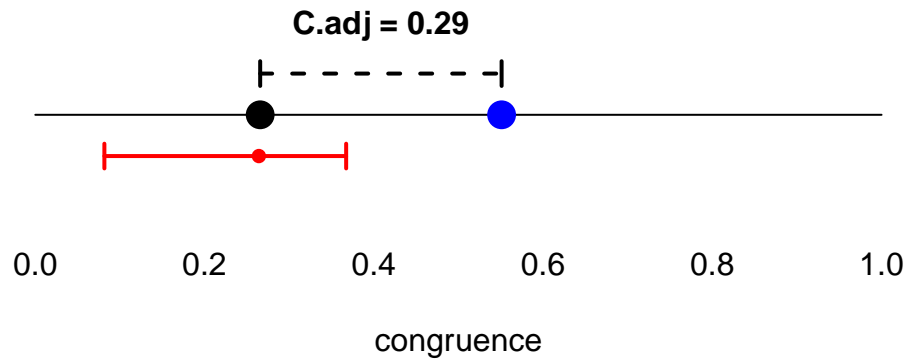


..



..
Adjusted Congruence: 0.29
Realized Congruence: 0.55
Hypermodularity: 0.32

Null Model 1

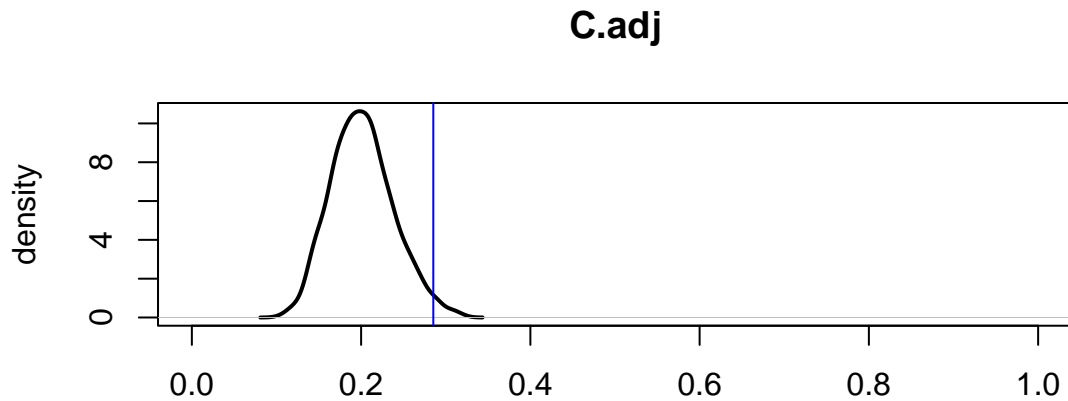


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.022

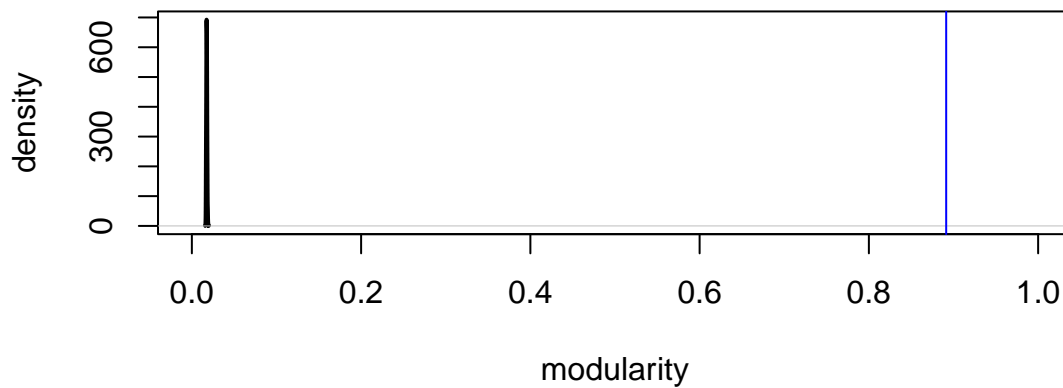
Dataset 19 : CORDOBA1

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.89
Number of Modules: 38

Comparison between observed modularity (blue line) and proportional null model (density in black)

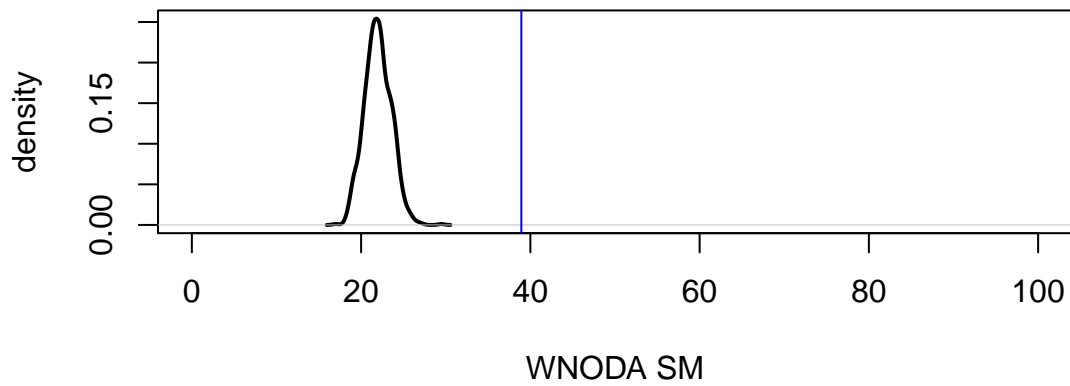


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 1.9
Nestedness between species in the same module: 39
Nestedness between species in different modules: 0.51

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

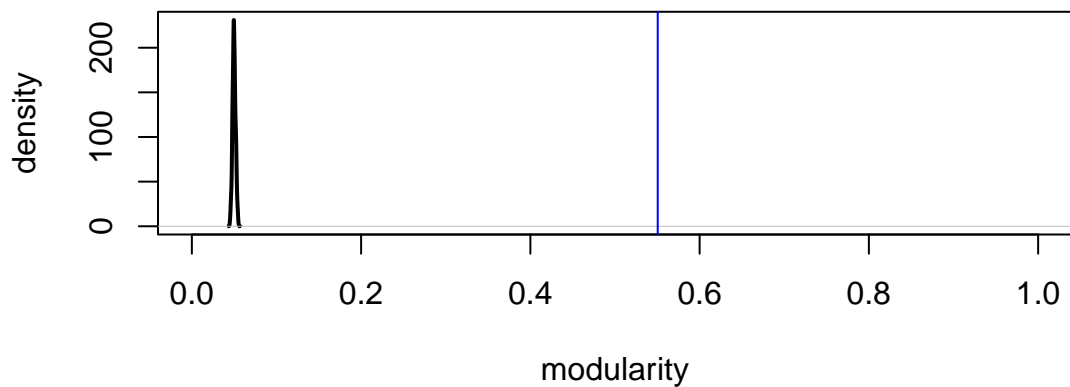
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.55
 Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

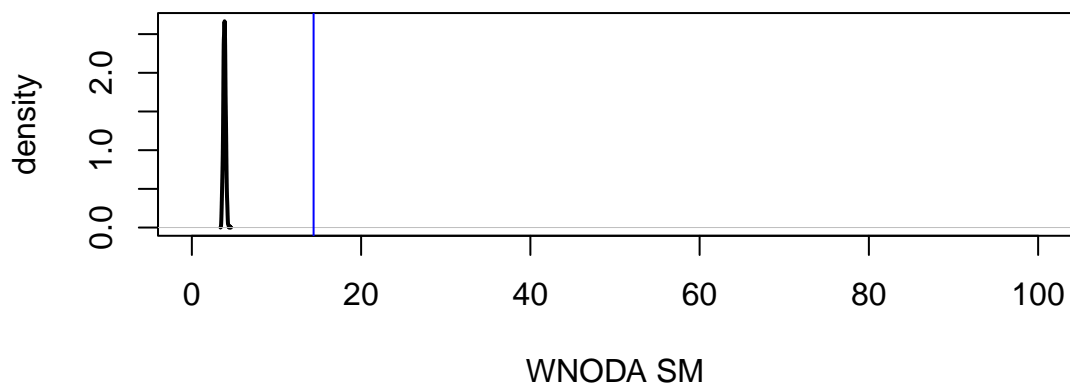


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 7.6
Nestedness between species in the same module 14
Nestedness between species in different modules 4.3

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

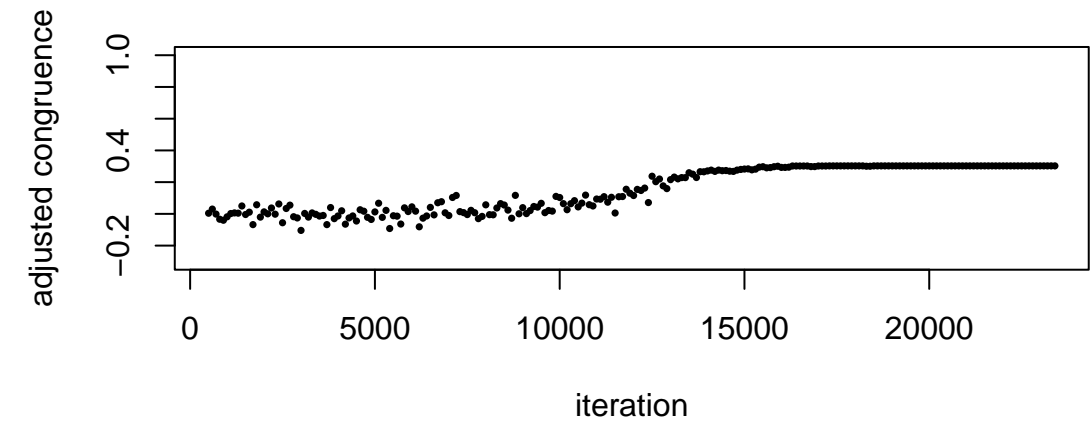
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

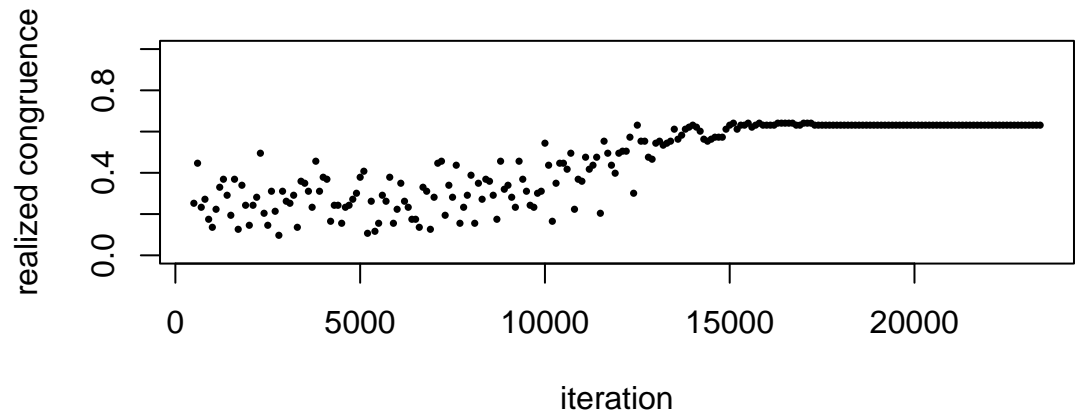
..
BN (A-B) Specialization (H2') 0.96
BN (A-B) Connectance 0.018
BN (B-C) Specialization (H2') 0.6
BN (B-C) Connectance 0.042
Plant richness in BN (A-B): 111
Herbivore richness in BN (A-B): 131
Herbivore richness in BN (B-C): 103
Parasitoid richness in BN (B-C): 232
Richness of shared Herbivores: 103
Number of modules in BN (A-B) 38
Number of modules in BN (B-C) 4

Number of modules in BN (A-B) (only for shared species) 35
Number of modules in BN (B-C) (only for shared species) 4

Hipermodule Congruence
Optmization procedure

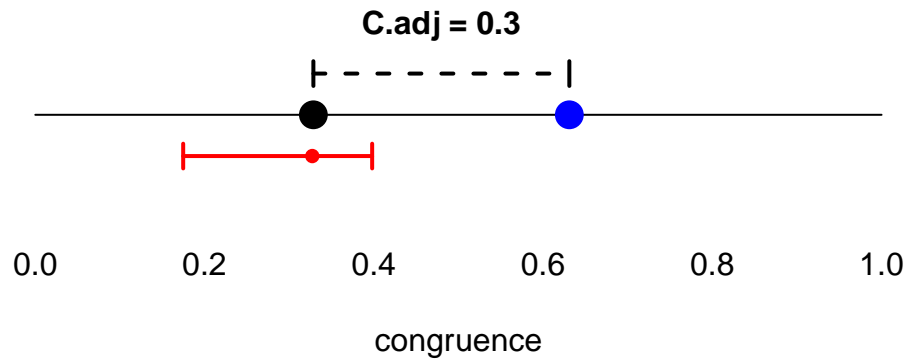


..



Adjusted Congruence: 0.3
Realized Congruence: 0.63
Hypermodularity: 0.12

Null Model 1

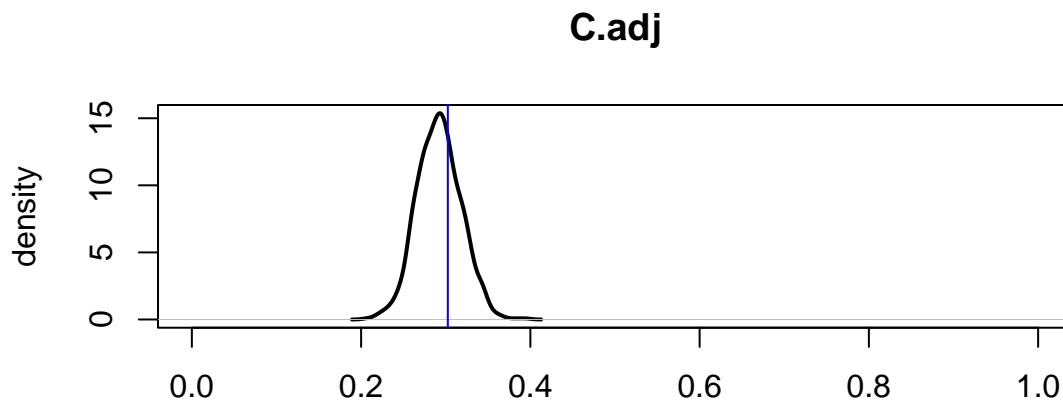


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.33

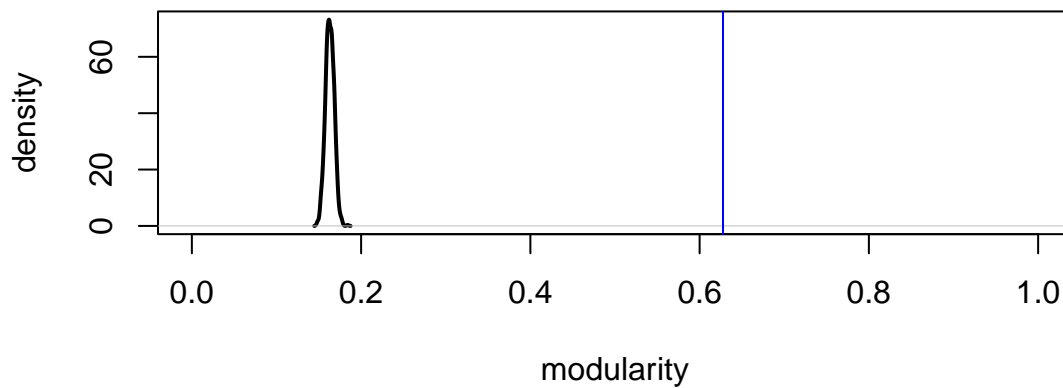
Dataset 20 : CORDOBA2

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.63
Number of Modules: 21

Comparison between observed modularity (blue line) and proportional null model (density in black)

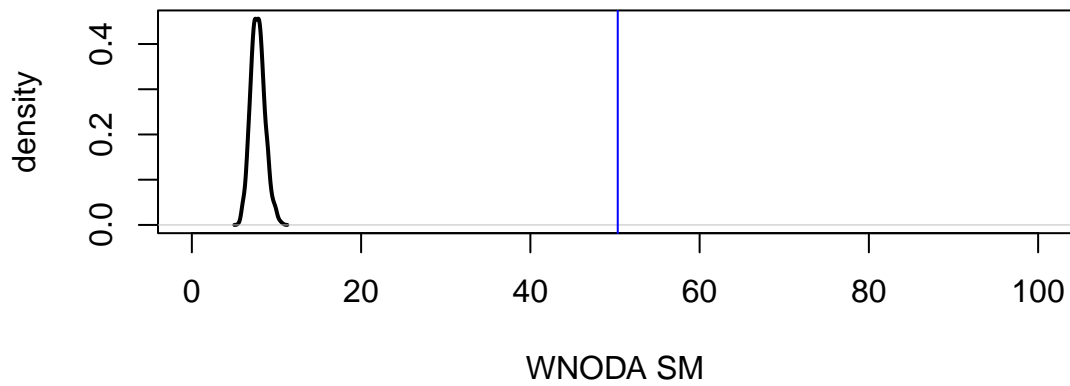


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 12
Nestedness between species in the same module: 50
Nestedness between species in different modules: 8.6

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

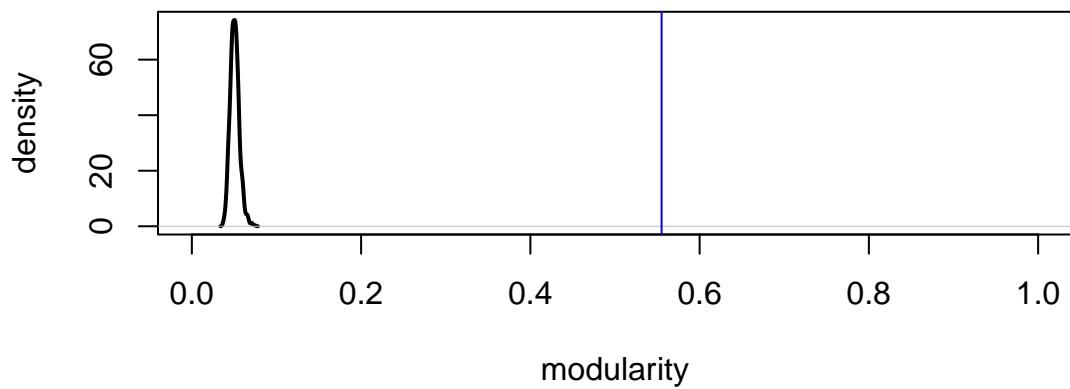
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.56
 Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

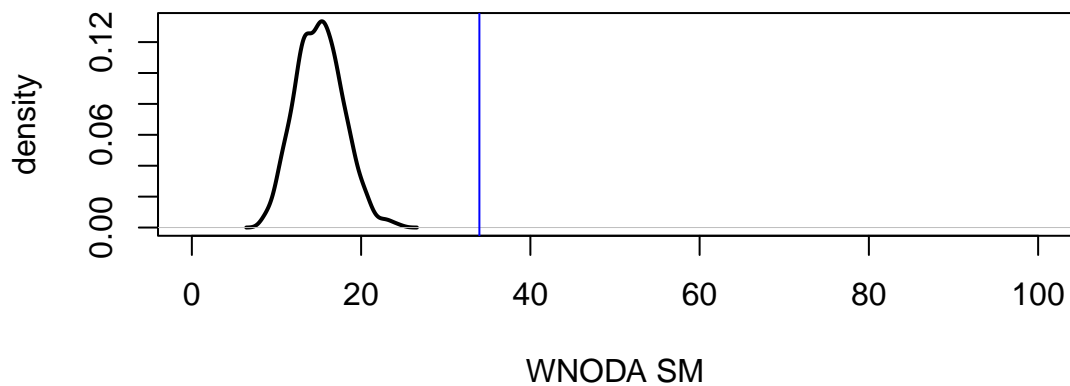


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 8.6
Nestedness between species in the same module 34
Nestedness between species in different modules 1.7

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

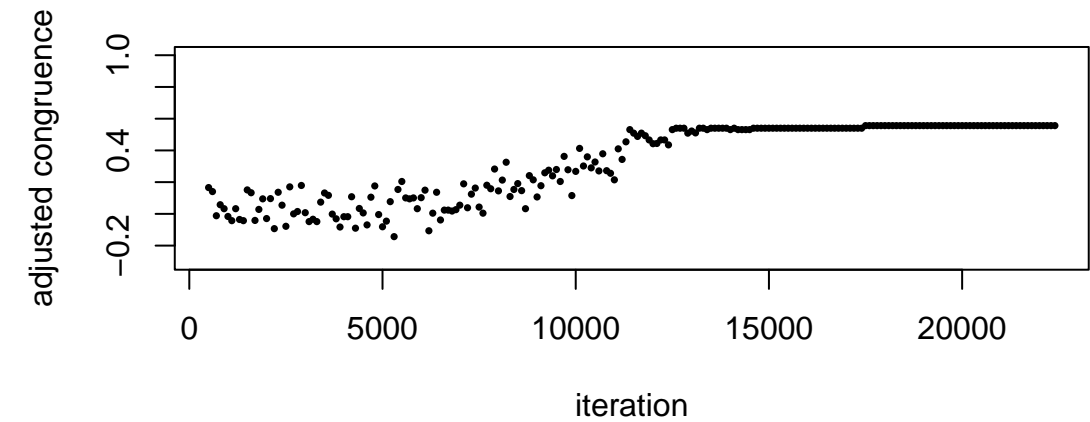
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

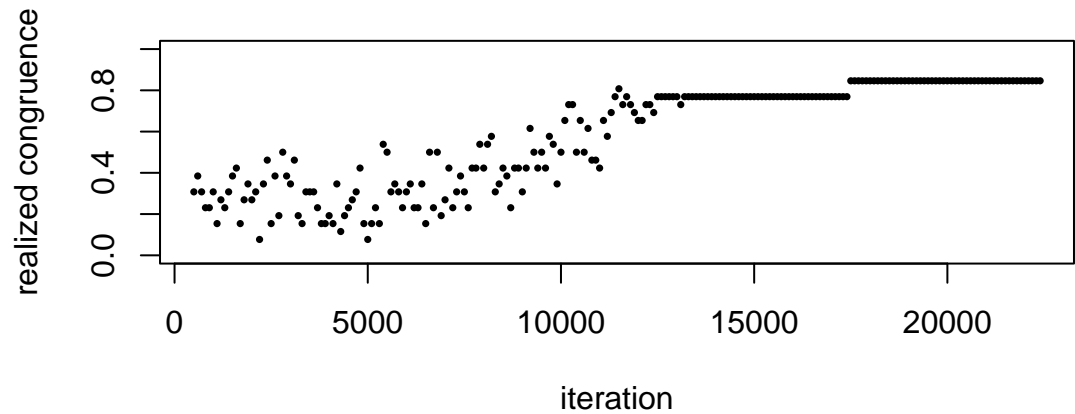
..
BN (A-B) Specialization (H2') 0.58
BN (A-B) Connectance 0.045
BN (B-C) Specialization (H2') 0.88
BN (B-C) Connectance 0.078
Plant richness in BN (A-B): 109
Herbivore richness in BN (A-B): 85
Herbivore richness in BN (B-C): 27
Parasitoid richness in BN (B-C): 27
Richness of shared Herbivores: 27
Number of modules in BN (A-B) 21
Number of modules in BN (B-C) 6

Number of modules in BN (A-B) (only for shared species) 16
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

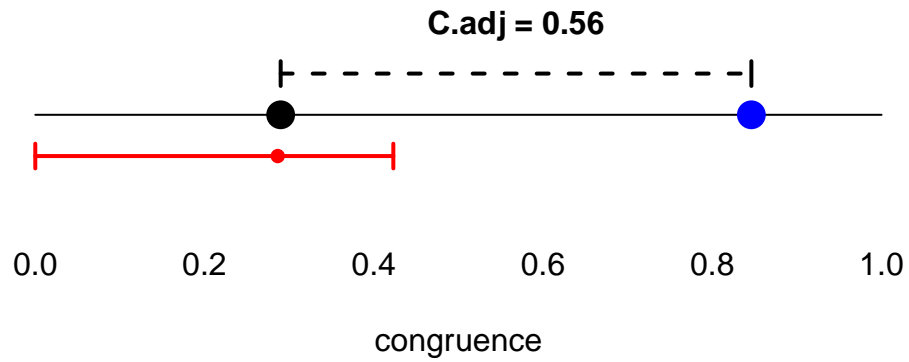


..



..
Adjusted Congruence: 0.56
Realized Congruence: 0.85
Hypermodularity: 0.39

Null Model 1

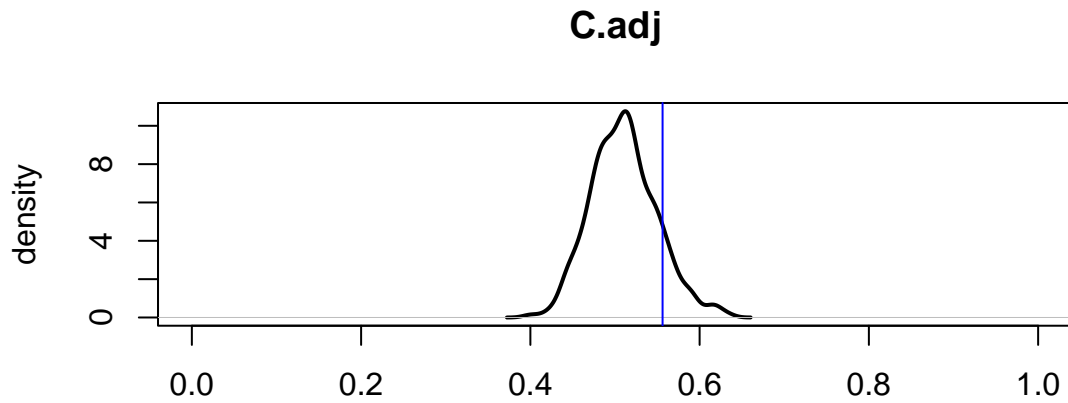


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.12

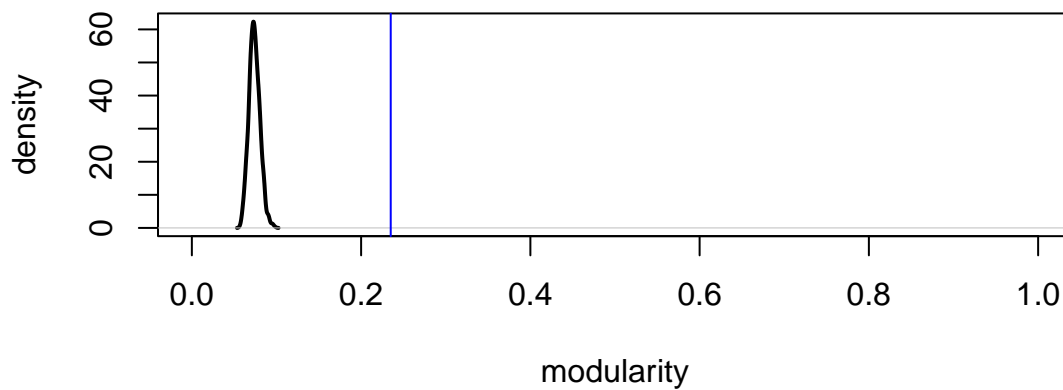
Dataset 21 : CORDOBA2

Topology BN (A-B): Plant defender - Plant

Modularity

..
Observed Modularity: 0.23
Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

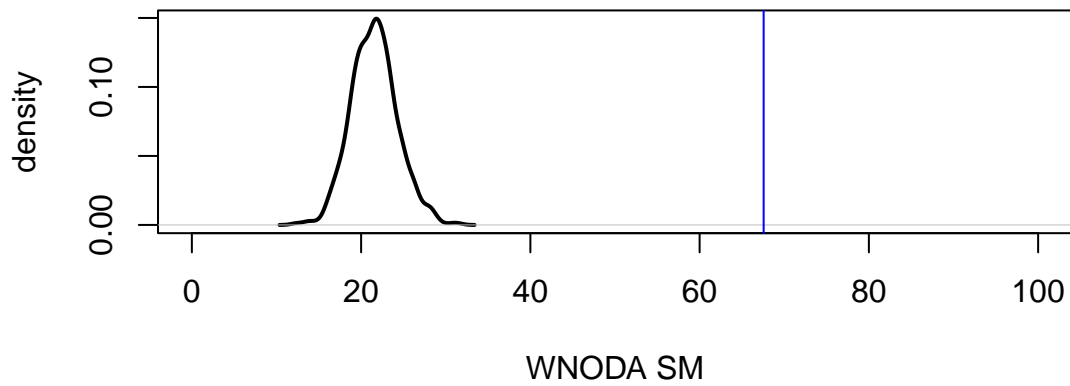


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 59
Nestedness between species in the same module: 68
Nestedness between species in different modules: 55

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

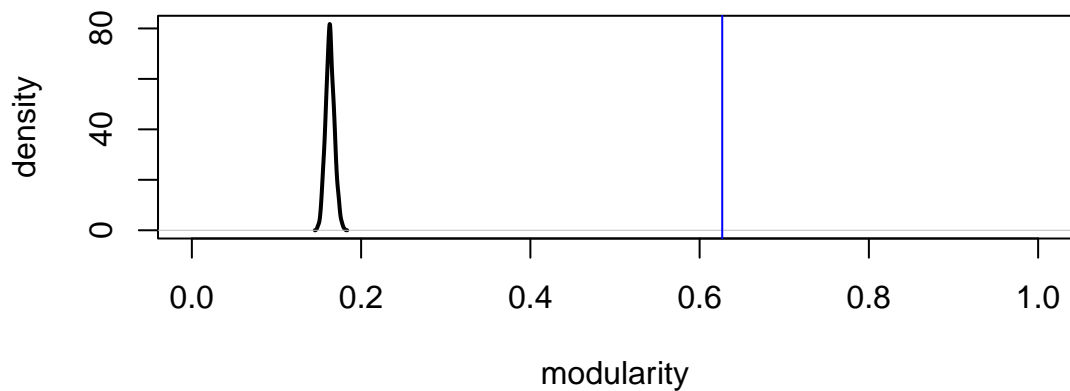
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Herbivore

Modularity

..
 Observed Modularity: 0.63
 Number of Modules: 20

Comparison between observed modularity (blue line) and proportional null model (density in black)

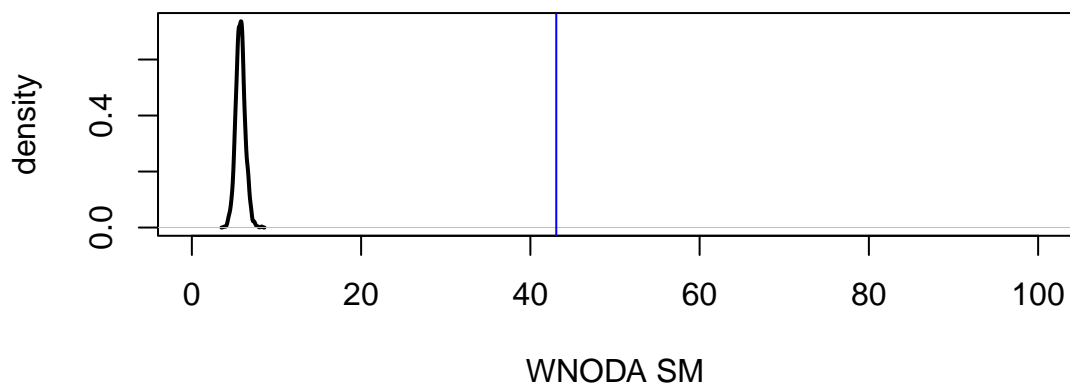


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 12
Nestedness between species in the same module 43
Nestedness between species in different modules 8.8

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

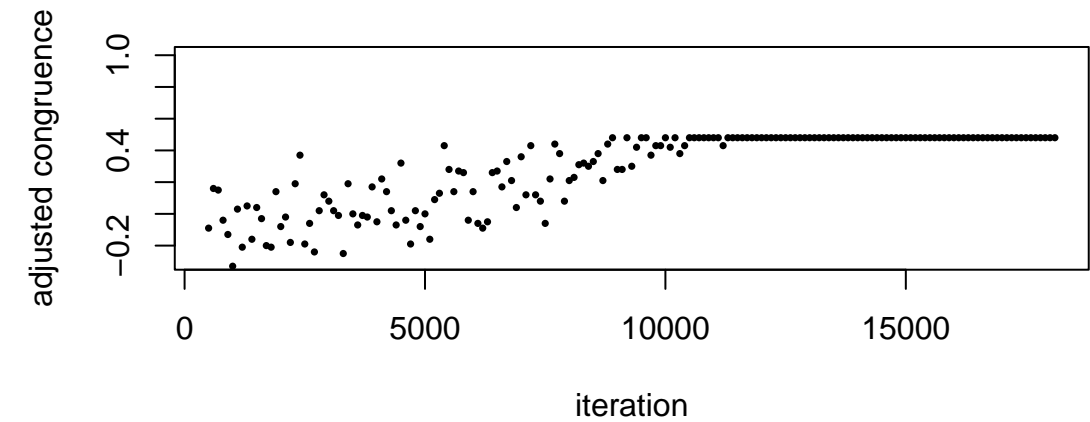
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

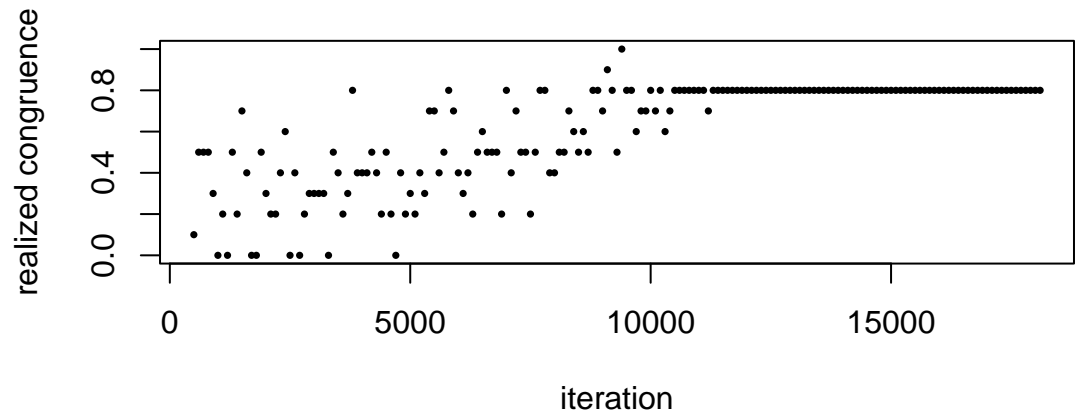
..
BN (A-B) Specialization (H2') 0.18
BN (A-B) Connectance 0.31
BN (B-C) Specialization (H2') 0.58
BN (B-C) Connectance 0.045
Plant defender richness in BN (A-B): 33
Plant richness in BN (A-B): 16
Plant richness in BN (B-C): 109
Herbivore richness in BN (B-C): 85
Richness of shared Plants: 109
Number of modules in BN (A-B) 4
Number of modules in BN (B-C) 20

Number of modules in BN (A-B) (only for shared species) 4
Number of modules in BN (B-C) (only for shared species) 6

Hipermodule Congruence
Optmization procedure

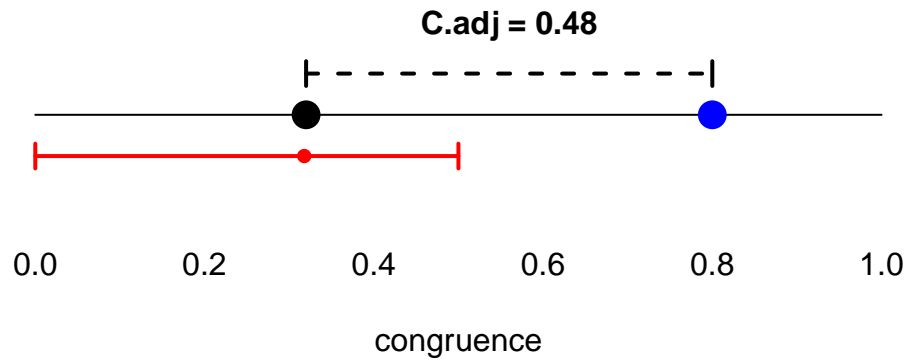


..



Adjusted Congruence: 0.48
Realized Congruence: 0.8
Hypermodularity: 0.26

Null Model 1

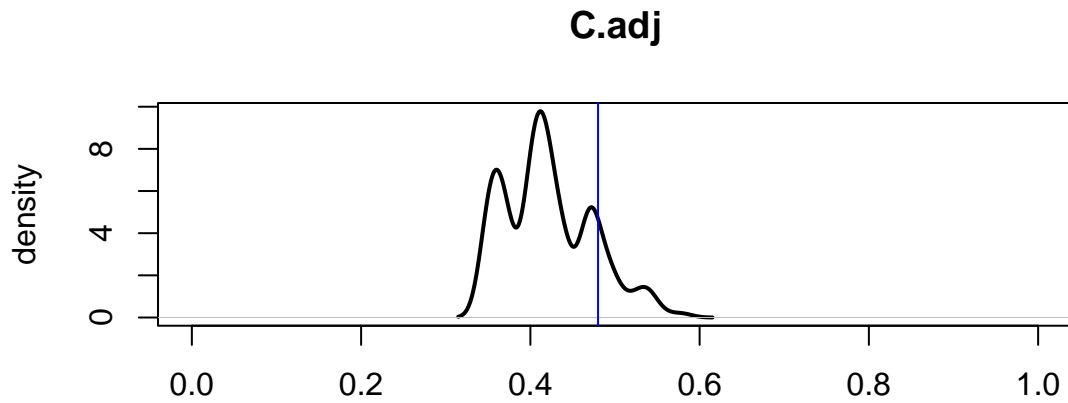


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.002

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.14

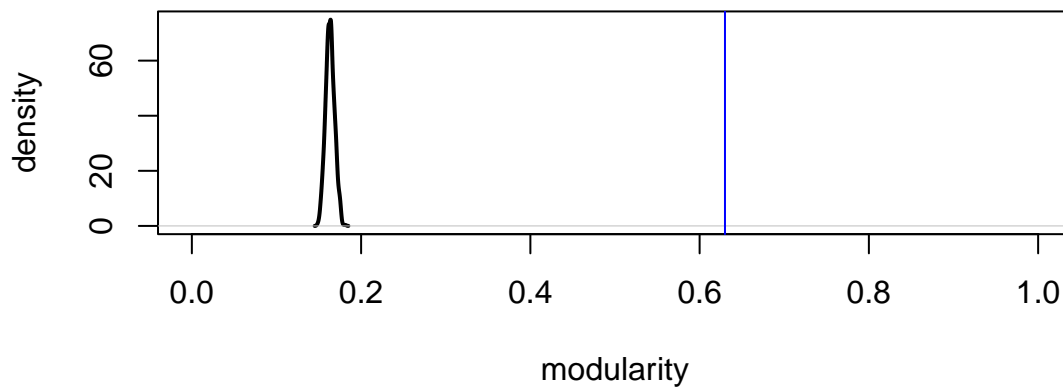
Dataset 22 : CORDOBA2

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.63
Number of Modules: 15

Comparison between observed modularity (blue line) and proportional null model (density in black)

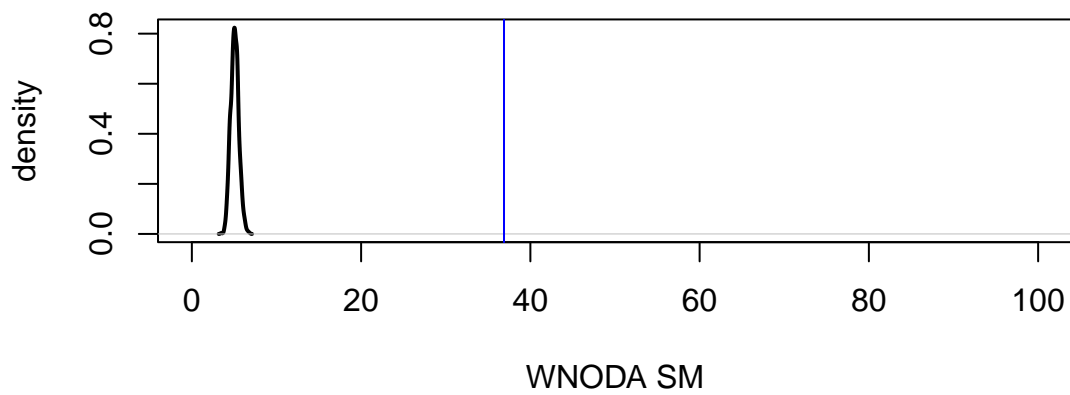


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 12
Nestedness between species in the same module: 37
Nestedness between species in different modules: 8.7

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

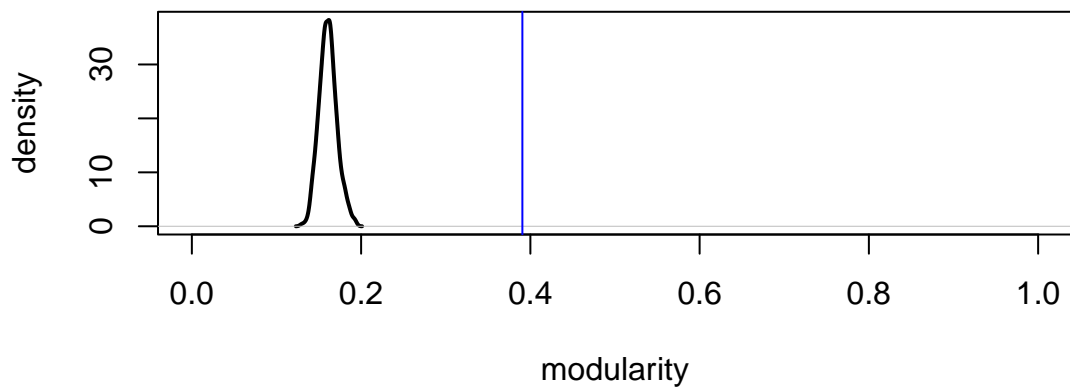
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Predator

Modularity

..
 Observed Modularity: 0.39
 Number of Modules: 7

Comparison between observed modularity (blue line) and proportional null model (density in black)

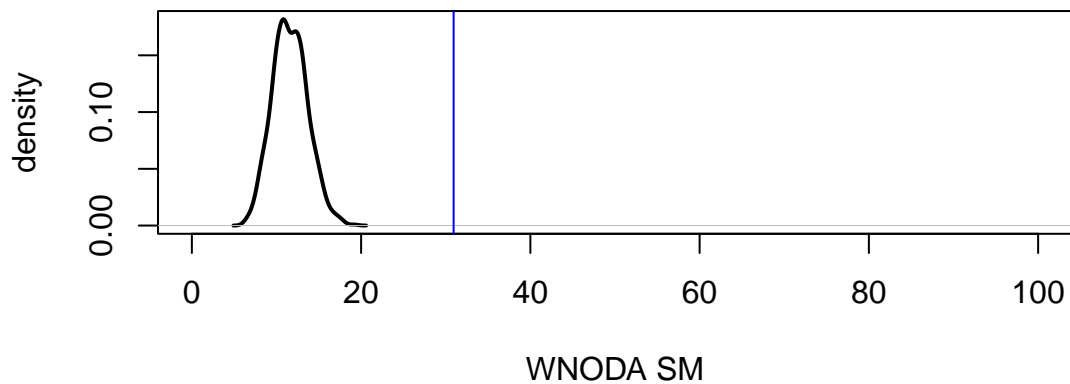


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 19
Nestedness between species in the same module 31
Nestedness between species in different modules 17

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

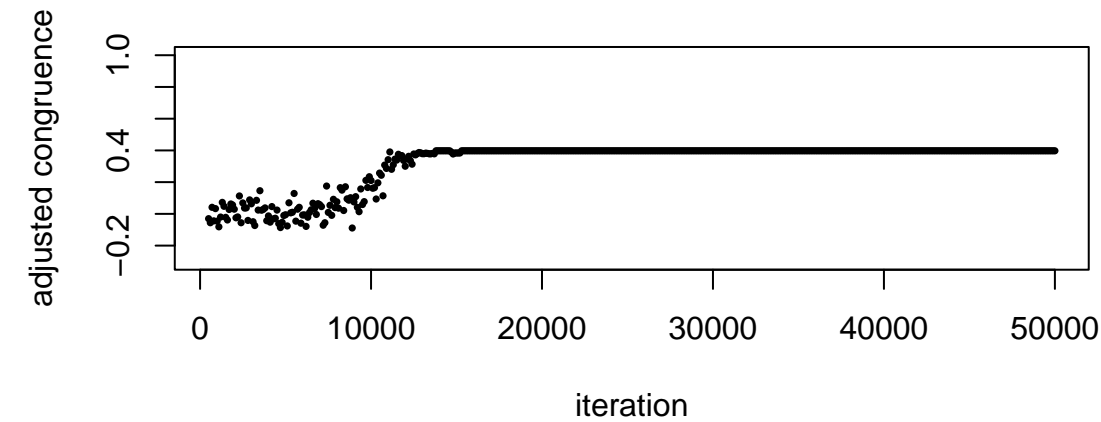
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

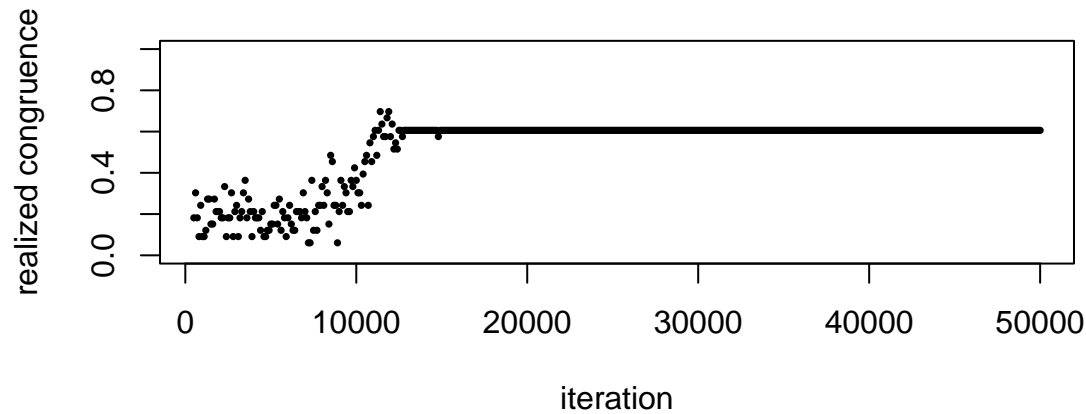
..
BN (A-B) Specialization (H2') 0.58
BN (A-B) Connectance 0.045
BN (B-C) Specialization (H2') 0.37
BN (B-C) Connectance 0.16
Plant richness in BN (A-B): 109
Herbivore richness in BN (A-B): 85
Herbivore richness in BN (B-C): 33
Predator richness in BN (B-C): 23
Richness of shared Herbivores: 33
Number of modules in BN (A-B) 15
Number of modules in BN (B-C) 7

Number of modules in BN (A-B) (only for shared species) 12
Number of modules in BN (B-C) (only for shared species) 7

Hipermodule Congruence
Optmization procedure

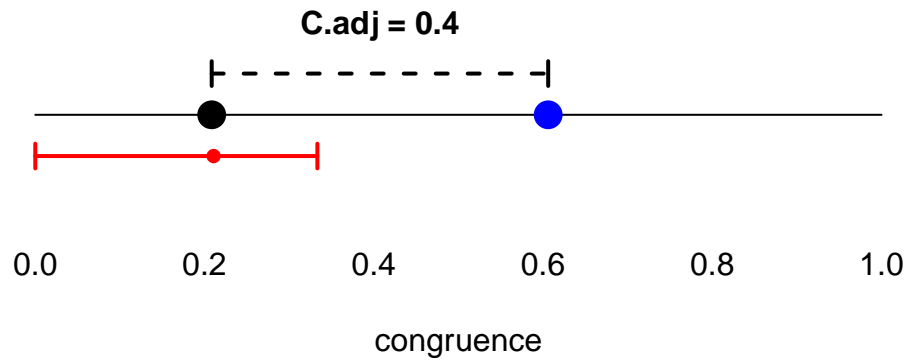


..



Adjusted Congruence: 0.4
Realized Congruence: 0.61
Hypermodularity: 0.16

Null Model 1

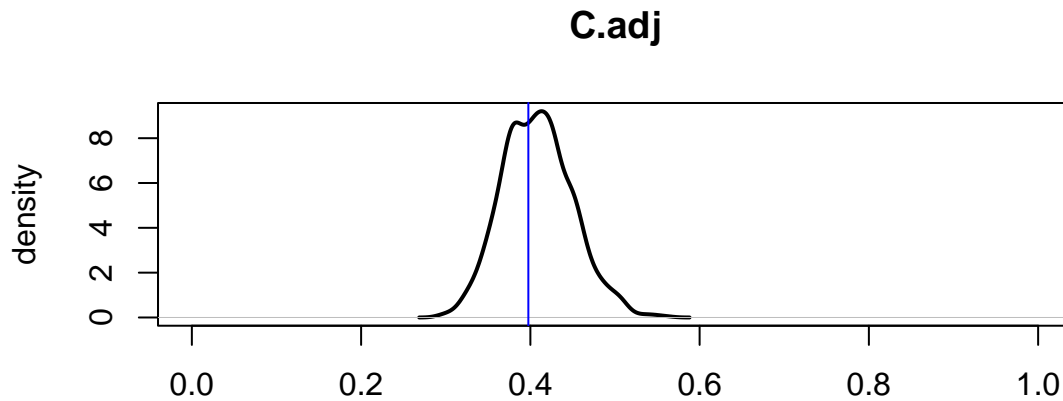


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.59

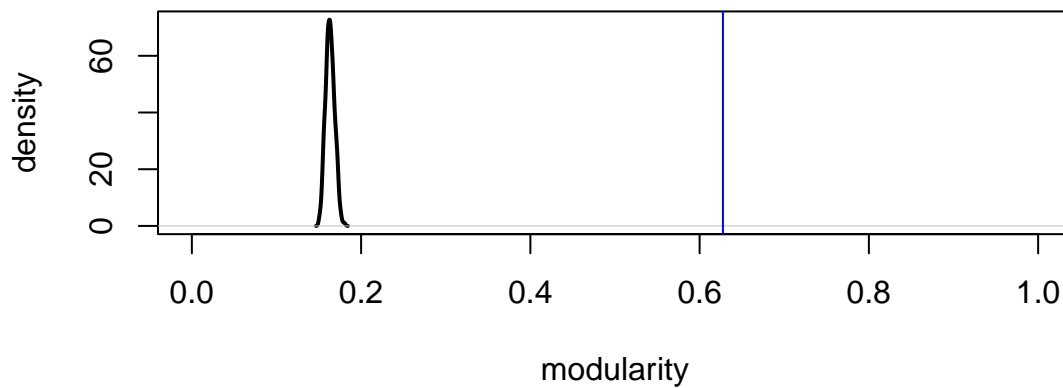
Dataset 23 : CORDOBA2

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.63
Number of Modules: 20

Comparison between observed modularity (blue line) and proportional null model (density in black)

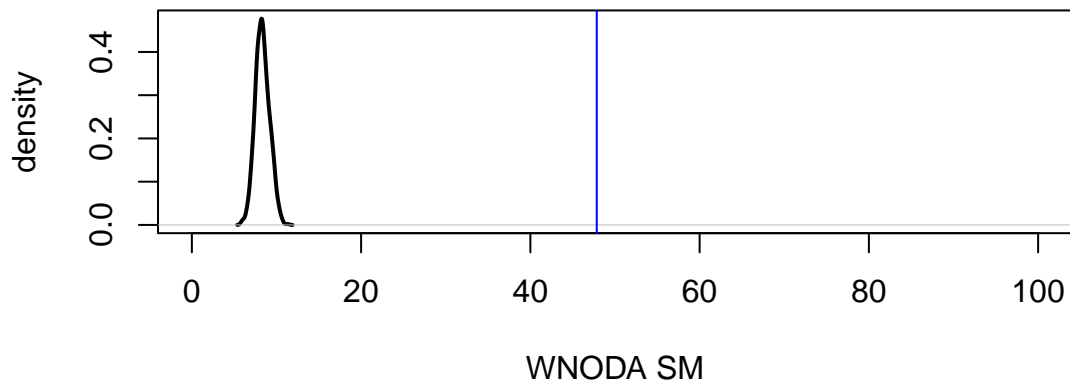


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 12
Nestedness between species in the same module: 48
Nestedness between species in different modules: 8.7

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

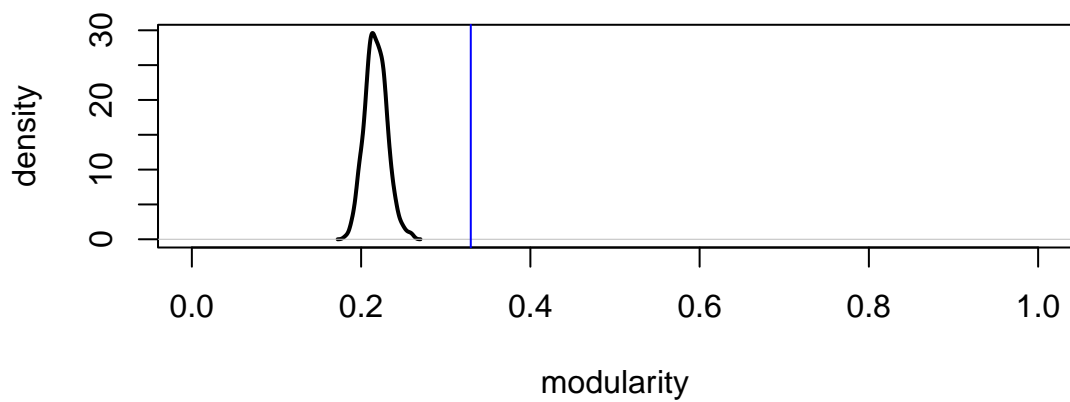
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Defender

Modularity

..
 Observed Modularity: 0.33
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

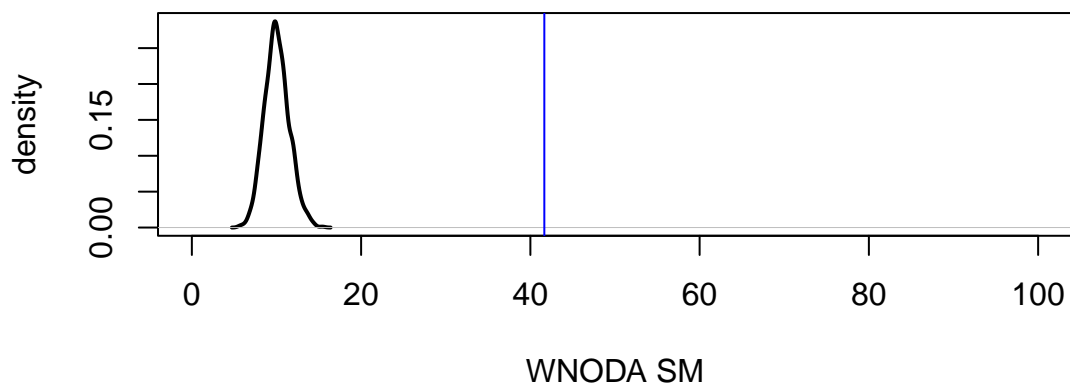


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 25
Nestedness between species in the same module 42
Nestedness between species in different modules 20

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

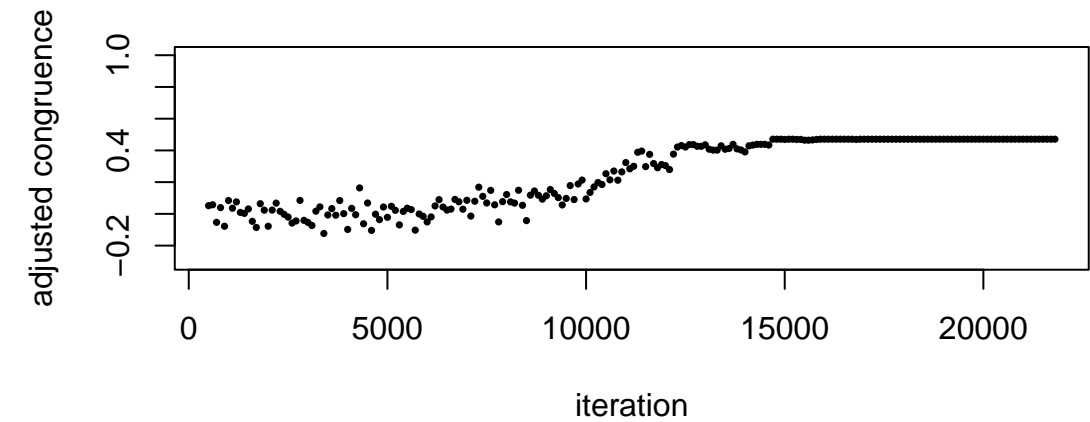
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

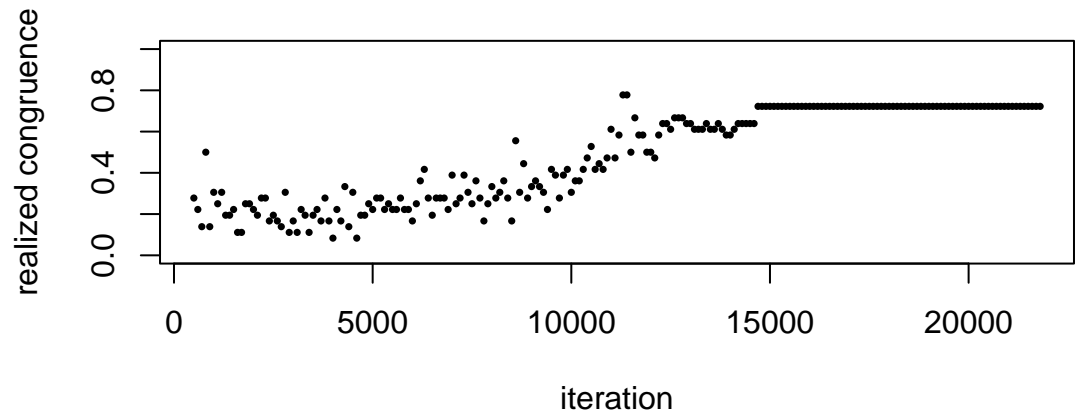
..
BN (A-B) Specialization (H2') 0.58
BN (A-B) Connectance 0.045
BN (B-C) Specialization (H2') 0.24
BN (B-C) Connectance 0.16
Plant richness in BN (A-B): 109
Herbivore richness in BN (A-B): 85
Herbivore richness in BN (B-C): 36
Defender richness in BN (B-C): 26
Richness of shared Herbivores: 36
Number of modules in BN (A-B) 20
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 18
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

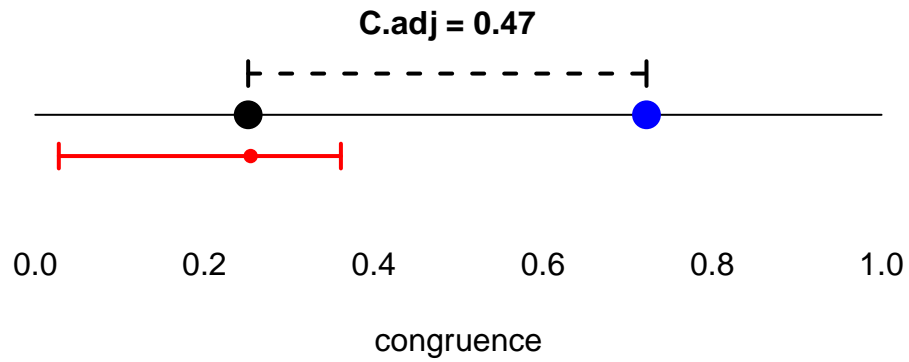


..



Adjusted Congruence: 0.47
Realized Congruence: 0.72
Hypermodularity: 0.28

Null Model 1

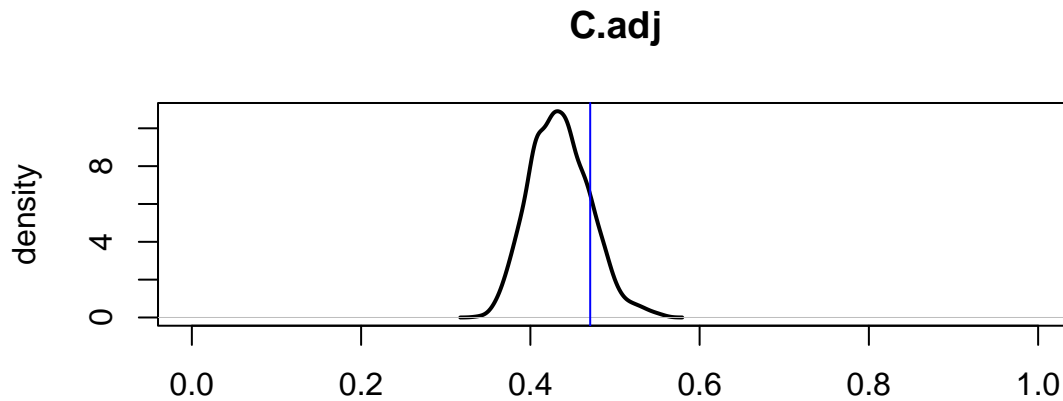


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.16

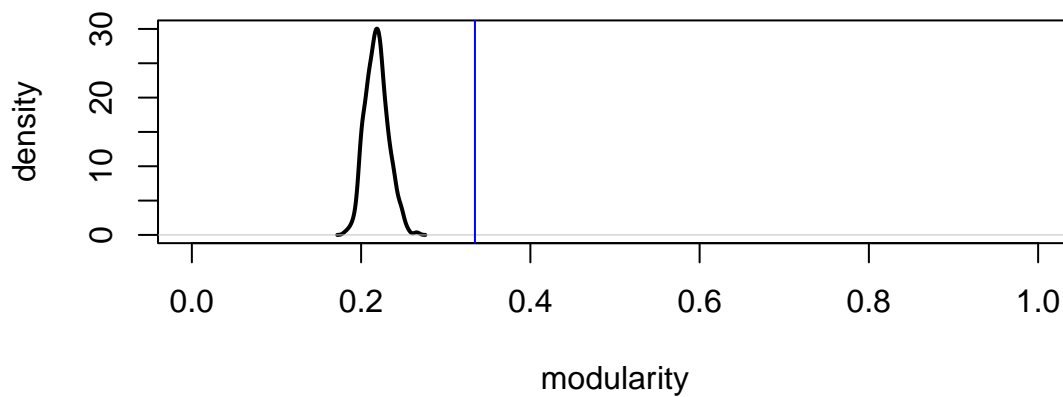
Dataset 24 : CORDOBA2

Topology BN (A-B): Defender - Herbivore

Modularity

..
Observed Modularity: 0.33
Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

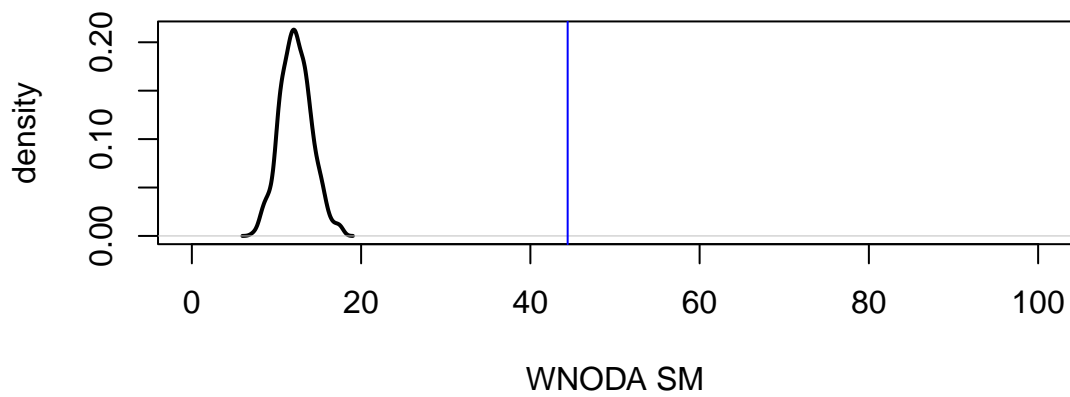


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 24
Nestedness between species in the same module: 44
Nestedness between species in different modules: 20

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

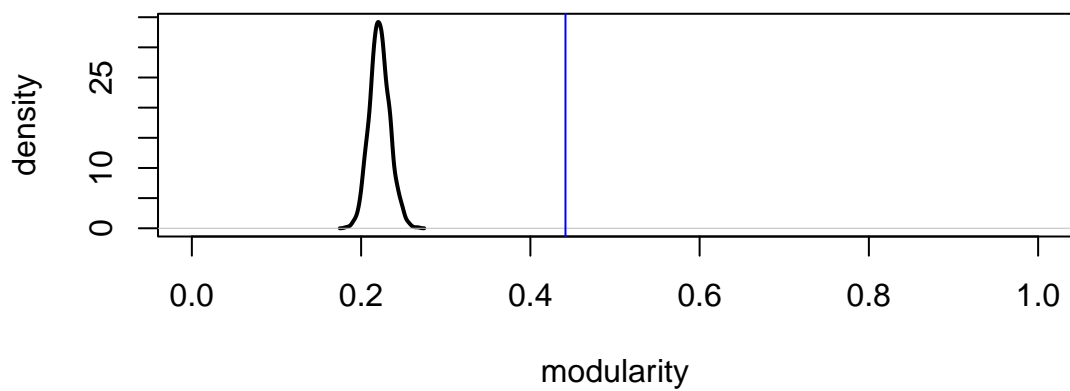
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Enemy

Modularity

..
Observed Modularity: 0.44
Number of Modules: 7

Comparison between observed modularity (blue line) and proportional null model (density in black)

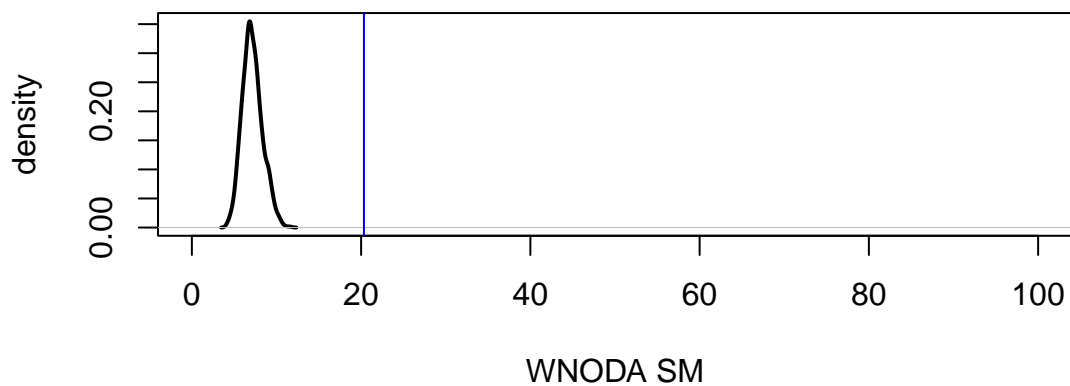


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 9.4
Nestedness between species in the same module 20
Nestedness between species in different modules 7.5

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

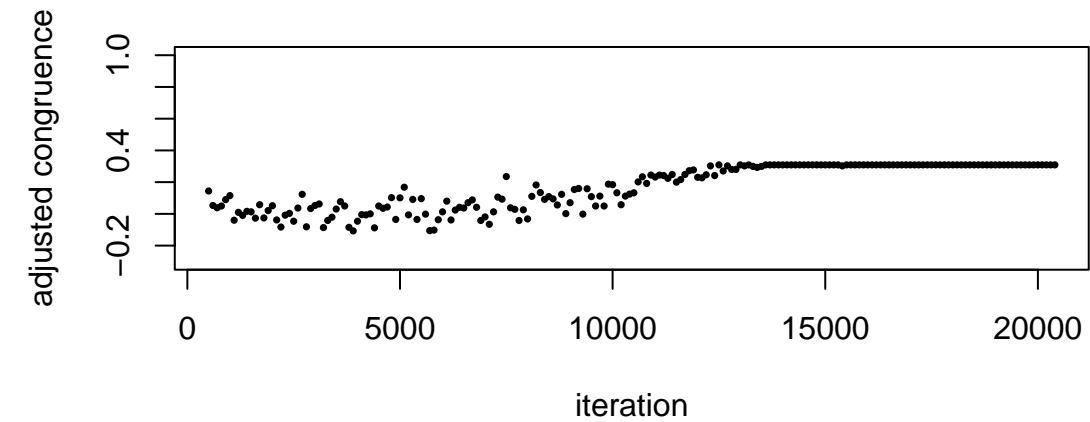
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

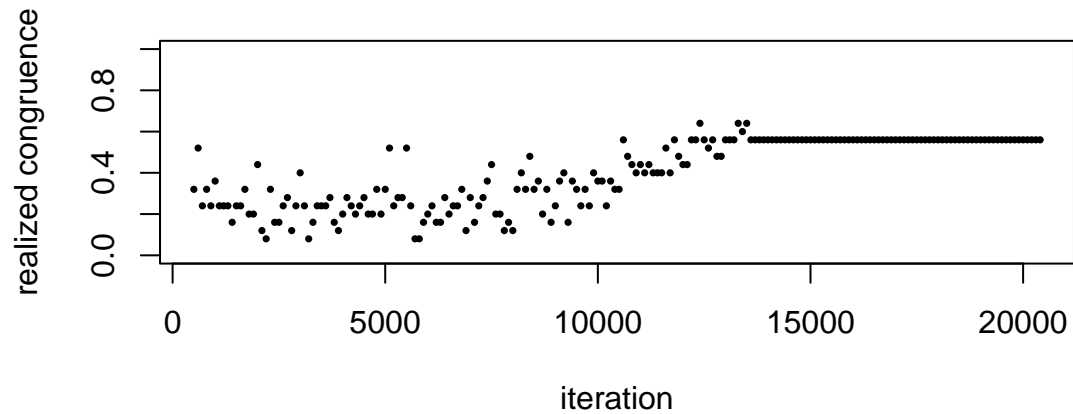
..
BN (A-B) Specialization (H2') 0.24
BN (A-B) Connectance 0.16
BN (B-C) Specialization (H2') 0.4
BN (B-C) Connectance 0.088
Defender richness in BN (A-B): 26
Herbivore richness in BN (A-B): 37
Herbivore richness in BN (B-C): 40
Enemy richness in BN (B-C): 50
Richness of shared Herbivores: 40
Number of modules in BN (A-B) 6
Number of modules in BN (B-C) 7

Number of modules in BN (A-B) (only for shared species) 6
Number of modules in BN (B-C) (only for shared species) 7

Hipermodule Congruence
Optmization procedure

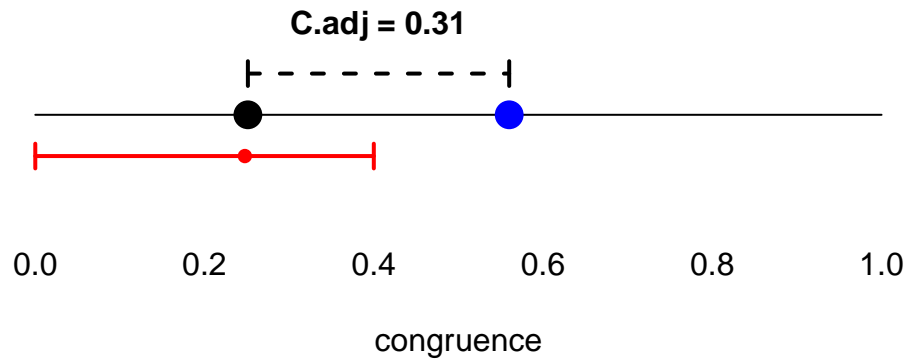


..



Adjusted Congruence: 0.31
Realized Congruence: 0.56
Hypermodularity: 0.077

Null Model 1

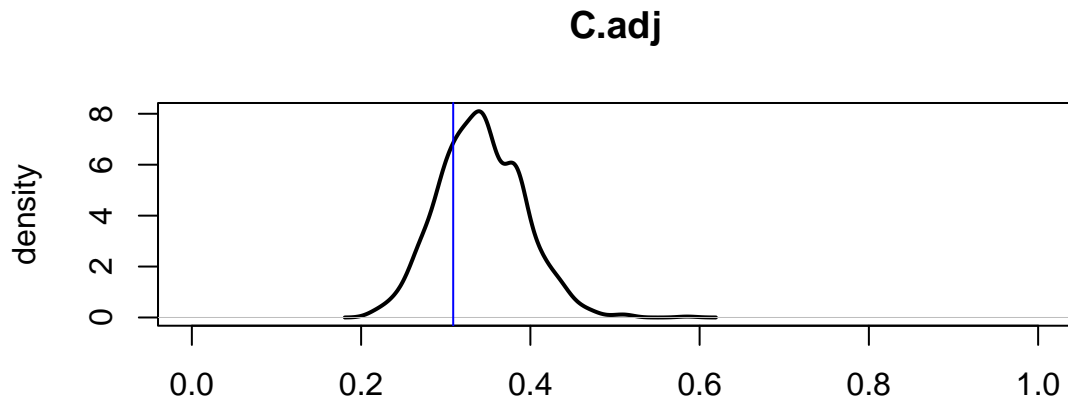


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.73

Dataset 25 : COSTA RICA

BINARY DATASET

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.91
Number of Modules: 20

Low-level nestedness

..
Nestedness in the entire matrix: 0.52
Nestedness between species in the same module: 5.9
Nestedness between species in different modules: 0.25

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
Observed Modularity: 0.61
Number of Modules: 9

Low-level nestedness

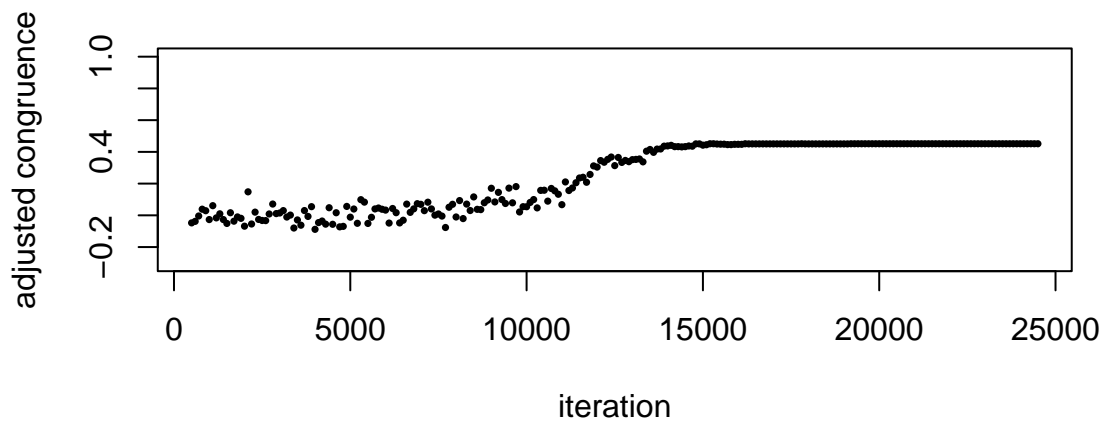
..
Nestedness in the entire matrix 7.1
Nestedness between species in the same module 24
Nestedness between species in different modules 5

Bipartite Networks and Intercept

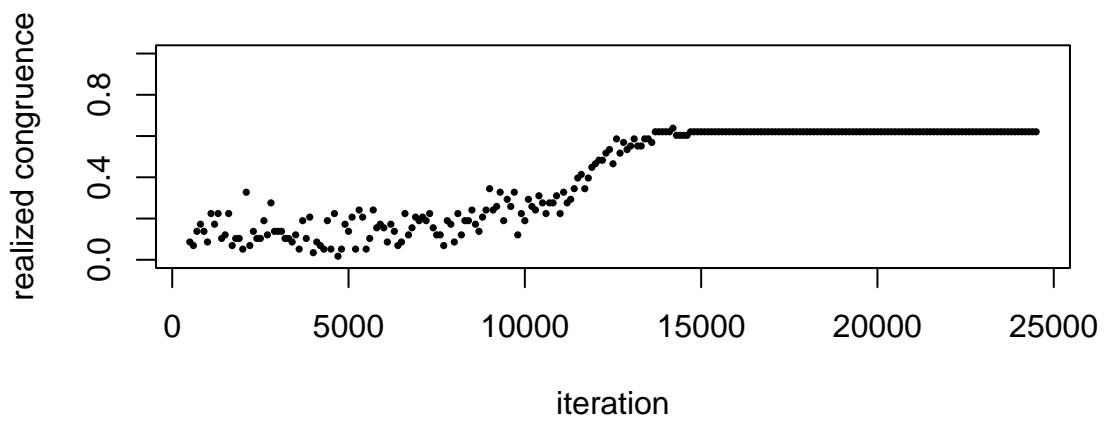
..
BN (A-B) Specialization (H2') NA
BN (A-B) Connectance 0.029
BN (B-C) Specialization (H2') NA
BN (B-C) Connectance 0.034
Plant richness in BN (A-B): 37
Herbivore richness in BN (A-B): 58
Herbivore richness in BN (B-C): 58
Parasitoid richness in BN (B-C): 102
Richness of shared Herbivores: 58
Number of modules in BN (A-B) 20
Number of modules in BN (B-C) 9
Number of modules in BN (A-B) (only for shared species) 20
Number of modules in BN (B-C) (only for shared species) 9

Hipermodule Congruence

Optimization procedure



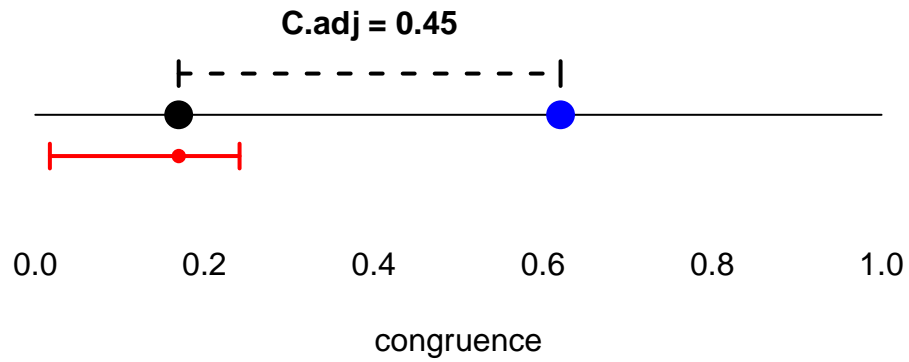
::



::

Adjusted Congruence: 0.45
 Realized Congruence: 0.62
 Hypermodularity: 0.42

Null Model 1

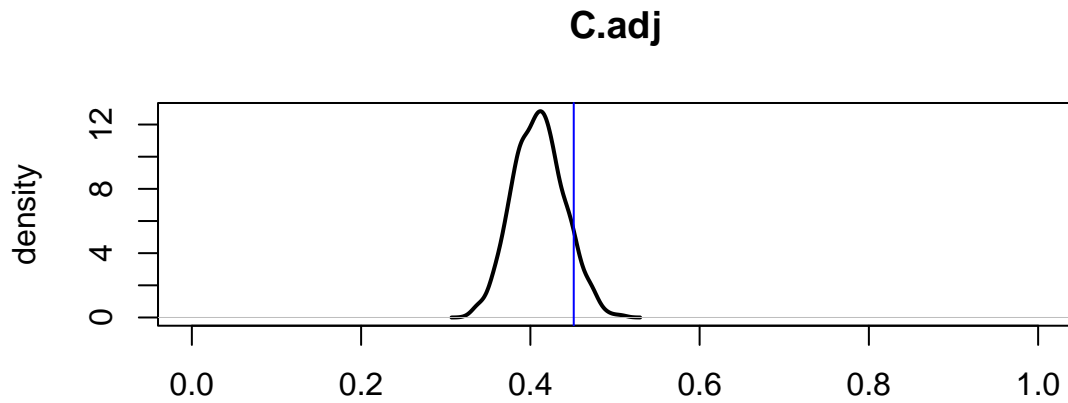


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.094

Dataset 26 : MULLER

BINARY DATASET

Topology BN (A-B): Plant - Herbivore

Modularity

..

Observed Modularity: 0.78

Number of Modules: 12

Low-level nestedness

..

Nestedness in the entire matrix: 3.7

Nestedness between species in the same module: 0

Nestedness between species in different modules: 4.1

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..

Observed Modularity: 0.55

Number of Modules: 6

Low-level nestedness

..

Nestedness in the entire matrix 24

Nestedness between species in the same module 68

Nestedness between species in different modules 15

Bipartite Networks and Intercept

..

BN (A-B) Specialization (H2') NA

BN (A-B) Connectance 0.082

BN (B-C) Specialization (H2') NA

BN (B-C) Connectance 0.14

Plant richness in BN (A-B): 21

Herbivore richness in BN (A-B): 14

Herbivore richness in BN (B-C): 14

Parasitoid richness in BN (B-C): 18

Richness of shared Herbivores:14

Number of modules in BN (A-B) 12

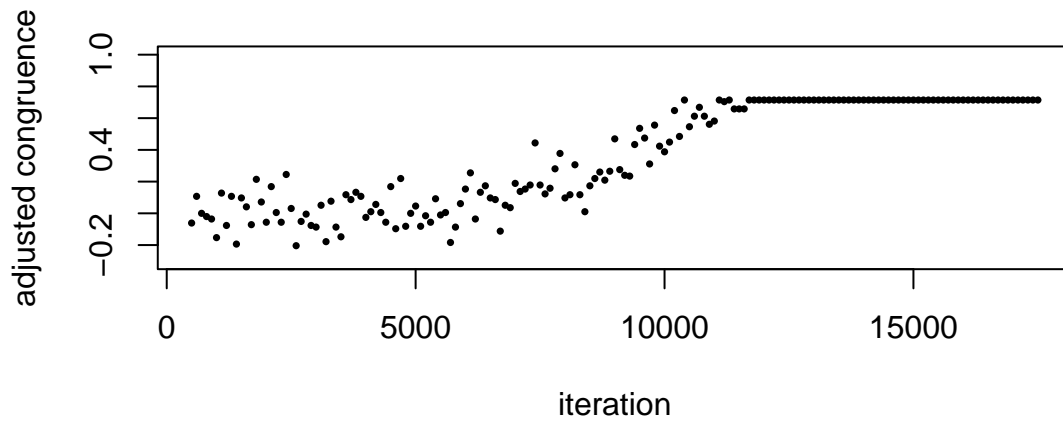
Number of modules in BN (B-C) 6

Number of modules in BN (A-B) (only for shared species) 12

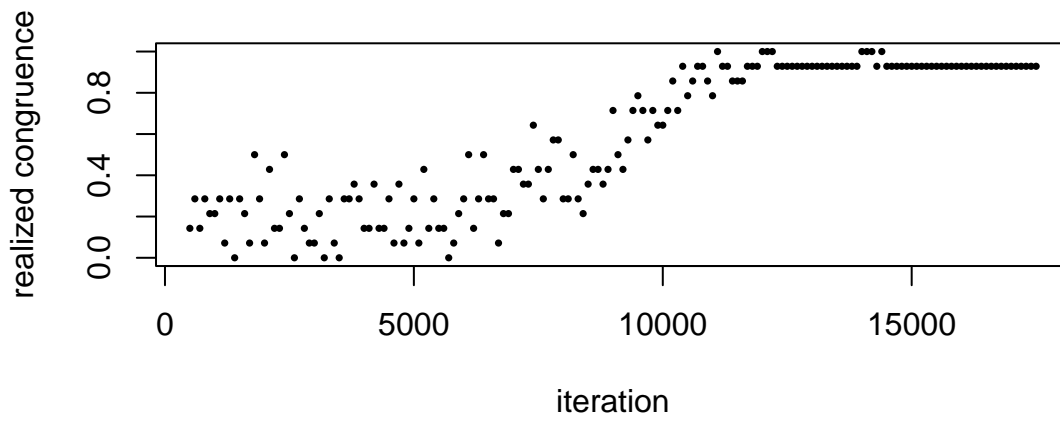
Number of modules in BN (B-C) (only for shared species) 6

Hipermodule Congruence

Optmization procedure



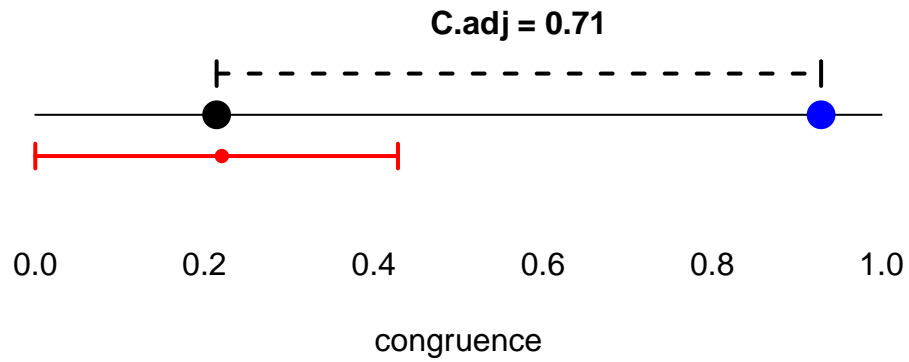
..



..

Adjusted Congruence: 0.71
 Realized Congruence: 0.93
 Hypermodularity: 0.55

Null Model 1

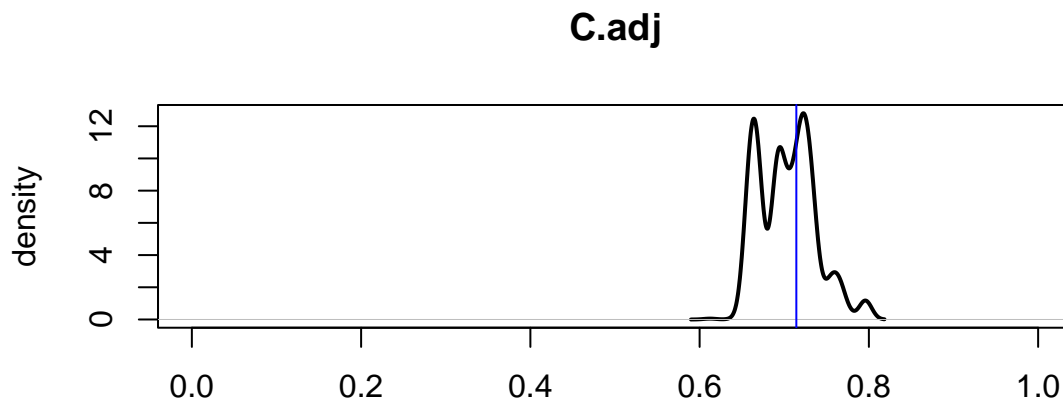


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.42

Dataset 27 : SERENQUETI

BINARY DATASET

Topology BN (A-B): Plant - Herbivore

Modularity

..

Observed Modularity: 0.4

Number of Modules: 6

Low-level nestedness

..

Nestedness in the entire matrix: 38

Nestedness between species in the same module: 67

Nestedness between species in different modules: 23

Topology BN (B-C): Herbivore - Predator

Modularity

..

Observed Modularity: 0.21

Number of Modules: 4

Low-level nestedness

..

Nestedness in the entire matrix 74

Nestedness between species in the same module 65

Nestedness between species in different modules 76

Bipartite Networks and Intercept

..

BN (A-B) Specialization (H2') NA

BN (A-B) Connectance 0.17

BN (B-C) Specialization (H2') NA

BN (B-C) Connectance 0.4

Plant richness in BN (A-B): 129

Herbivore richness in BN (A-B): 23

Herbivore richness in BN (B-C): 22

Predator richness in BN (B-C): 9

Richness of shared Herbivores: 22

Number of modules in BN (A-B) 6

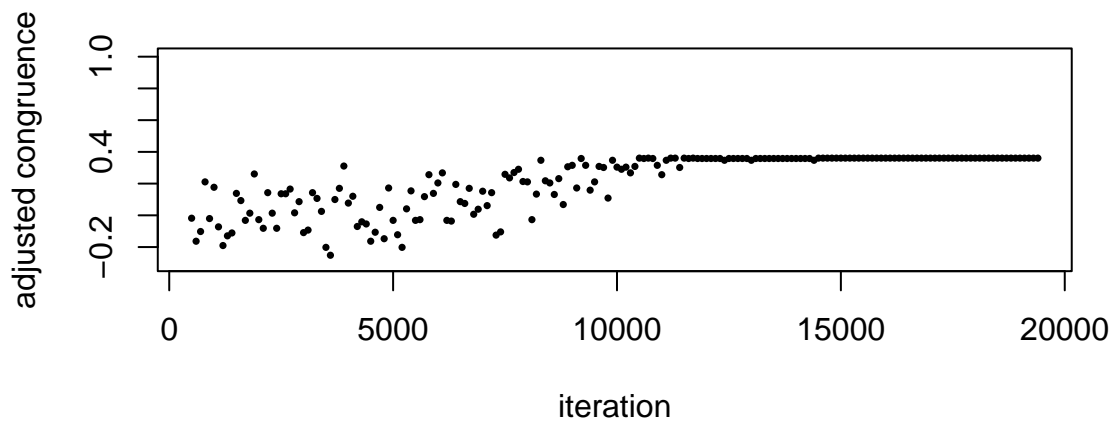
Number of modules in BN (B-C) 4

Number of modules in BN (A-B) (only for shared species) 6

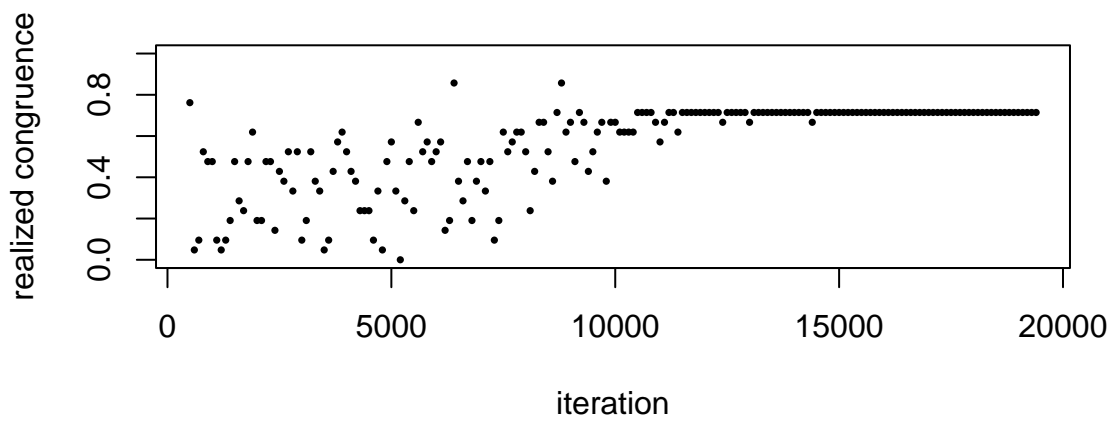
Number of modules in BN (B-C) (only for shared species) 4

Hipermodule Congruence

Optimization procedure



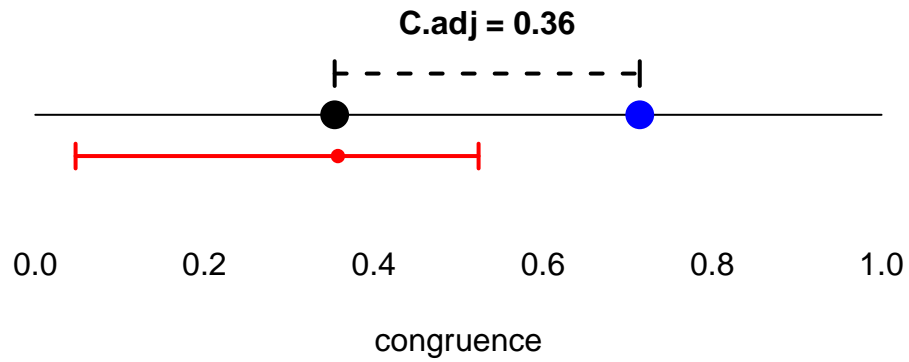
..



..

Adjusted Congruence: 0.36
 Realized Congruence: 0.71
 Hypermodularity: 0.17

Null Model 1

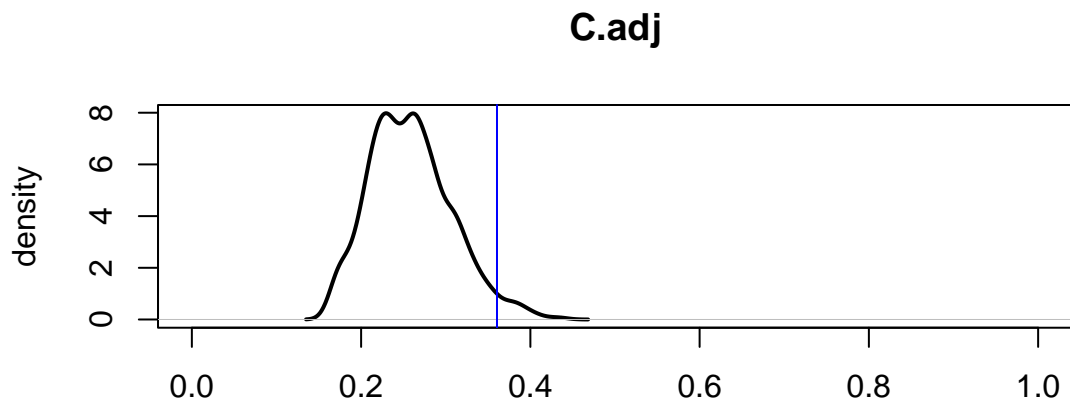


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.03

Dataset 28 : dattilo

BINARY DATASET

Topology BN (A-B): Plant defender - Plant

Modularity

..

Observed Modularity: 0.29

Number of Modules: 7

Low-level nestedness

..

Nestedness in the entire matrix: 49

Nestedness between species in the same module: 60

Nestedness between species in different modules: 46

Topology BN (B-C): Plant - Pollinator

Modularity

..

Observed Modularity: 0.54

Number of Modules: 13

Low-level nestedness

..

Nestedness in the entire matrix 7.9

Nestedness between species in the same module 26

Nestedness between species in different modules 6.4

Bipartite Networks and Intercept

..

BN (A-B) Specialization (H2') NA

BN (A-B) Connectance 0.17

BN (B-C) Specialization (H2') NA

BN (B-C) Connectance 0.026

Plant defender richness in BN (A-B): 30

Plant richness in BN (A-B): 40

Plant richness in BN (B-C): 93

Pollinator richness in BN (B-C): 173

Richness of shared Plants:93

Number of modules in BN (A-B) 7

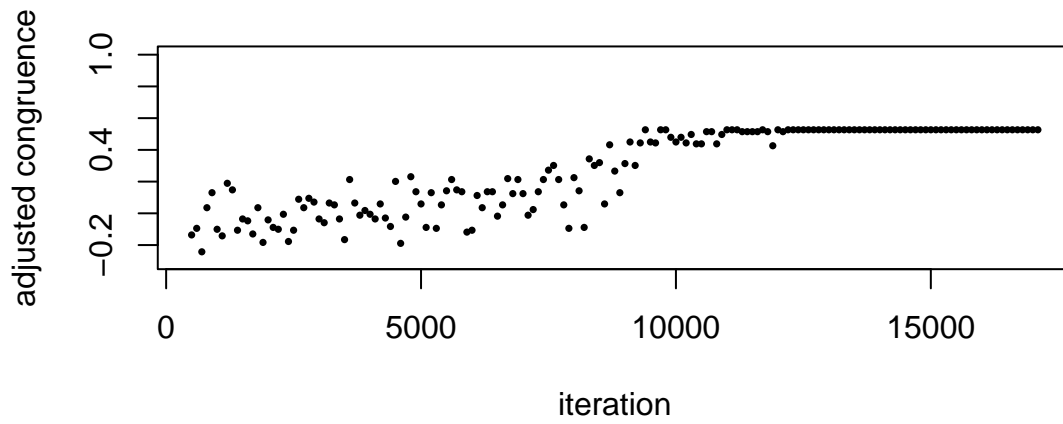
Number of modules in BN (B-C) 13

Number of modules in BN (A-B) (only for shared species) 4

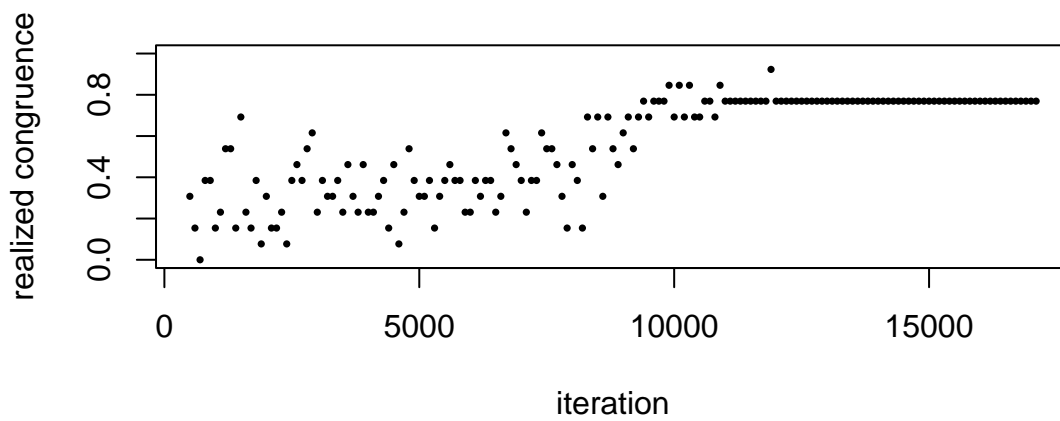
Number of modules in BN (B-C) (only for shared species) 9

Hipermodule Congruence

Optmization procedure



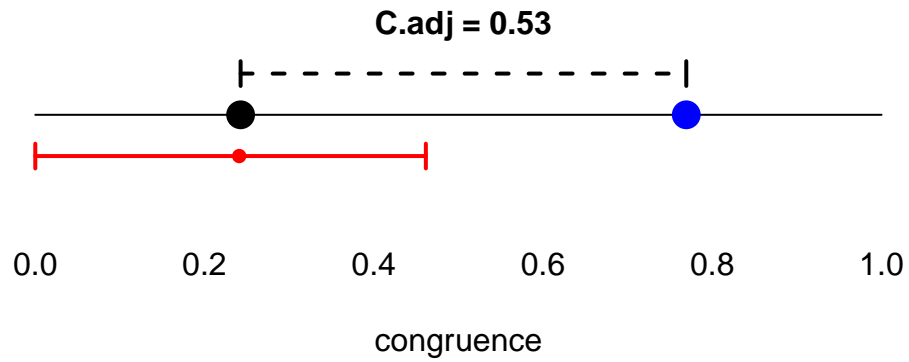
::



::

Adjusted Congruence: 0.53
 Realized Congruence: 0.77
 Hypermodularity: 0.24

Null Model 1

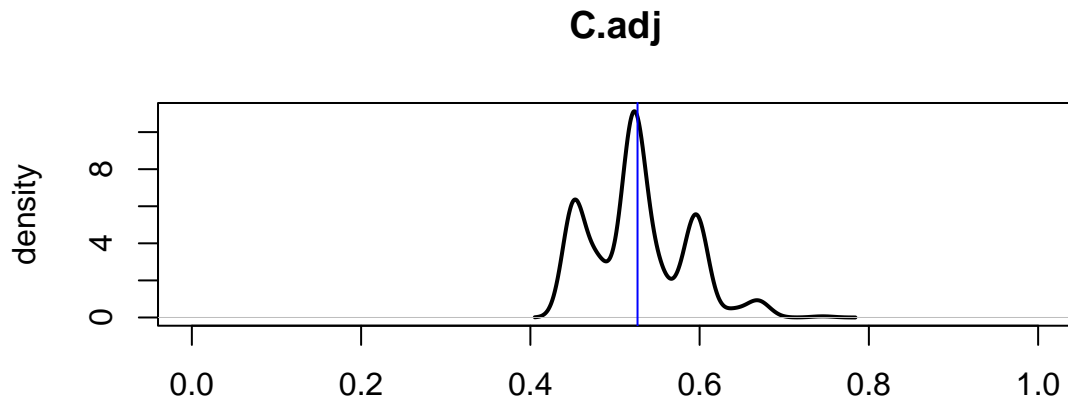


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.5

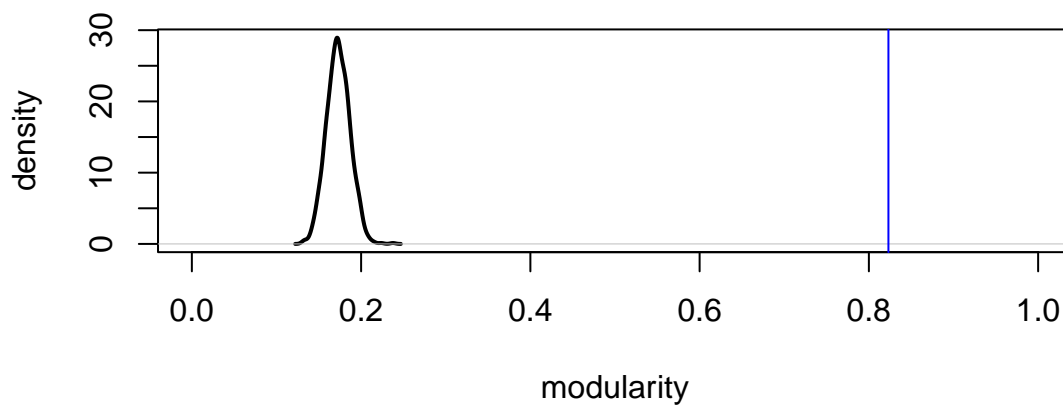
Dataset 29 : hackett HH

Topology BN (A-B): Herbivore - Plant

Modularity

..
Observed Modularity: 0.82
Number of Modules: 15

Comparison between observed modularity (blue line) and proportional null model (density in black)

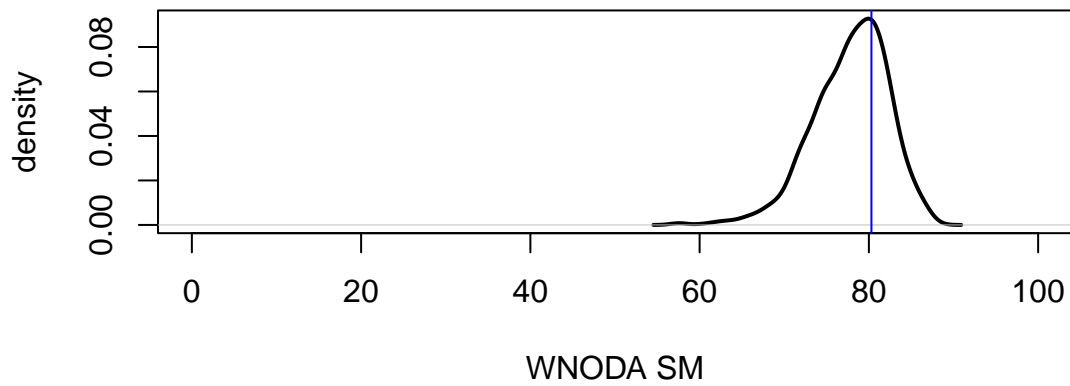


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 6.3
Nestedness between species in the same module: 80
Nestedness between species in different modules: 0.032

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.37

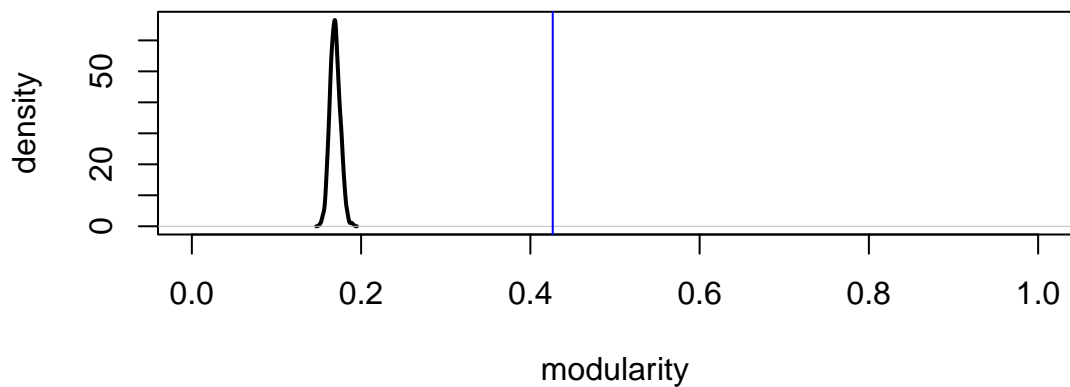
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Plant - Pollinator

Modularity

..
 Observed Modularity: 0.43
 Number of Modules: 10

Comparison between observed modularity (blue line) and proportional null model (density in black)

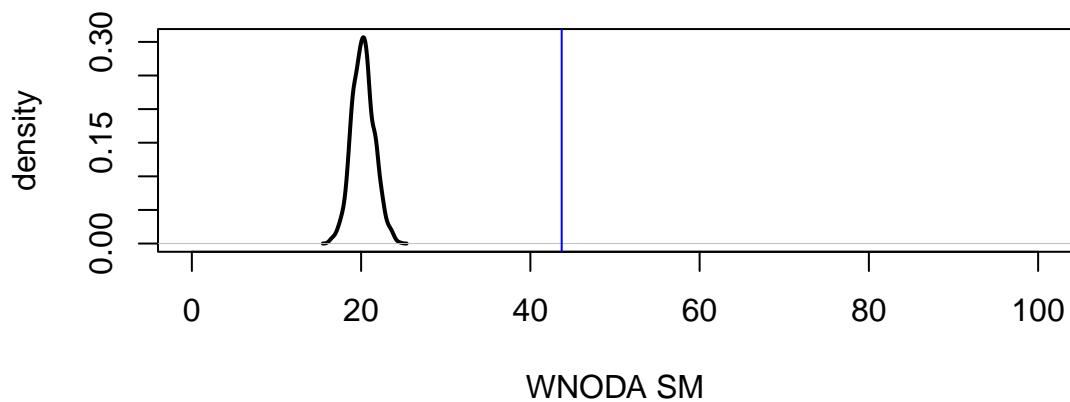


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 13
Nestedness between species in the same module 44
Nestedness between species in different modules 7.8

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

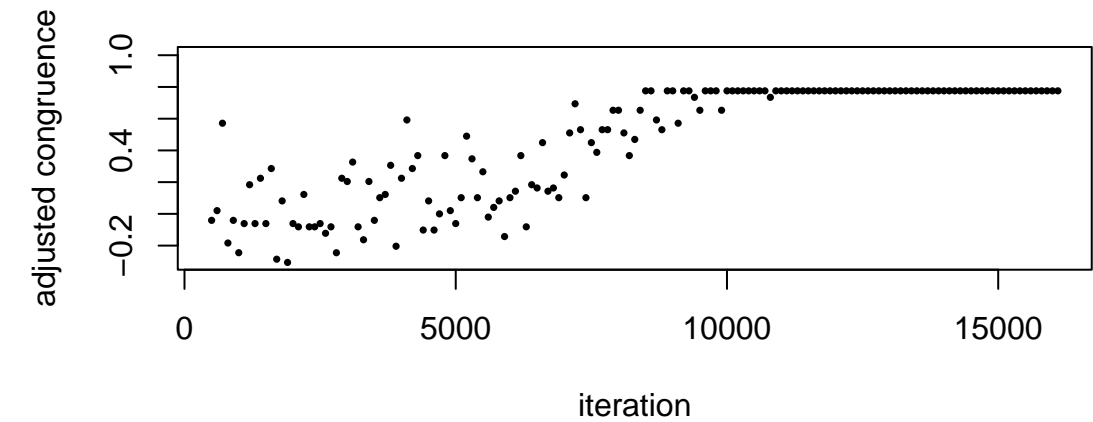
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

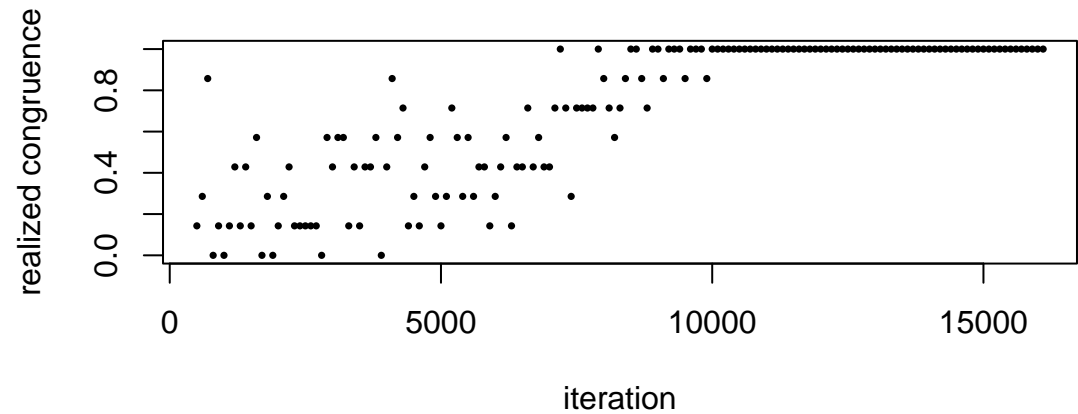
..
BN (A-B) Specialization (H2') 1
BN (A-B) Connectance 0.068
BN (B-C) Specialization (H2') 0.41
BN (B-C) Connectance 0.056
Herbivore richness in BN (A-B): 39
Plant richness in BN (A-B): 15
Plant richness in BN (B-C): 43
Pollinator richness in BN (B-C): 220
Richness of shared Plants: 43
Number of modules in BN (A-B) 15
Number of modules in BN (B-C) 10

Number of modules in BN (A-B) (only for shared species) 7
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

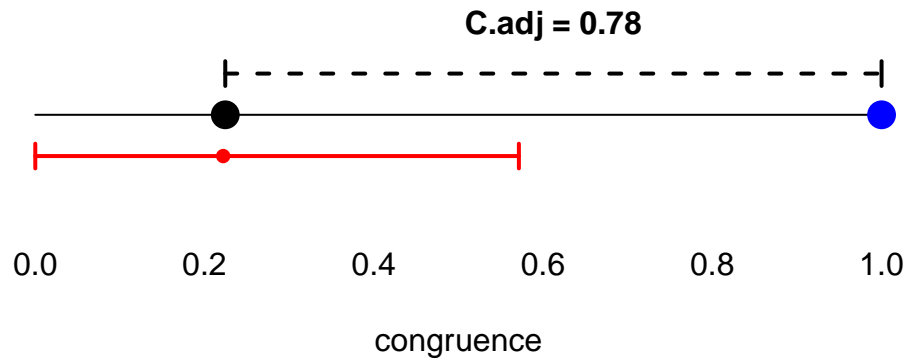


..



Adjusted Congruence: 0.78
Realized Congruence: 1
Hypermodularity: 0.58

Null Model 1

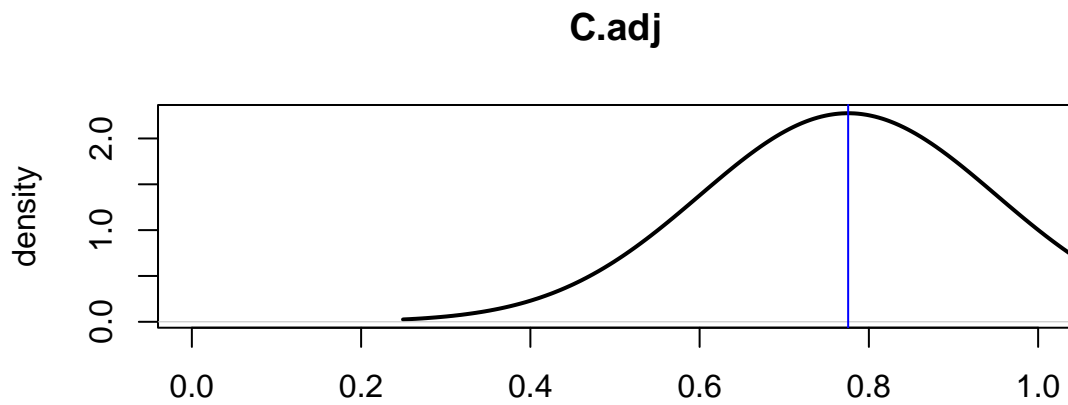


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

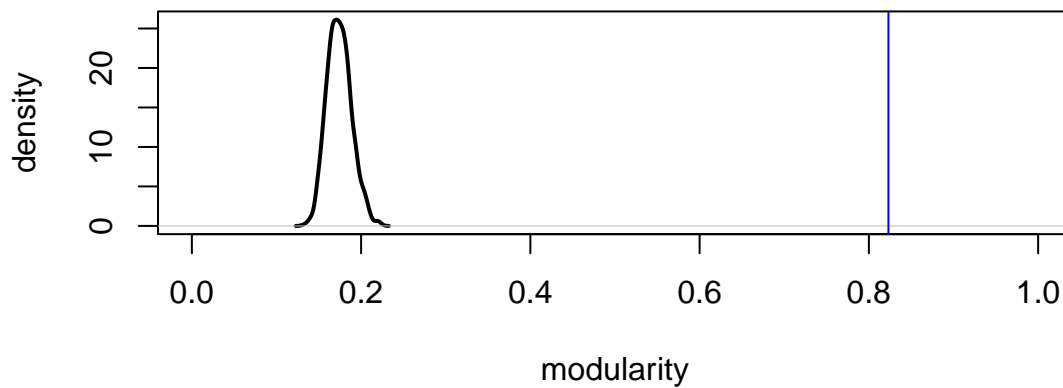
Dataset 30 : hackett HH

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.82
Number of Modules: 15

Comparison between observed modularity (blue line) and proportional null model (density in black)

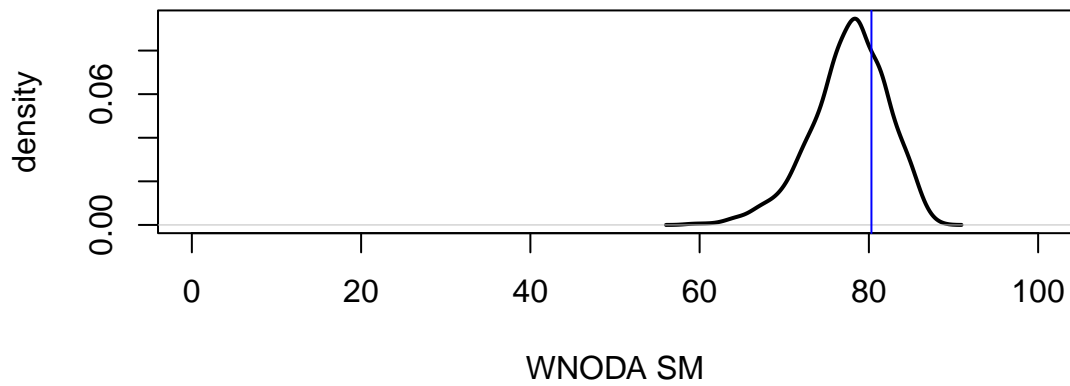


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 6.3
Nestedness between species in the same module: 80
Nestedness between species in different modules: 0.032

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.33

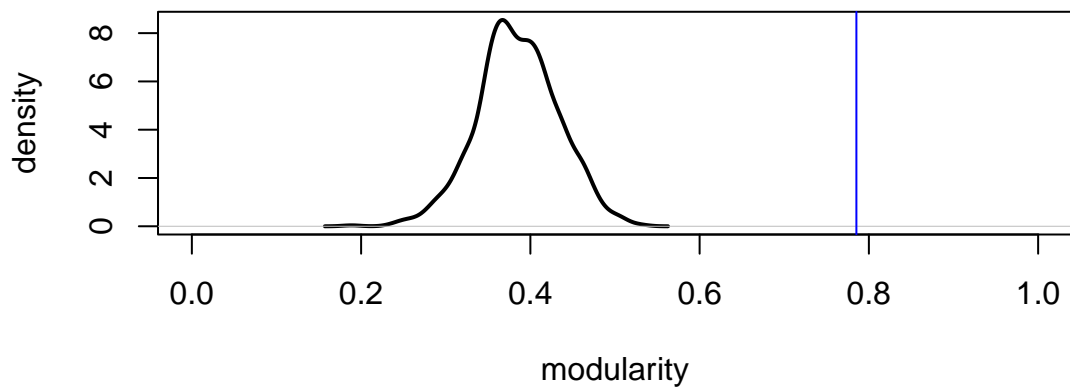
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.79
 Number of Modules: 12

Comparison between observed modularity (blue line) and proportional null model (density in black)

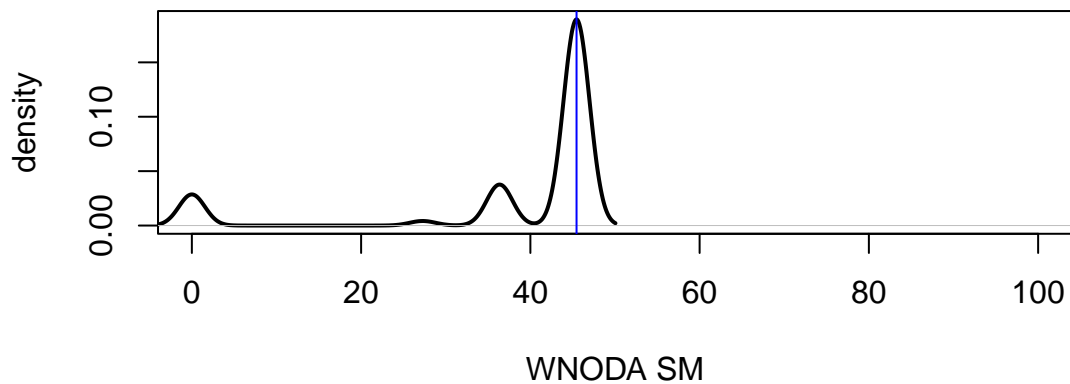


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 2.4
Nestedness between species in the same module 45
Nestedness between species in different modules 0.21

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.73

CONCLUSION: BN (B-C) has a purely modular topology

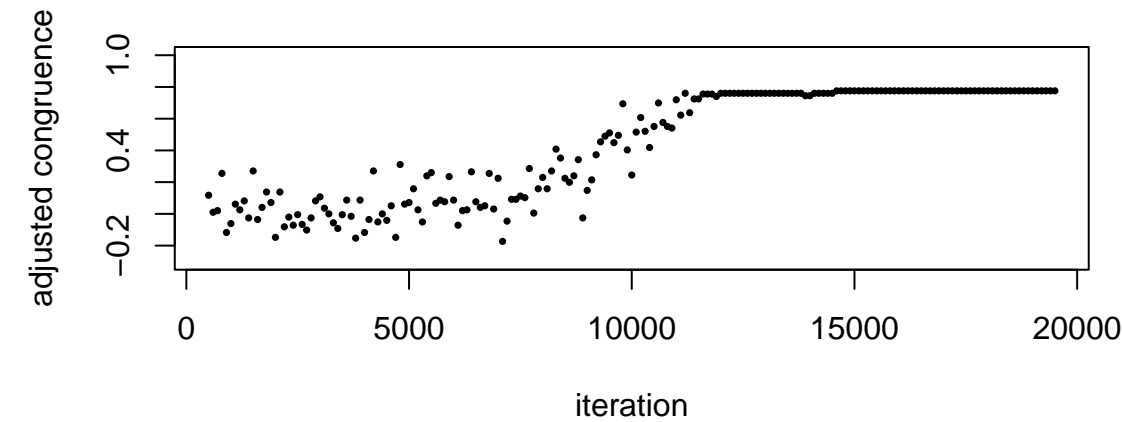
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 1
BN (A-B) Connectance 0.068
BN (B-C) Specialization (H2') 0.82
BN (B-C) Connectance 0.088
Plant richness in BN (A-B): 15
Herbivore richness in BN (A-B): 39
Herbivore richness in BN (B-C): 14
Parasitoid richness in BN (B-C): 17
Richness of shared Herbivores:14
Number of modules in BN (A-B) 15
Number of modules in BN (B-C) 12

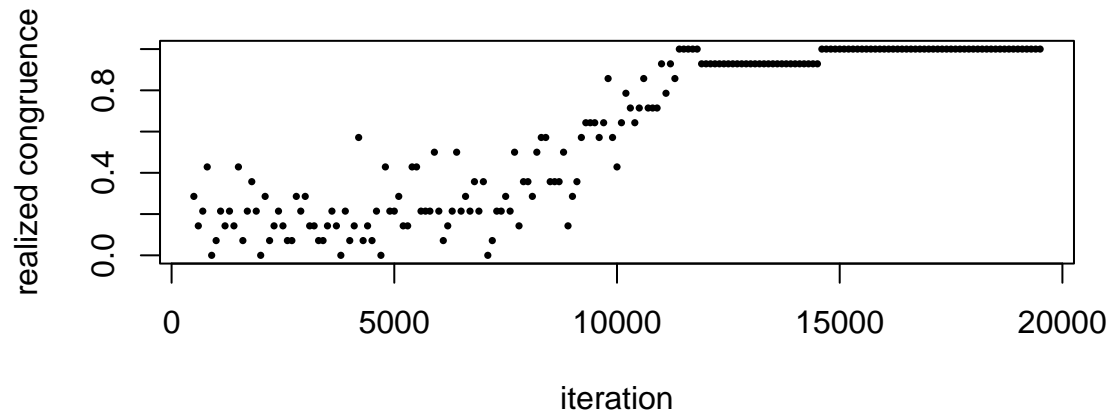
Number of modules in BN (A-B) (only for shared species) 8
Number of modules in BN (B-C) (only for shared species) 12

Hipermodule Congruence

Optmization procedure



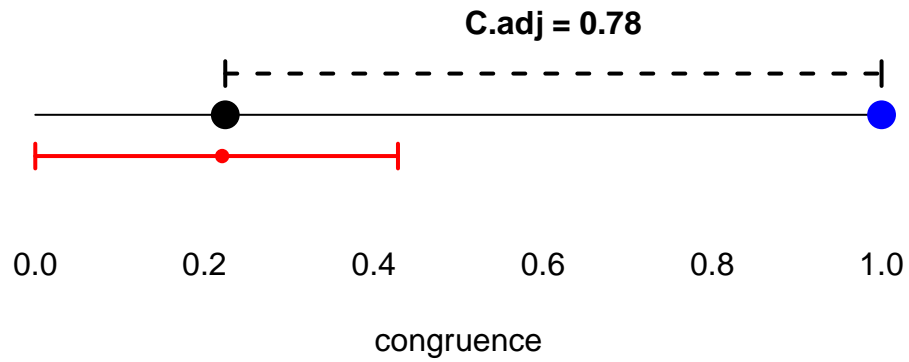
..



..

Adjusted Congruence: 0.78
Realized Congruence: 1
Hypermodularity: 0.72

Null Model 1

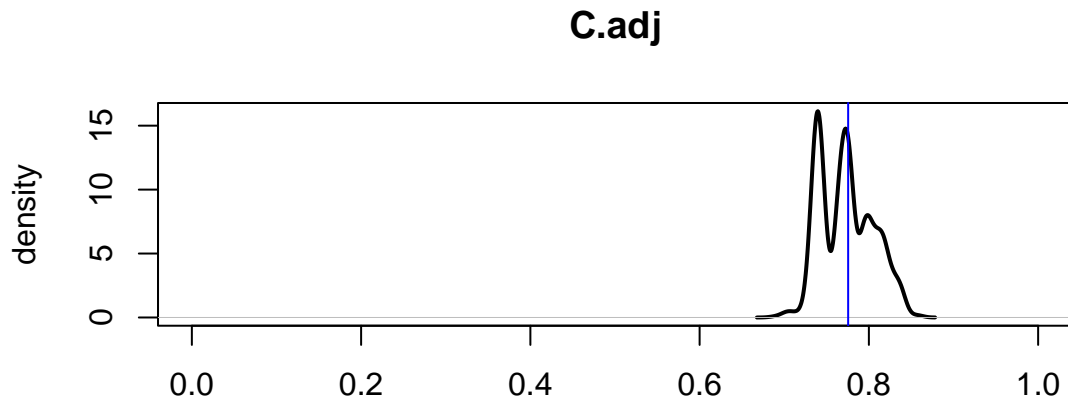


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.53

Dataset 31 : SMOKY MOUNTAINS

BINARY DATASET

Topology BN (A-B): Plant - Herbivore

Modularity

..

Observed Modularity: 0.78

Number of Modules: 27

Low-level nestedness

..

Nestedness in the entire matrix: 3.6

Nestedness between species in the same module: 19

Nestedness between species in different modules: 2.9

Topology BN (B-C): Herbivore - Defender

Modularity

..

Observed Modularity: 0.63

Number of Modules: 5

Low-level nestedness

..

Nestedness in the entire matrix 16

Nestedness between species in the same module 32

Nestedness between species in different modules 12

Bipartite Networks and Intercept

..

BN (A-B) Specialization (H2') NA

BN (A-B) Connectance 0.017

BN (B-C) Specialization (H2') NA

BN (B-C) Connectance 0.15

Plant richness in BN (A-B): 120

Herbivore richness in BN (A-B): 97

Herbivore richness in BN (B-C): 19

Defender richness in BN (B-C): 10

Richness of shared Herbivores: 19

Number of modules in BN (A-B) 27

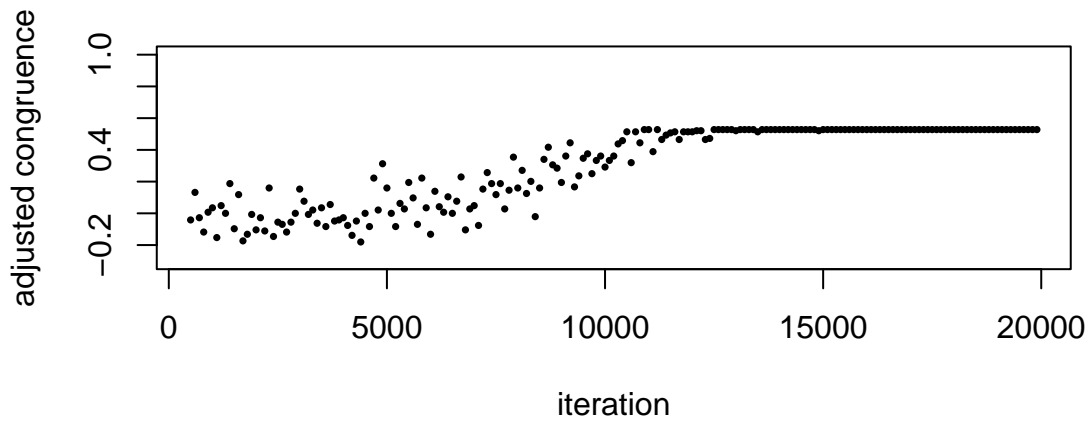
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 9

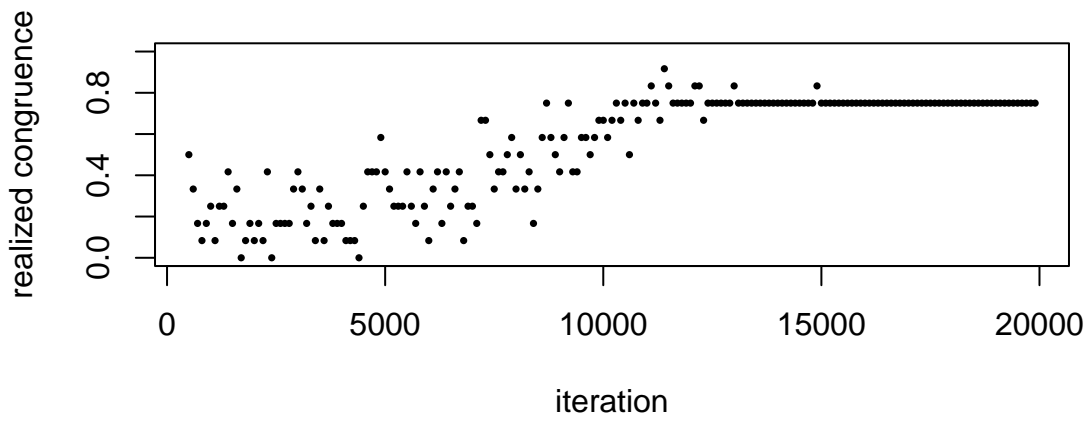
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence

Optimization procedure



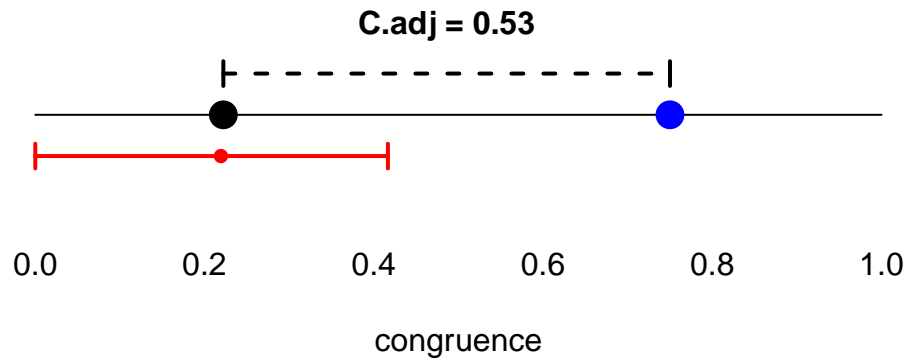
..



..

Adjusted Congruence: 0.53
 Realized Congruence: 0.75
 Hypermodularity: 0.37

Null Model 1

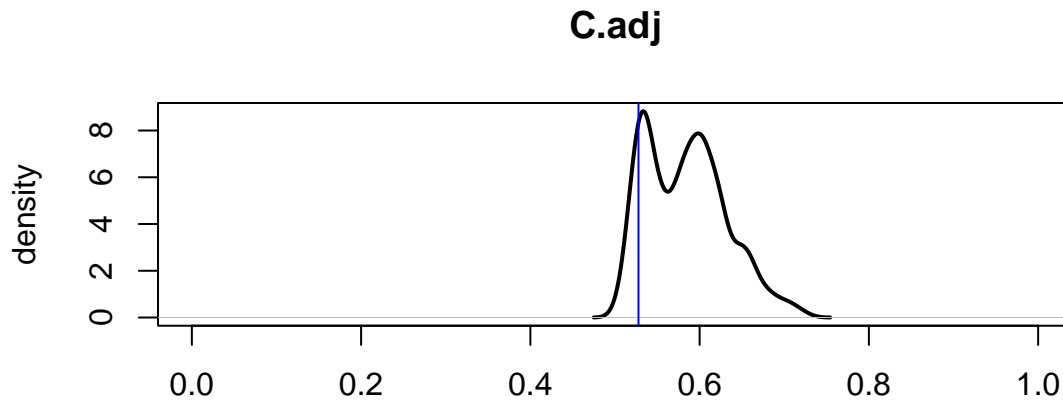


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.91

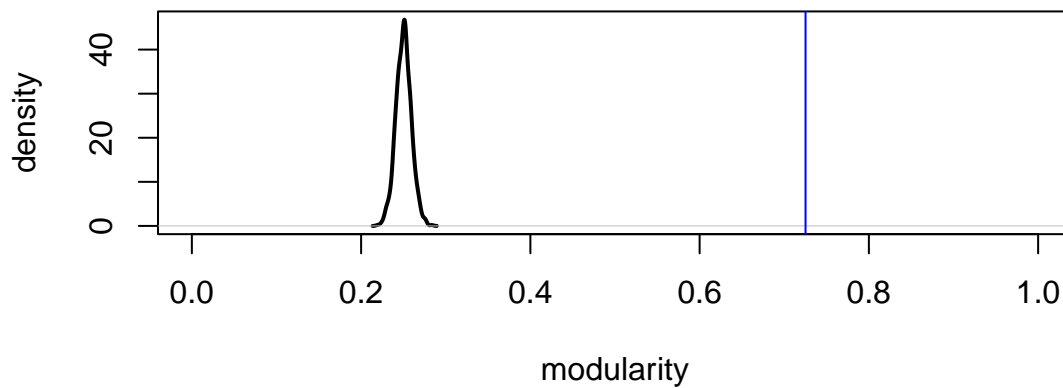
Dataset 32 : SHINOHARA

Topology BN (A-B): Herbivore - Plant

Modularity

..
Observed Modularity: 0.73
Number of Modules: 21

Comparison between observed modularity (blue line) and proportional null model (density in black)

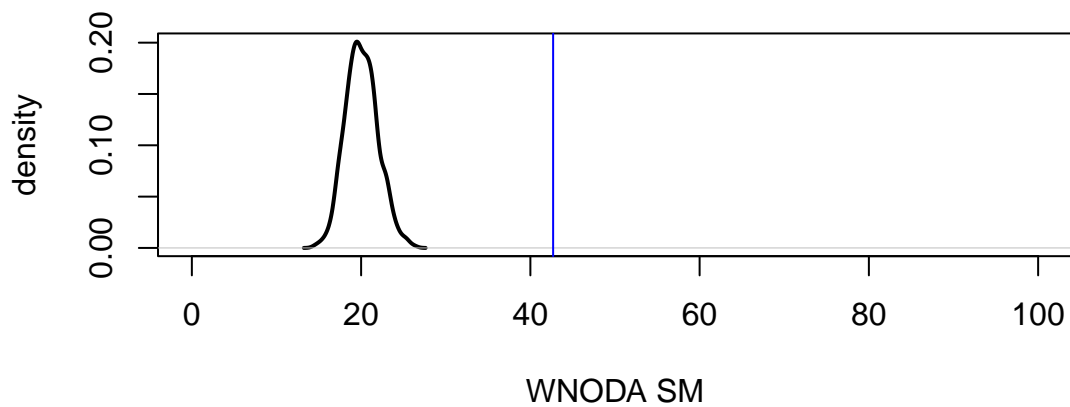


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 4.6
Nestedness between species in the same module: 43
Nestedness between species in different modules: 2.1

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

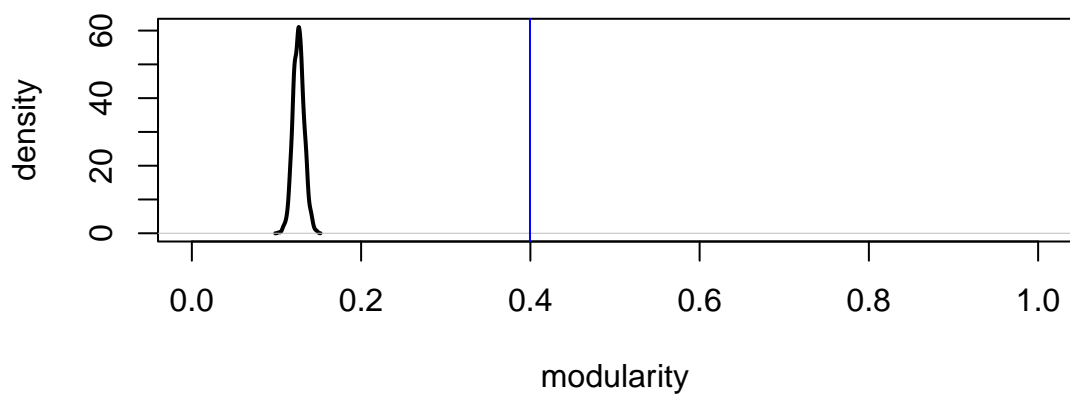
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Pollinator

Modularity

..
 Observed Modularity: 0.4
 Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

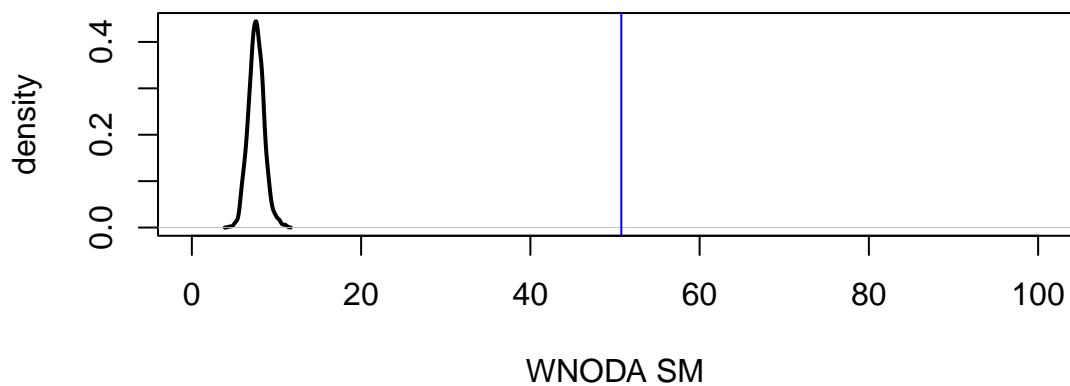


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 21
Nestedness between species in the same module 51
Nestedness between species in different modules 14

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

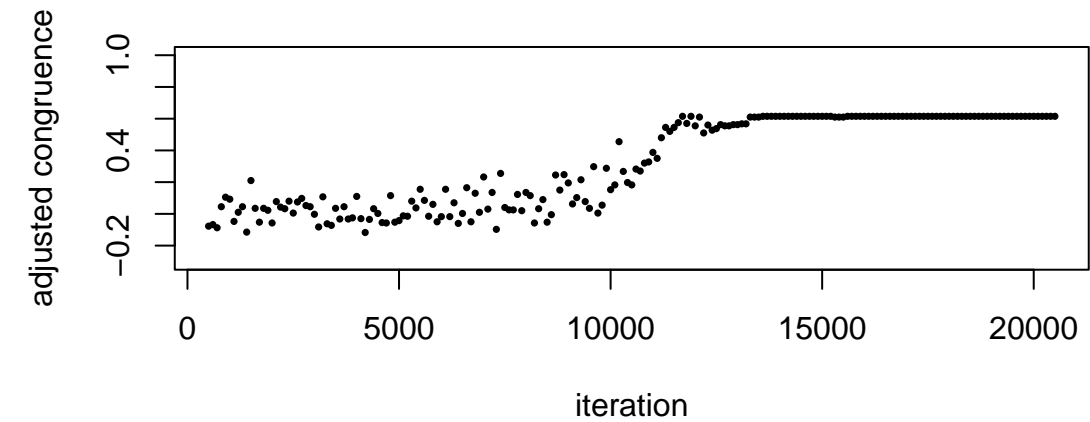
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

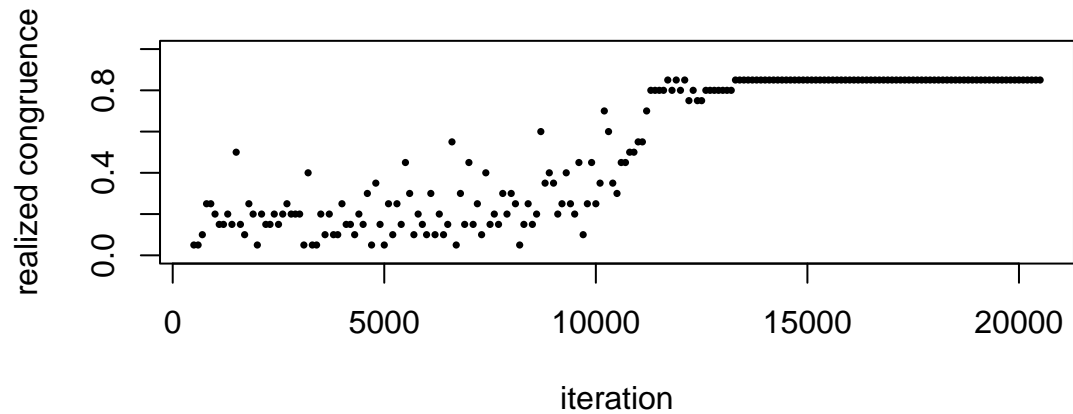
..
BN (A-B) Specialization (H2') 0.67
BN (A-B) Connectance 0.036
BN (B-C) Specialization (H2') 0.42
BN (B-C) Connectance 0.081
Herbivore richness in BN (A-B): 93
Plant richness in BN (A-B): 58
Plant richness in BN (B-C): 48
Pollinator richness in BN (B-C): 52
Richness of shared Plants: 48
Number of modules in BN (A-B) 21
Number of modules in BN (B-C) 9

Number of modules in BN (A-B) (only for shared species) 13
Number of modules in BN (B-C) (only for shared species) 8

Hipermodule Congruence
Optmization procedure

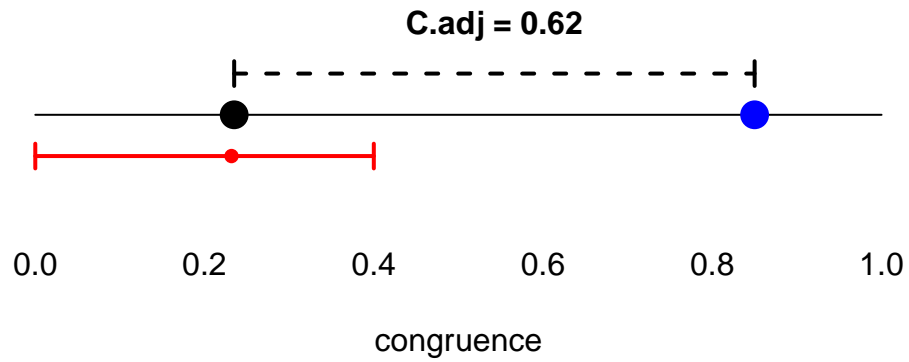


..



Adjusted Congruence: 0.61
Realized Congruence: 0.85
Hypermodularity: 0.47

Null Model 1

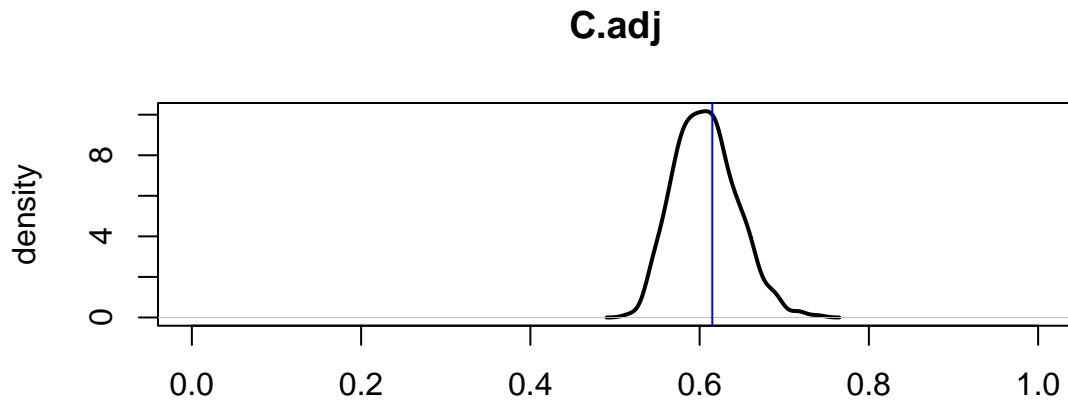


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.41

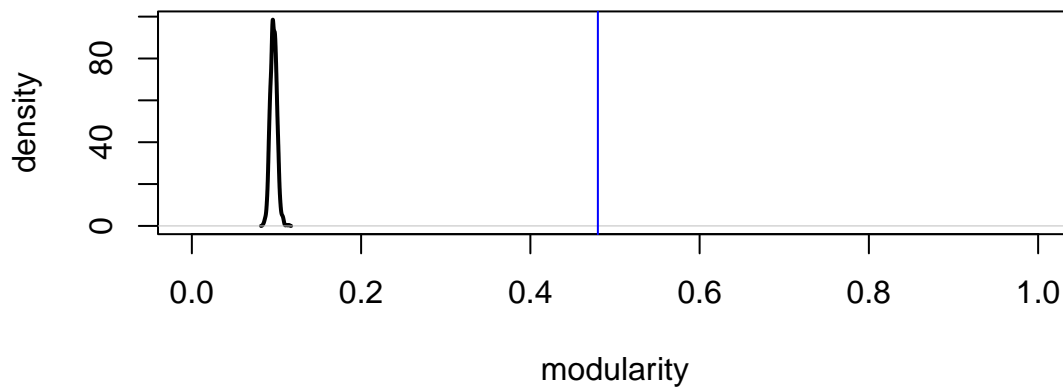
Dataset 33 : Vitali

Topology BN (A-B): Pollinator - Plant

Modularity

..
Observed Modularity: 0.48
Number of Modules: 10

Comparison between observed modularity (blue line) and proportional null model (density in black)

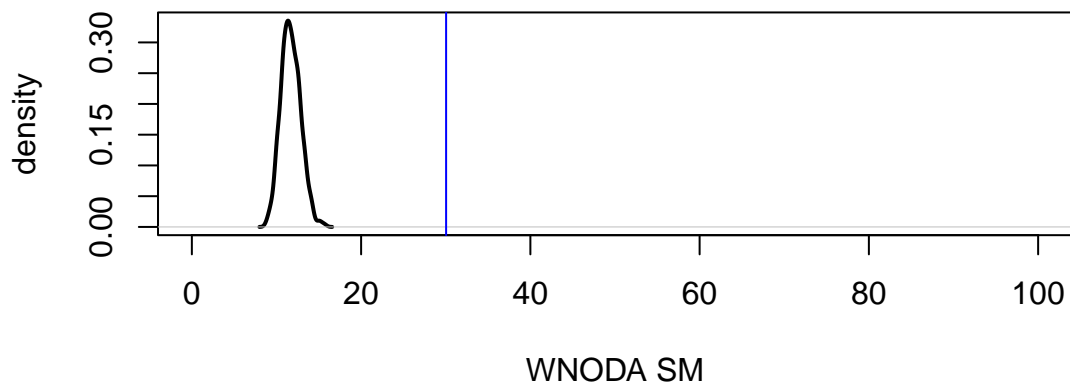


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 12
Nestedness between species in the same module: 30
Nestedness between species in different modules: 9

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

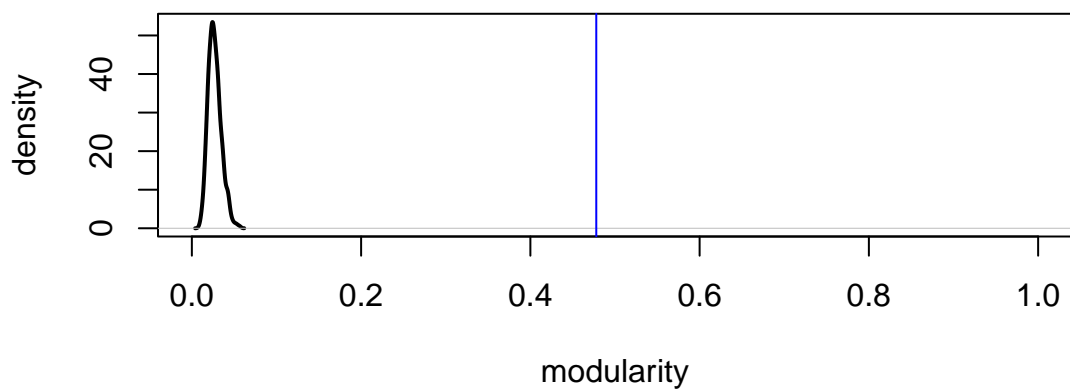
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Seed disperser

Modularity

..
 Observed Modularity: 0.48
 Number of Modules: 3

Comparison between observed modularity (blue line) and proportional null model (density in black)

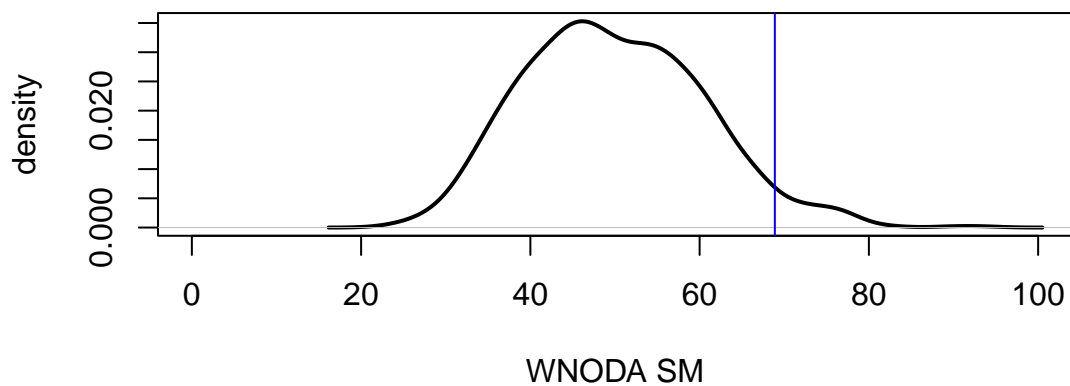


..
 Number of Matrices in Null Model: 1000
 P-Value: 0

Low-level nestedness

..
 Nestedness in the entire matrix 48
 Nestedness between species in the same module 69
 Nestedness between species in different modules 40

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.043

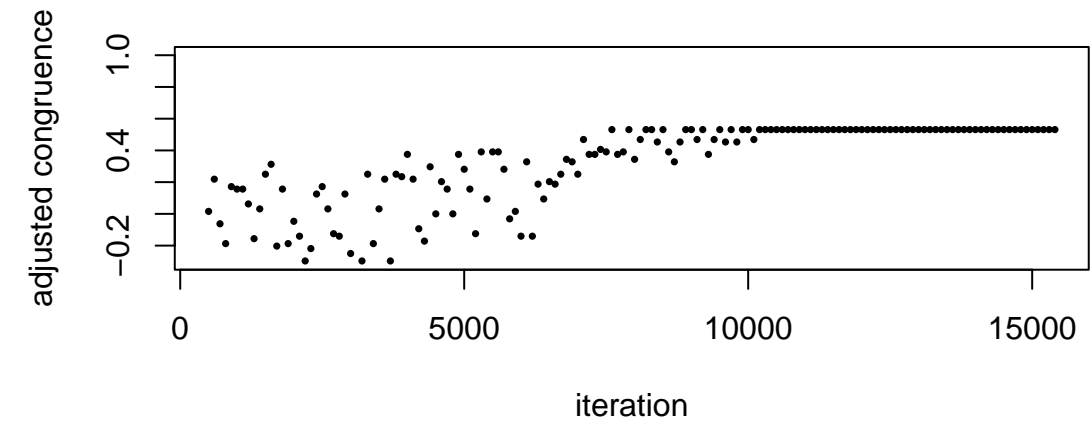
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

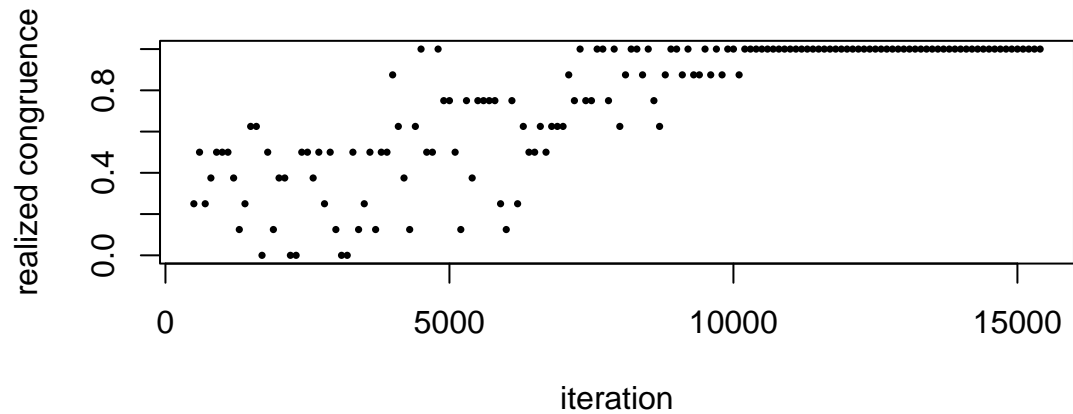
..
 BN (A-B) Specialization (H2') 0.51
 BN (A-B) Connectance 0.096
 BN (B-C) Specialization (H2') 0.88
 BN (B-C) Connectance 0.47
 Pollinator richness in BN (A-B): 95
 Plant richness in BN (A-B): 34
 Plant richness in BN (B-C): 10
 Seed disperser richness in BN (B-C): 4
 Richness of shared Plants:10
 Number of modules in BN (A-B) 10
 Number of modules in BN (B-C) 3

Number of modules in BN (A-B) (only for shared species) 6
Number of modules in BN (B-C) (only for shared species) 3

Hipermodule Congruence
Optimization procedure

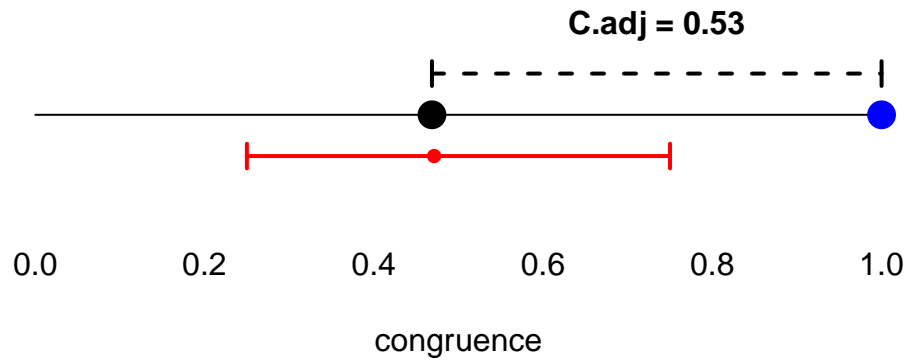


..



Adjusted Congruence: 0.53
Realized Congruence: 1
Hypermodularity: 0.41

Null Model 1

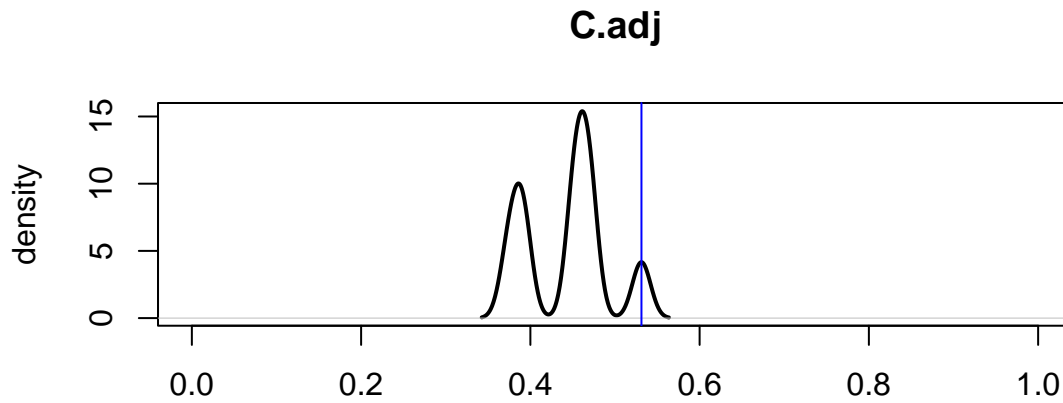


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.005

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.11

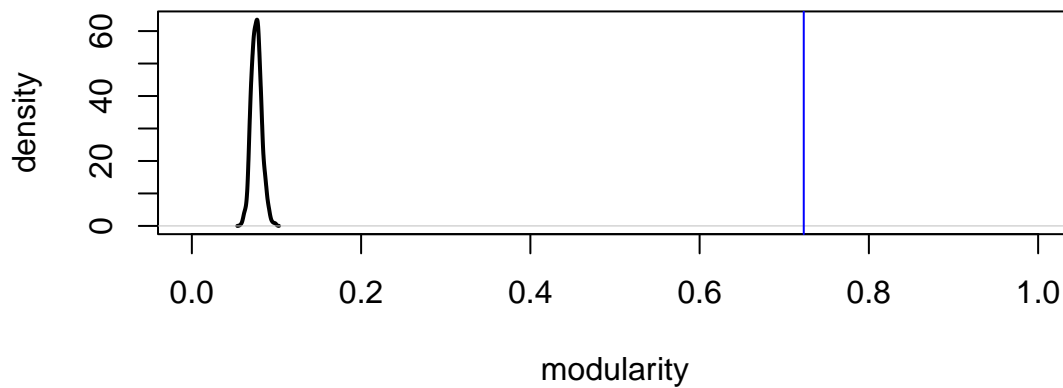
Dataset 34 : Zhang

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.72
Number of Modules: 19

Comparison between observed modularity (blue line) and proportional null model (density in black)

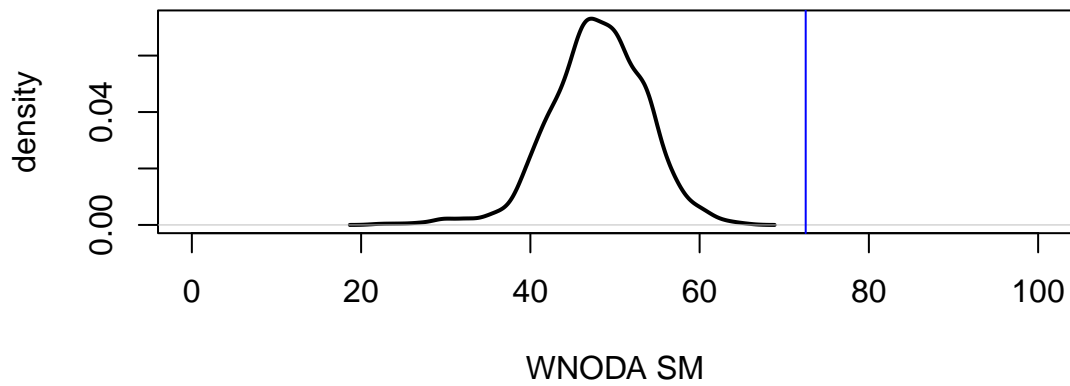


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 8
Nestedness between species in the same module: 73
Nestedness between species in different modules: 3.5

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

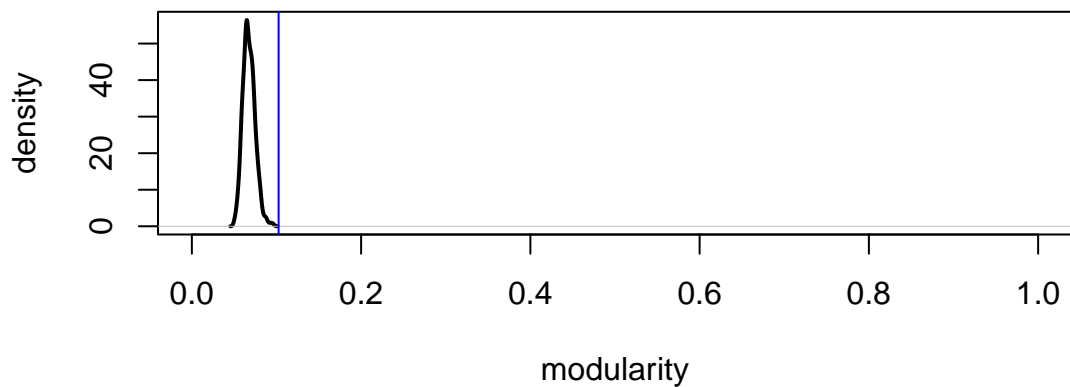
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Herbivore - Defender

Modularity

..
 Observed Modularity: 0.1
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

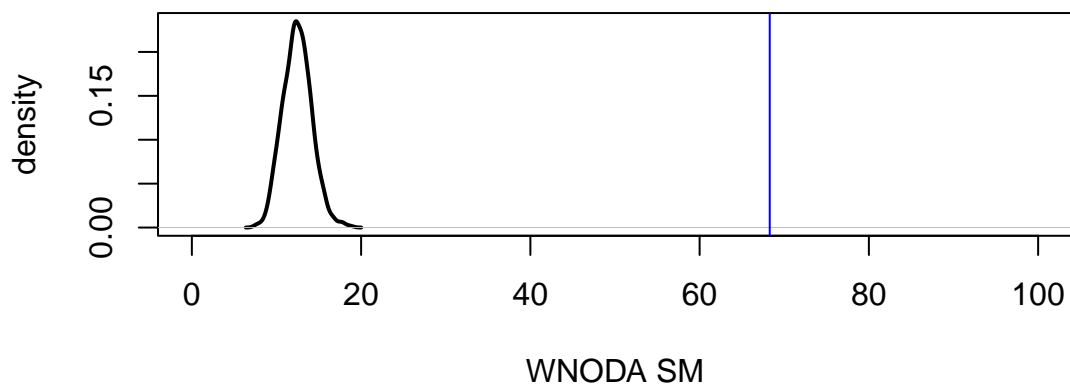


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 57
Nestedness between species in the same module 68
Nestedness between species in different modules 54

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

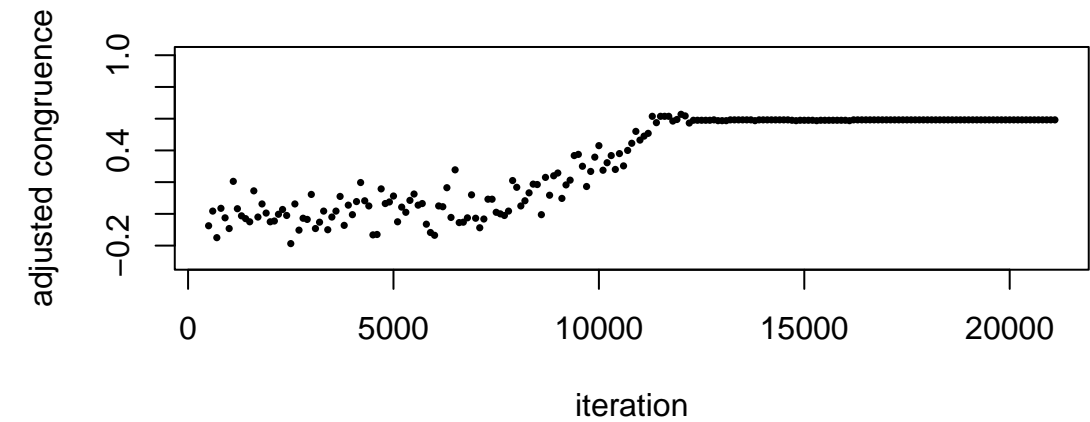
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

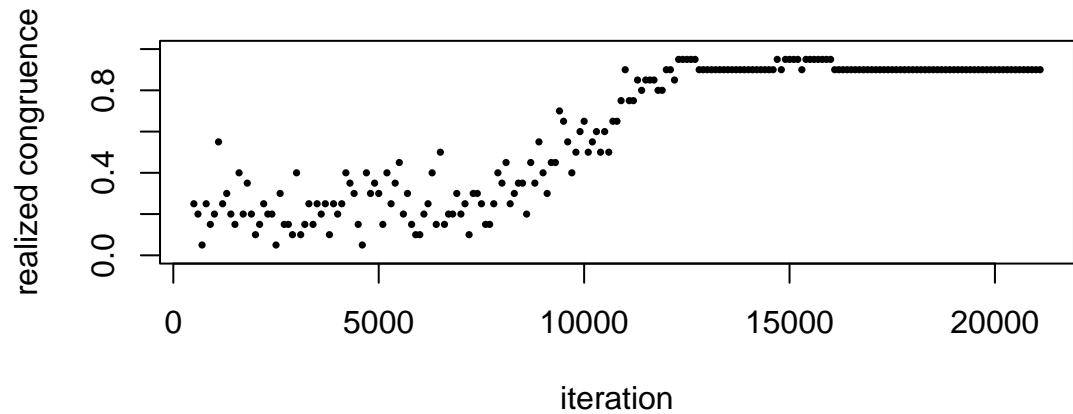
..
BN (A-B) Specialization (H2') 0.91
BN (A-B) Connectance 0.078
BN (B-C) Specialization (H2') 0.062
BN (B-C) Connectance 0.21
Plant richness in BN (A-B): 41
Herbivore richness in BN (A-B): 24
Herbivore richness in BN (B-C): 20
Defender richness in BN (B-C): 35
Richness of shared Herbivores: 20
Number of modules in BN (A-B) 19
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 16
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

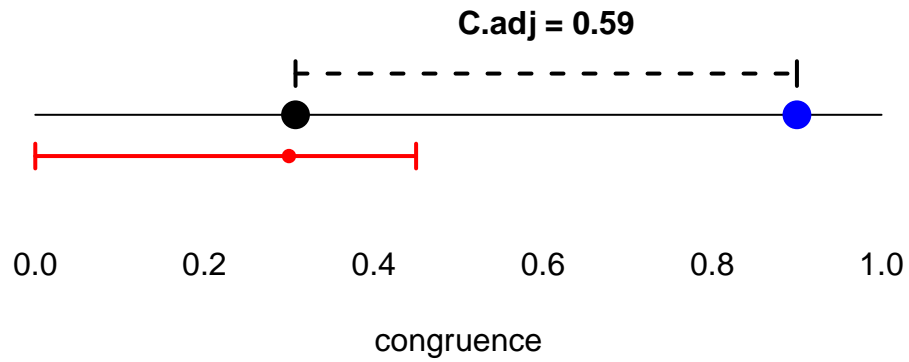


..



..
Adjusted Congruence: 0.59
Realized Congruence: 0.9
Hypermodularity: 0.3

Null Model 1

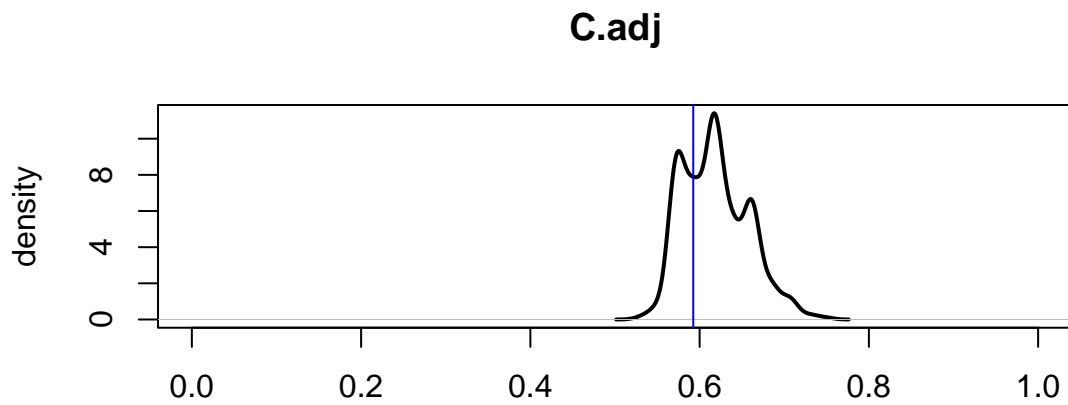


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.72

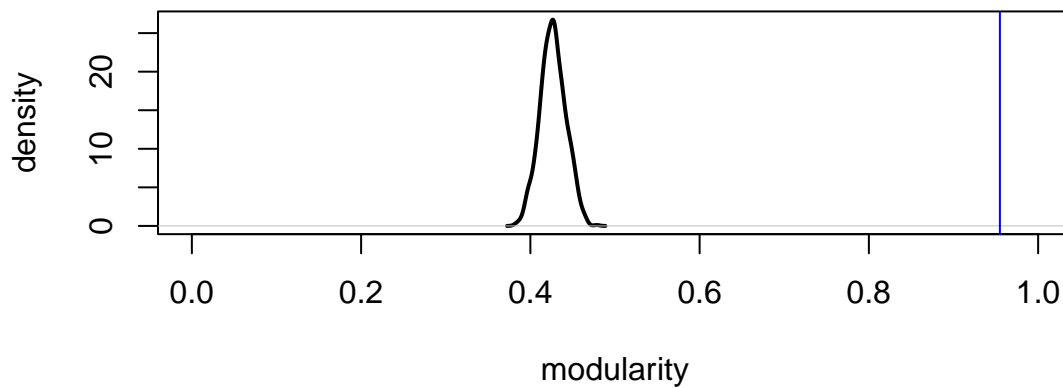
Dataset 35 : ARAUJO

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.95
Number of Modules: 44

Comparison between observed modularity (blue line) and proportional null model (density in black)

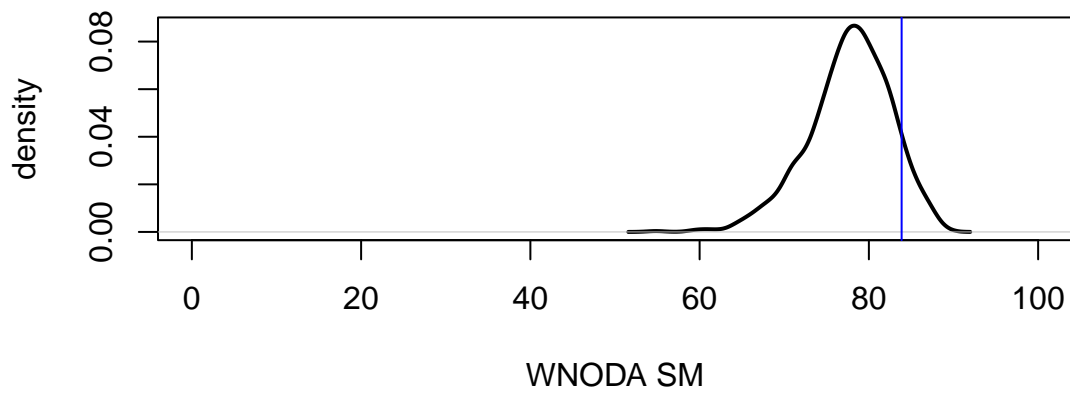


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 1.3
Nestedness between species in the same module: 84
Nestedness between species in different modules: 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.12

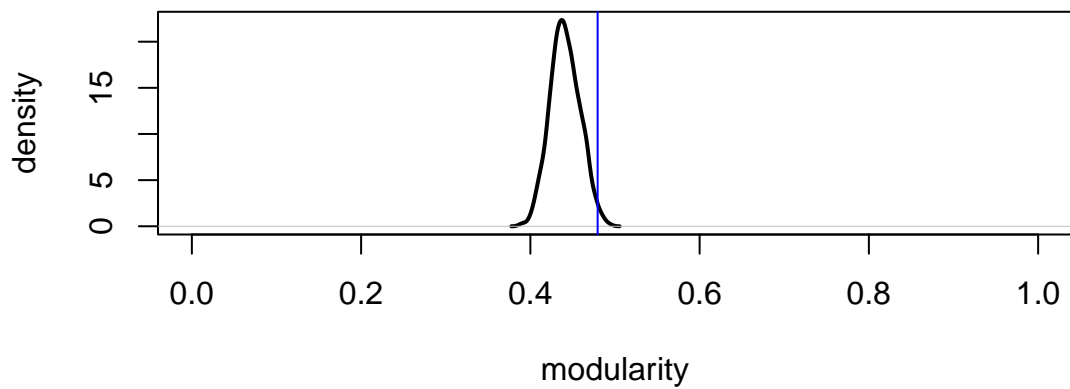
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.48
 Number of Modules: 18

Comparison between observed modularity (blue line) and proportional null model (density in black)

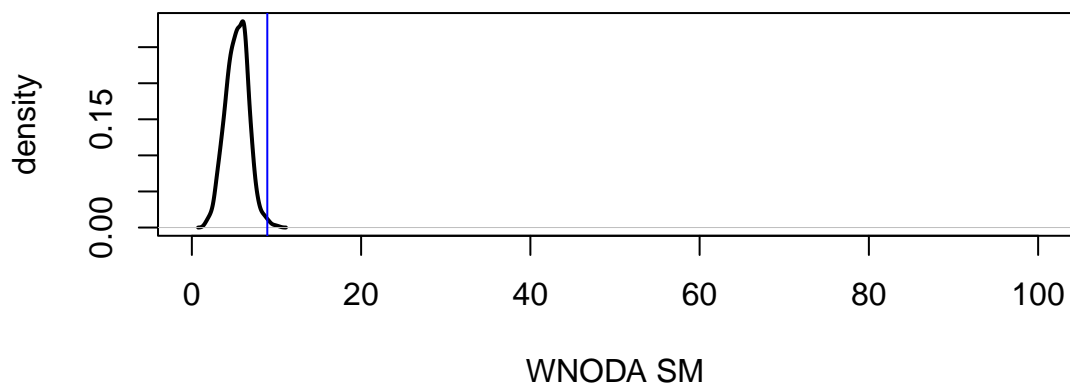


..
Number of Matrices in Null Model: 1000
P-Value: 0.015

Low-level nestedness

..
Nestedness in the entire matrix 2.4
Nestedness between species in the same module 8.9
Nestedness between species in different modules 1.9

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.008

CONCLUSION: BN (B-C) has a compound topology

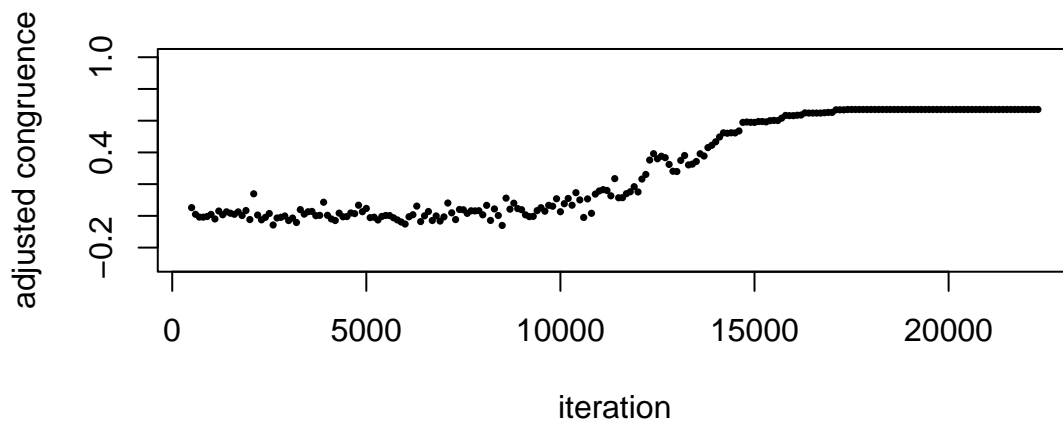
Bipartite Networks and Intercept

..
BN (A-B) Specialization (H2') 1
BN (A-B) Connectance 0.023
BN (B-C) Specialization (H2') 0.049
BN (B-C) Connectance 0.05
Plant richness in BN (A-B): 44
Herbivore richness in BN (A-B): 80
Herbivore richness in BN (B-C): 59
Parasitoid richness in BN (B-C): 68
Richness of shared Herbivores: 59
Number of modules in BN (A-B) 44
Number of modules in BN (B-C) 18

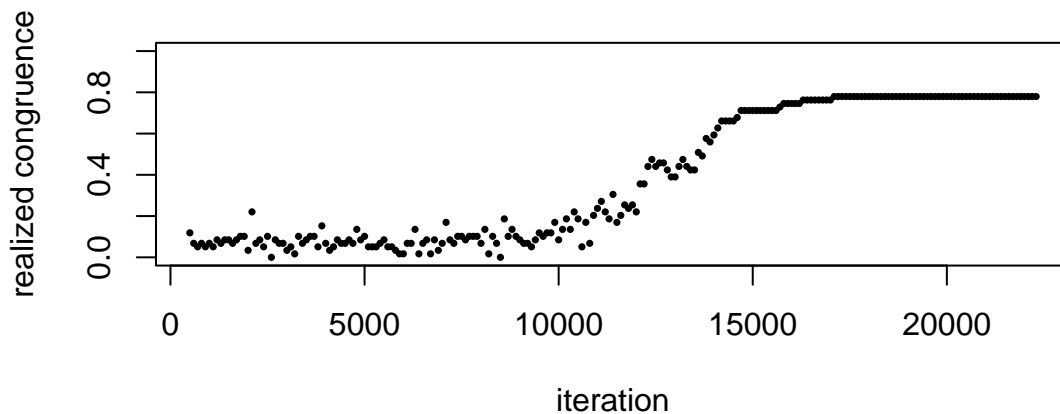
Number of modules in BN (A-B) (only for shared species) 35
Number of modules in BN (B-C) (only for shared species) 18

Hipermodule Congruence

Optmization procedure



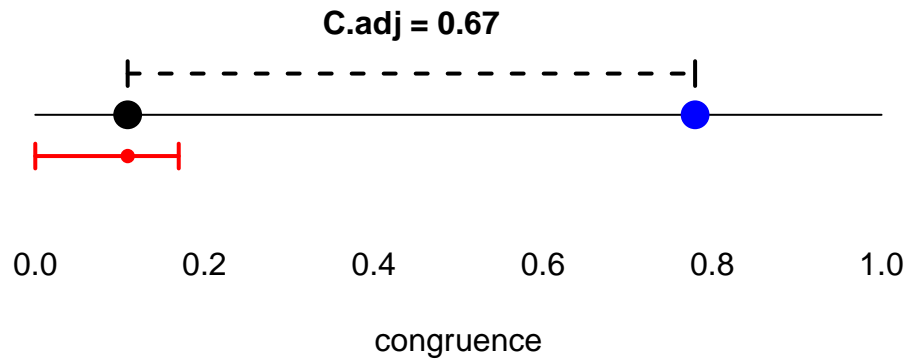
..



..

Adjusted Congruence: 0.67
Realized Congruence: 0.78
Hypermodularity: 0.51

Null Model 1

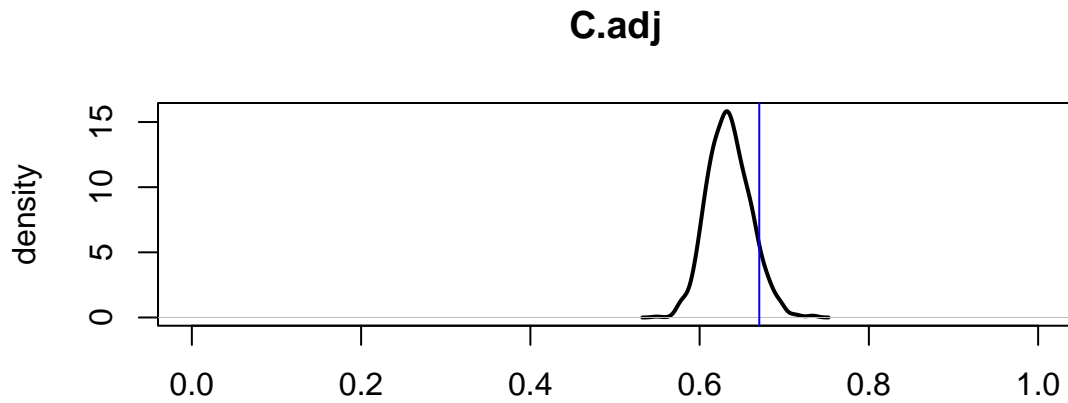


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.084

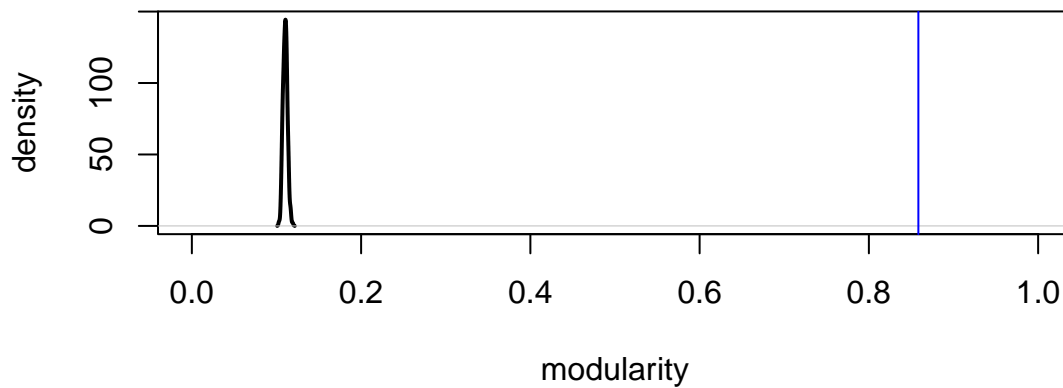
Dataset 36 : BASSET BCI

Topology BN (A-B): Plant - pulp.feeder

Modularity

..
Observed Modularity: 0.86
Number of Modules: 63

Comparison between observed modularity (blue line) and proportional null model (density in black)

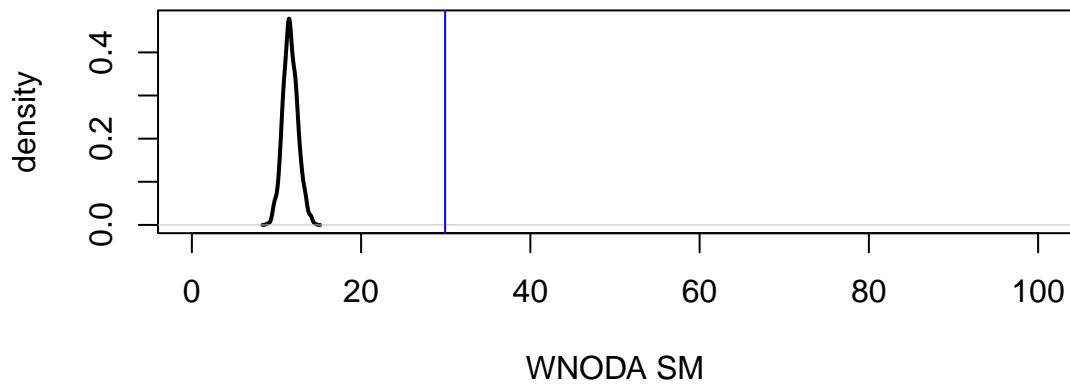


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 1.4
Nestedness between species in the same module: 30
Nestedness between species in different modules: 0.66

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

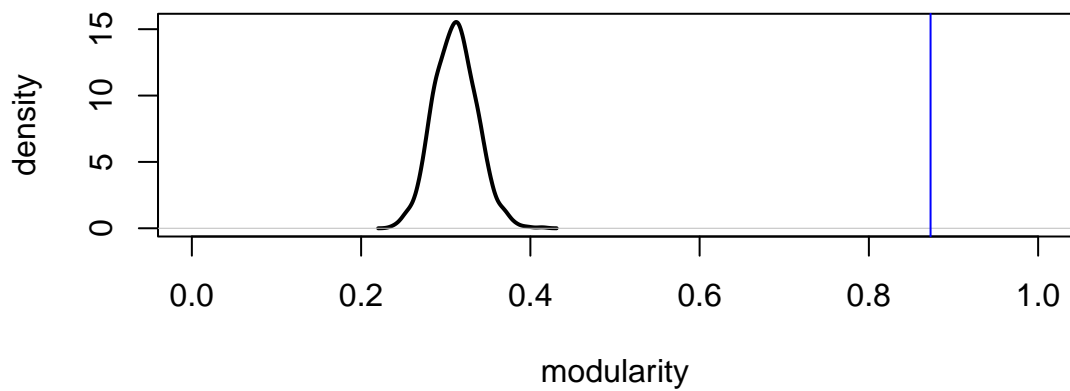
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): pulp.feeder - Parasitoid

Modularity

..
 Observed Modularity: 0.87
 Number of Modules: 19

Comparison between observed modularity (blue line) and proportional null model (density in black)

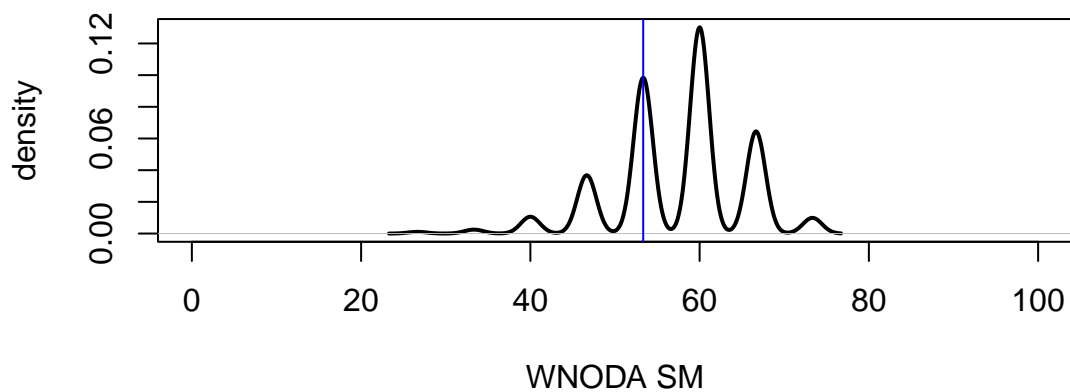


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 1.3
Nestedness between species in the same module 53
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.86

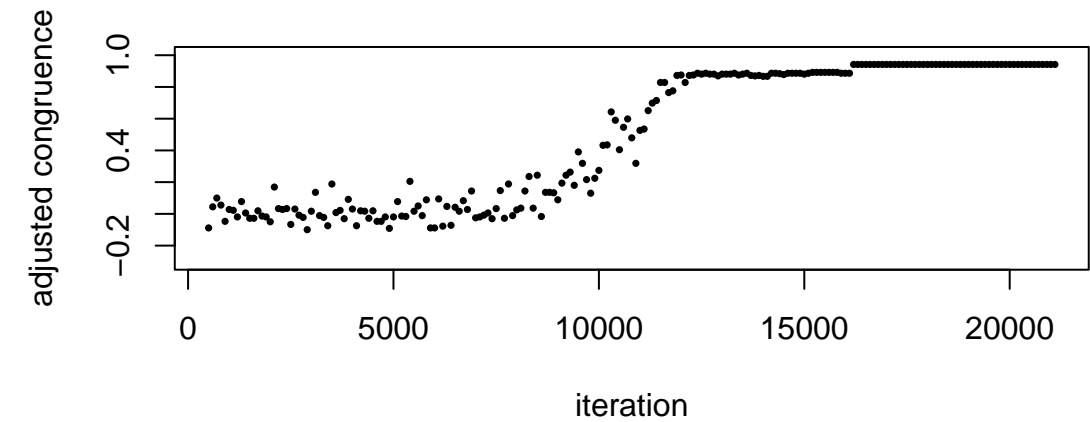
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

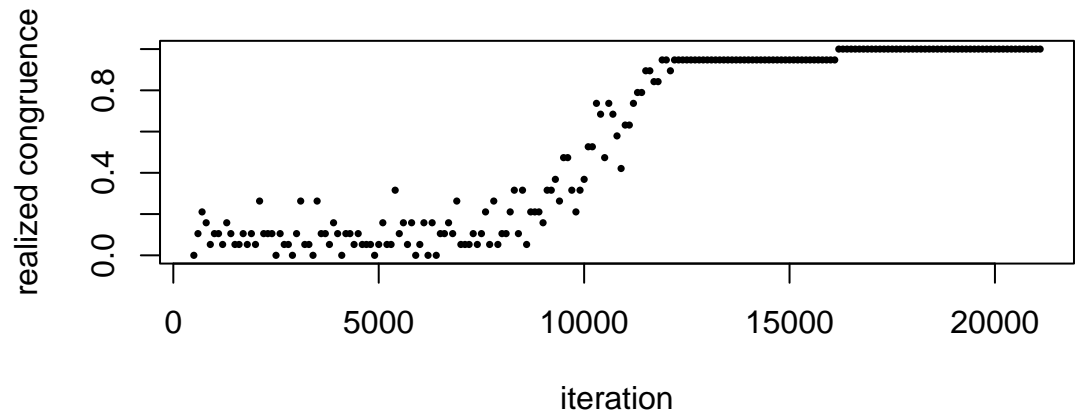
..
BN (A-B) Specialization (H2') 0.86
BN (A-B) Connectance 0.012
BN (B-C) Specialization (H2') 1
BN (B-C) Connectance 0.053
Plant richness in BN (A-B): 157
pulp.feeder richness in BN (A-B): 214
pulp.feeder richness in BN (B-C): 19
Parasitoid richness in BN (B-C): 30
Richness of shared pulp.feeders:19
Number of modules in BN (A-B) 63
Number of modules in BN (B-C) 19

Number of modules in BN (A-B) (only for shared species) 18
Number of modules in BN (B-C) (only for shared species) 19

Hipermodule Congruence
Optmization procedure

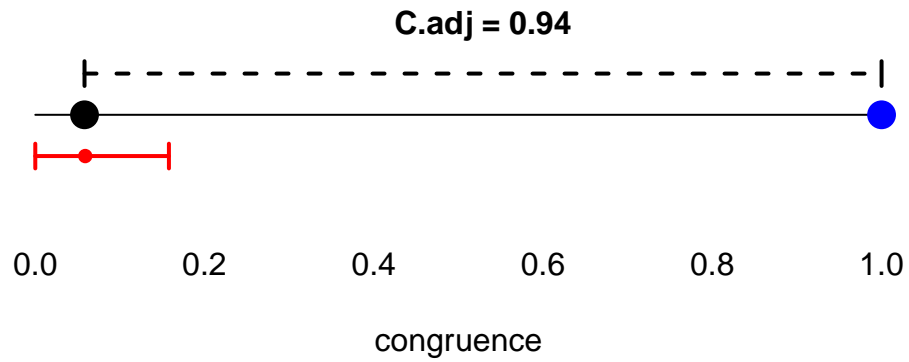


..



Adjusted Congruence: 0.94
Realized Congruence: 1
Hypermodularity: 0.83

Null Model 1

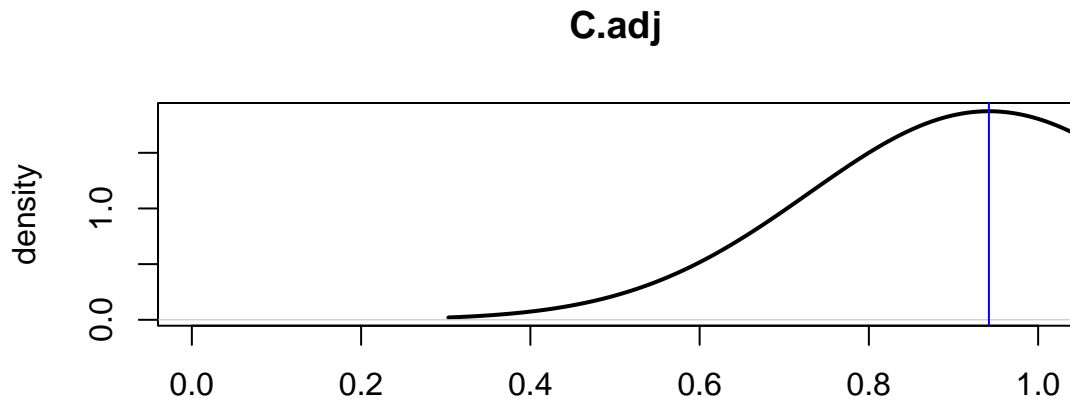


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

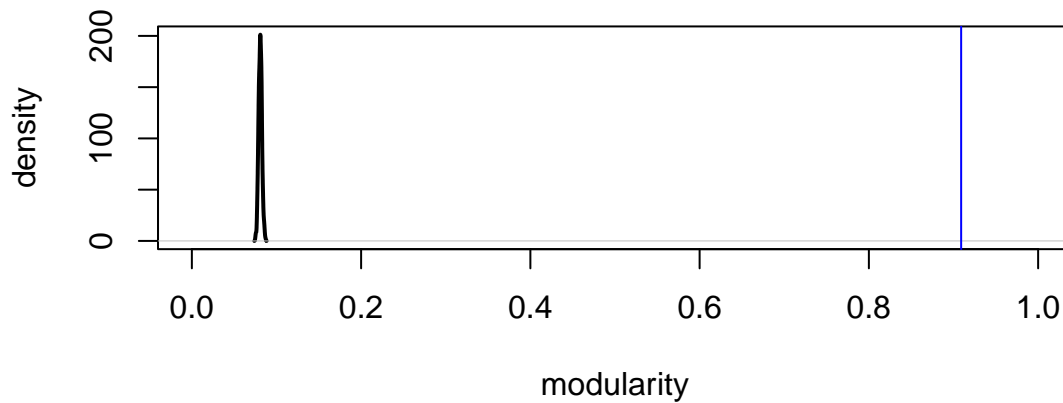
Dataset 37 : BASSET BCI

Topology BN (A-B): Plant - seed predator

Modularity

..
Observed Modularity: 0.91
Number of Modules: 89

Comparison between observed modularity (blue line) and proportional null model (density in black)

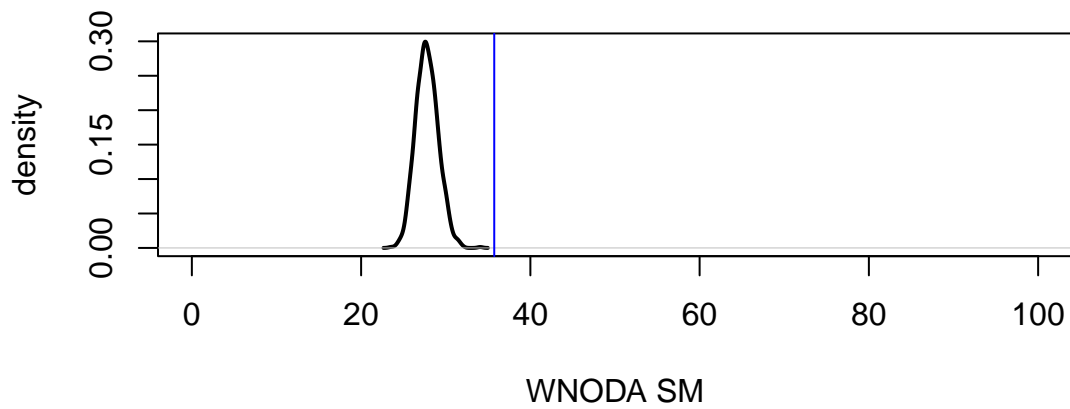


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 0.6
Nestedness between species in the same module: 36
Nestedness between species in different modules: 0.11

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

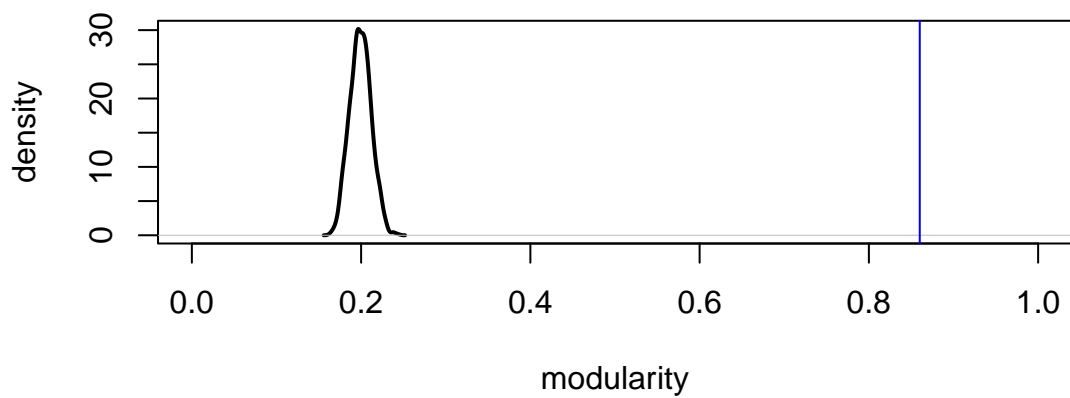
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): seed predator - Parasitoid

Modularity

..
 Observed Modularity: 0.86
 Number of Modules: 28

Comparison between observed modularity (blue line) and proportional null model (density in black)

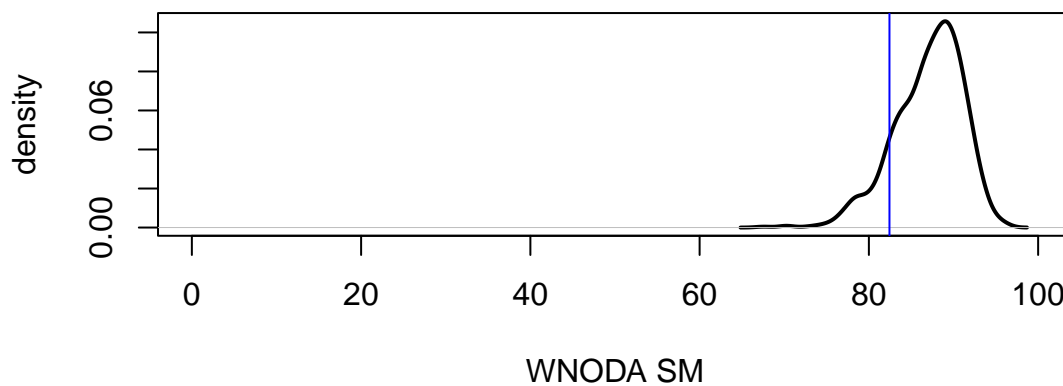


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 3.5
Nestedness between species in the same module 82
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.9

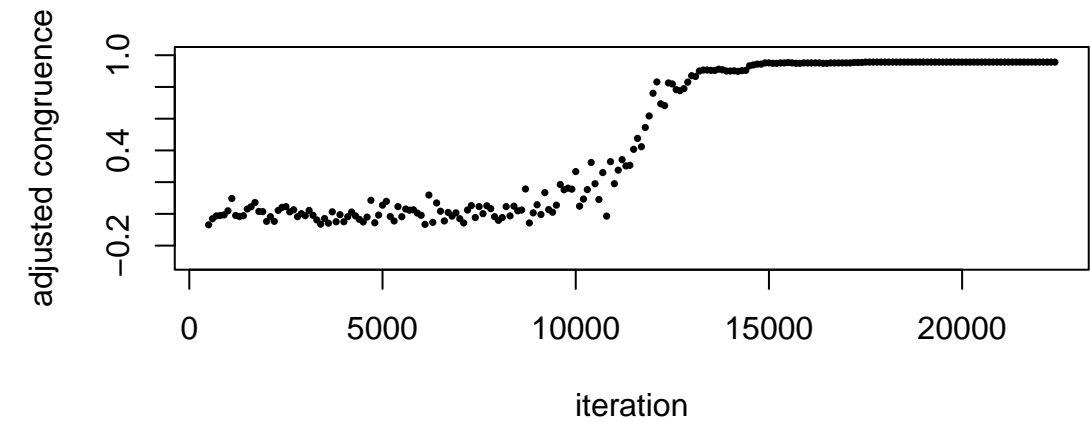
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

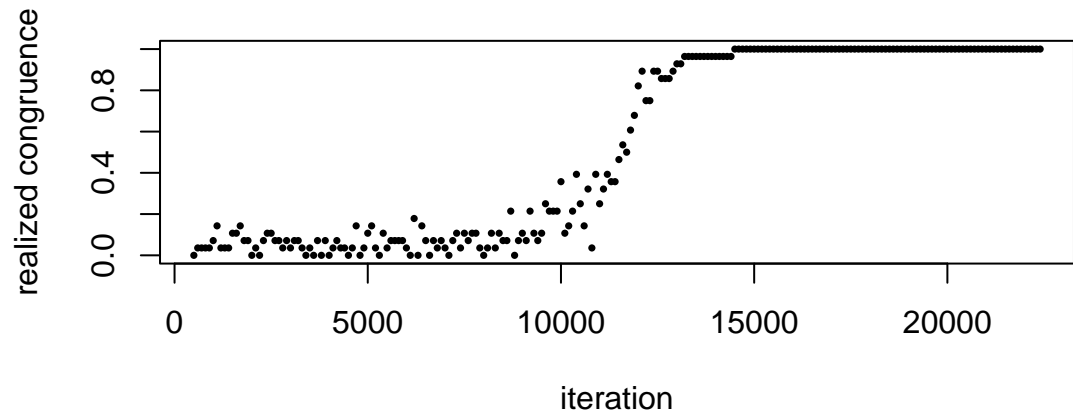
..
BN (A-B) Specialization (H2') 0.97
BN (A-B) Connectance 0.0072
BN (B-C) Specialization (H2') 1
BN (B-C) Connectance 0.036
Plant richness in BN (A-B): 181
seed predator richness in BN (A-B): 311
seed predator richness in BN (B-C): 28
Parasitoid richness in BN (B-C): 53
Richness of shared seed predators: 28
Number of modules in BN (A-B) 89
Number of modules in BN (B-C) 28

Number of modules in BN (A-B) (only for shared species) 25
Number of modules in BN (B-C) (only for shared species) 28

Hipermodule Congruence
Optmization procedure

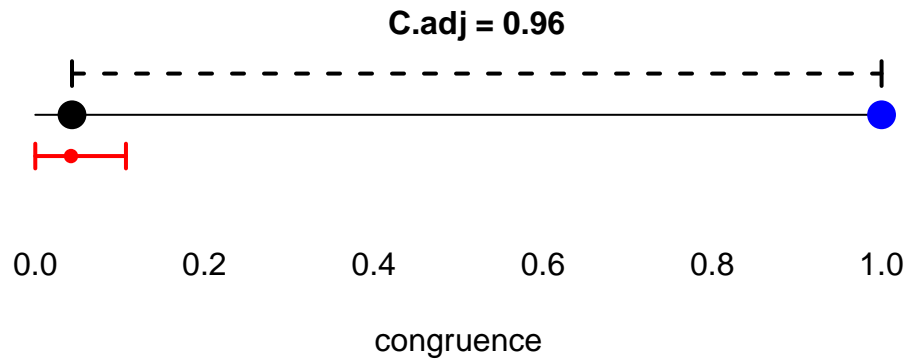


..



Adjusted Congruence: 0.96
Realized Congruence: 1
Hypermodularity: 0.81

Null Model 1

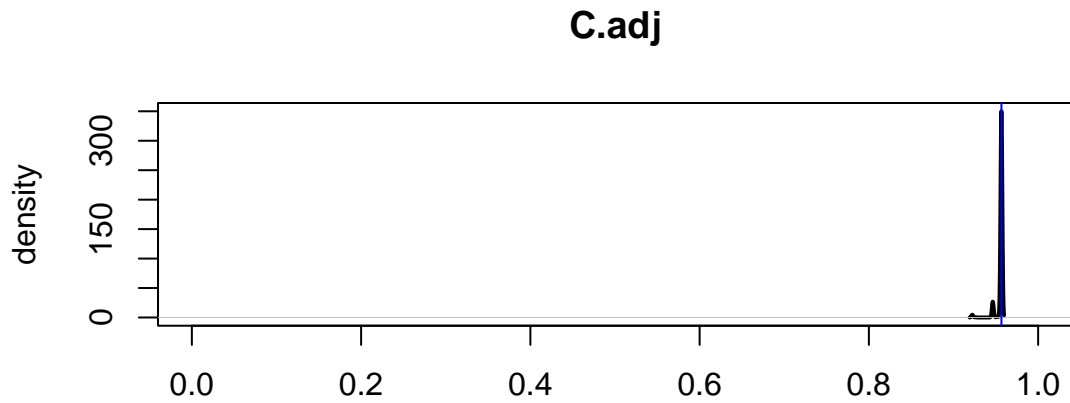


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.91

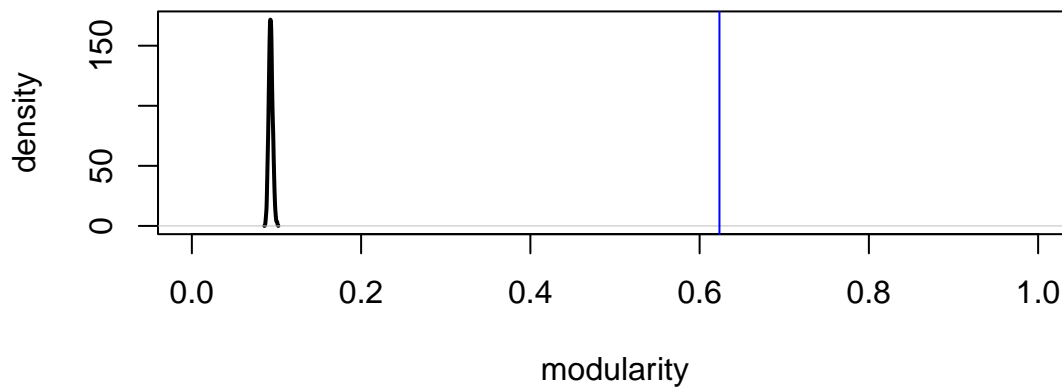
Dataset 38 : BASSET KHC

Topology BN (A-B): Plant - pulp.feeder

Modularity

..
Observed Modularity: 0.62
Number of Modules: 26

Comparison between observed modularity (blue line) and proportional null model (density in black)

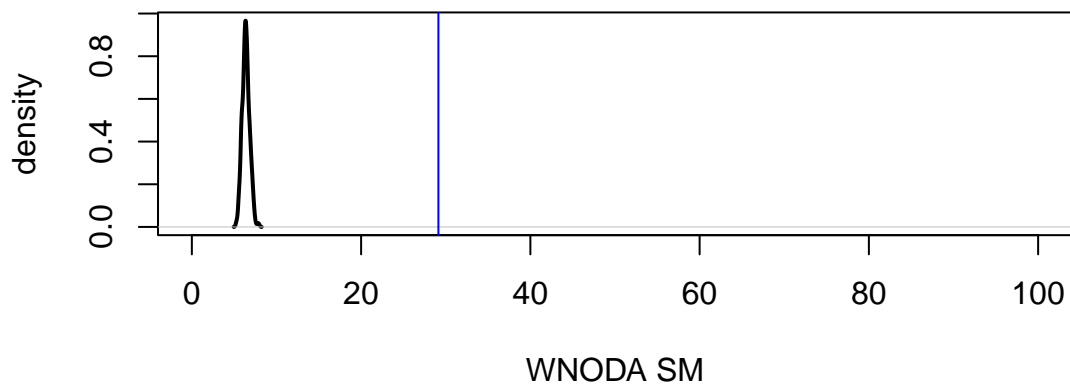


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 5.8
Nestedness between species in the same module: 29
Nestedness between species in different modules: 4.2

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

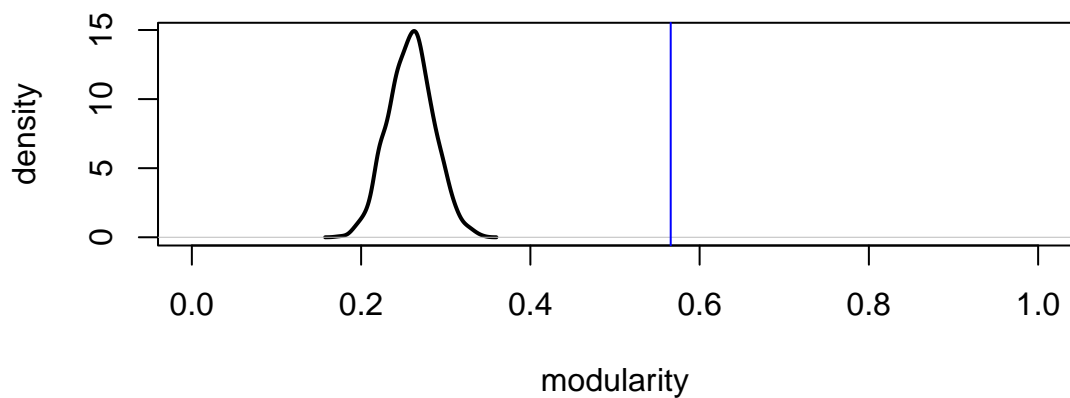
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): pulp.feeder - Parasitoid

Modularity

..
 Observed Modularity: 0.57
 Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

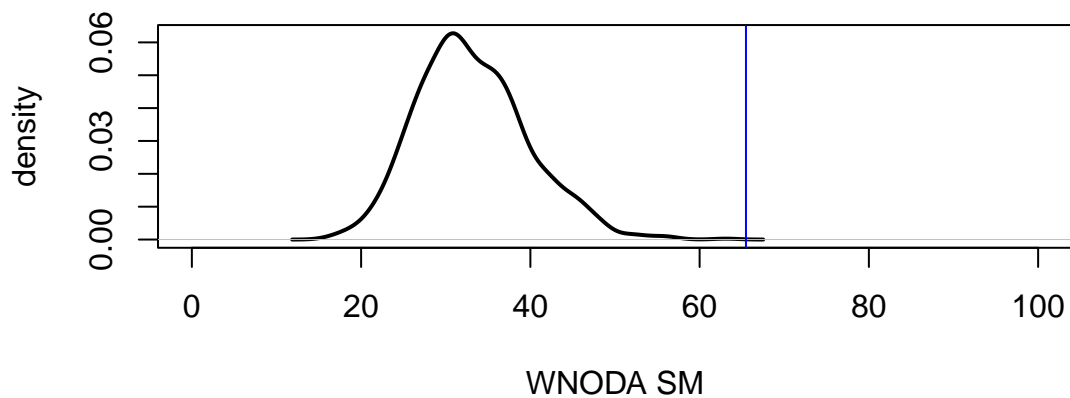


..
 Number of Matrices in Null Model: 1000
 P-Value: 0

Low-level nestedness

..
 Nestedness in the entire matrix 12
 Nestedness between species in the same module 65
 Nestedness between species in different modules 4.6

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

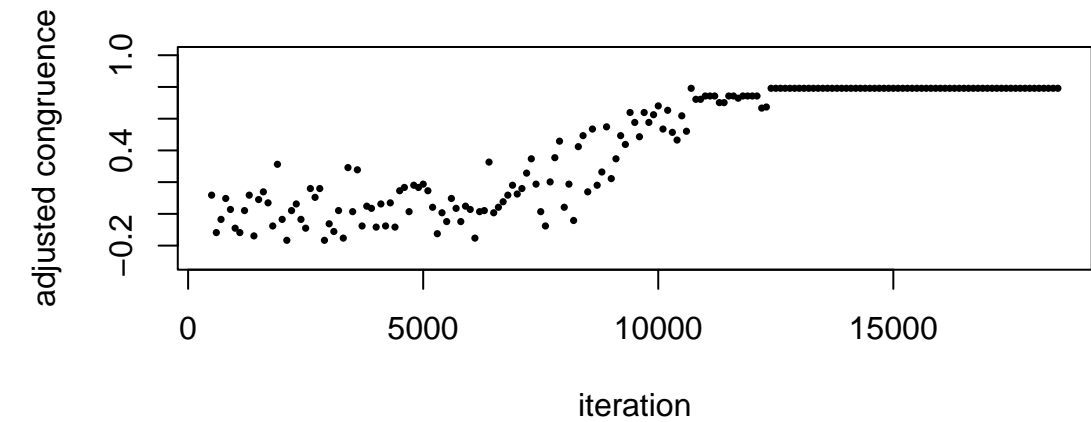
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

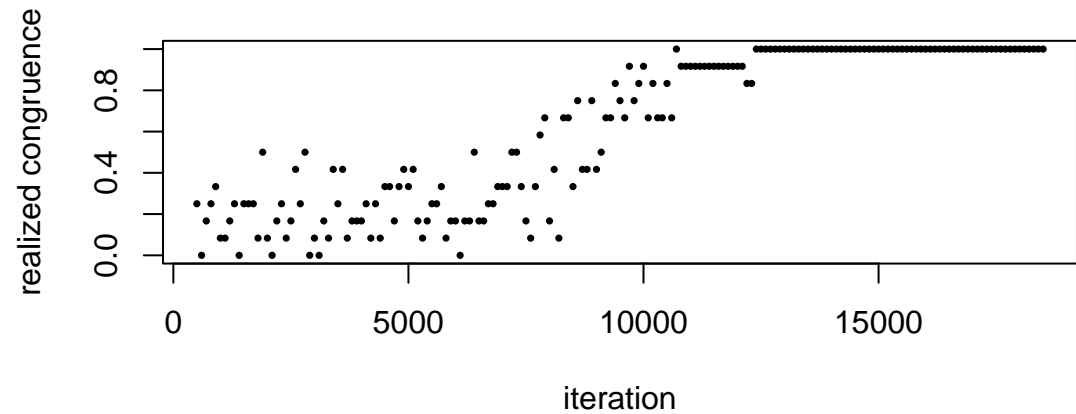
..
 BN (A-B) Specialization (H2') 0.63
 BN (A-B) Connectance 0.027
 BN (B-C) Specialization (H2') 0.64
 BN (B-C) Connectance 0.12
 Plant richness in BN (A-B): 170
 pulp.feeder richness in BN (A-B): 161
 pulp.feeder richness in BN (B-C): 12
 Parasitoid richness in BN (B-C): 24
 Richness of shared pulp.feeders:12
 Number of modules in BN (A-B) 26
 Number of modules in BN (B-C) 9

Number of modules in BN (A-B) (only for shared species) 8
Number of modules in BN (B-C) (only for shared species) 9

Hipermodule Congruence
Optmization procedure

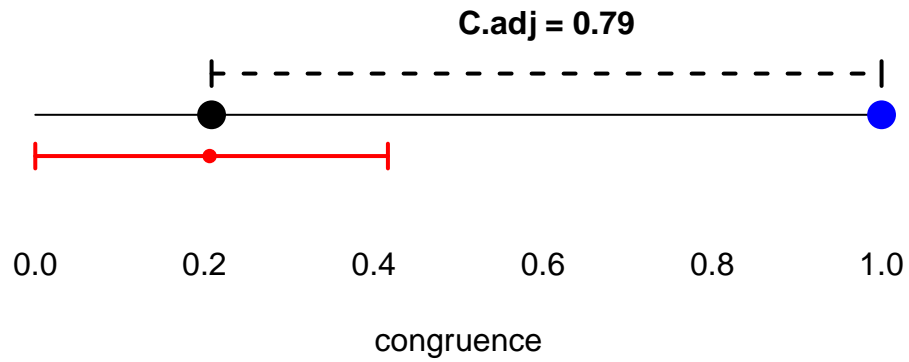


..



Adjusted Congruence: 0.79
Realized Congruence: 1
Hypermodularity: 0.54

Null Model 1

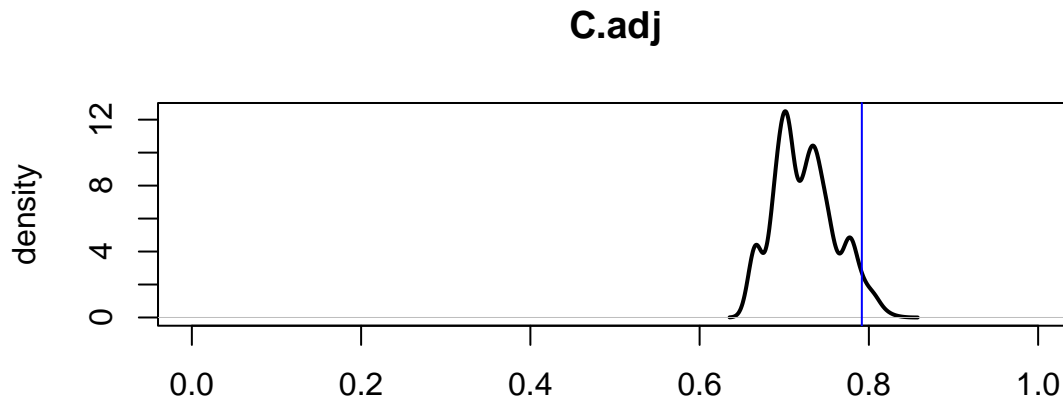


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.059

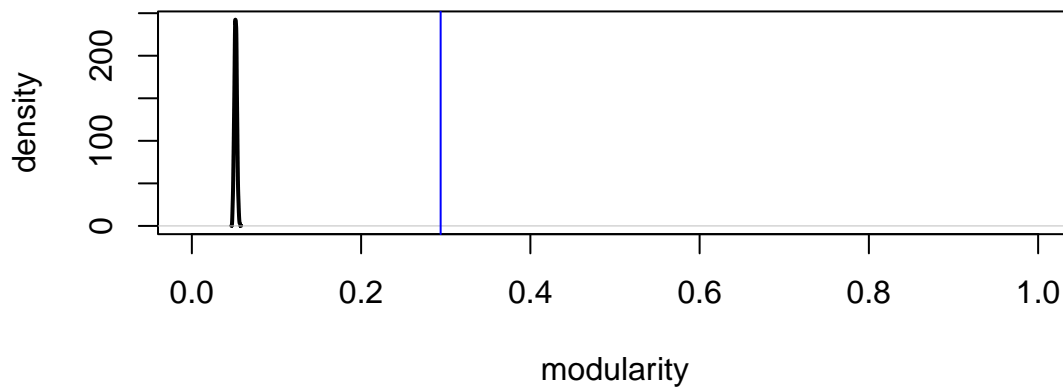
Dataset 39 : BASSET WAN

Topology BN (A-B): Plant - pulp.feeder

Modularity

..
Observed Modularity: 0.29
Number of Modules: 29

Comparison between observed modularity (blue line) and proportional null model (density in black)

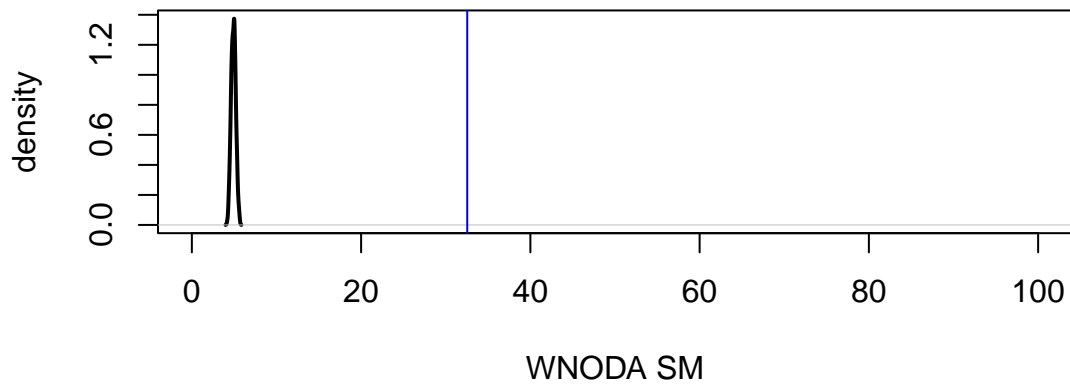


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 19
Nestedness between species in the same module: 33
Nestedness between species in different modules: 18

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

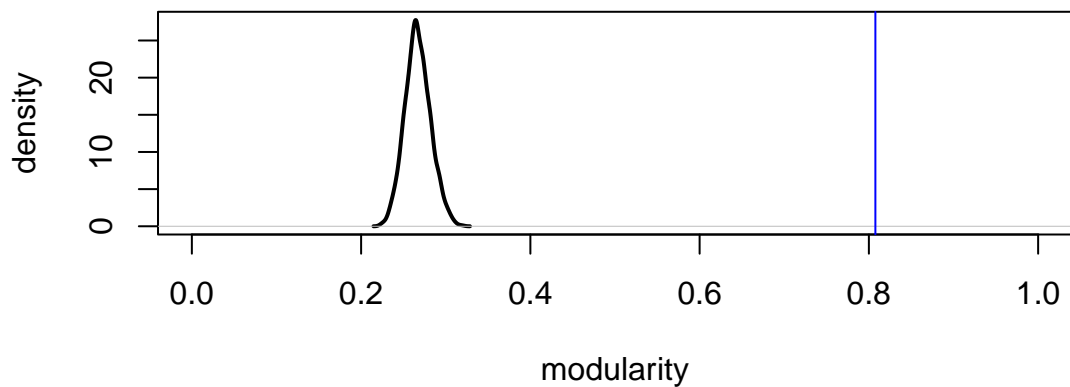
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): pulp.feeder - Parasitoid

Modularity

..
 Observed Modularity: 0.81
 Number of Modules: 20

Comparison between observed modularity (blue line) and proportional null model (density in black)

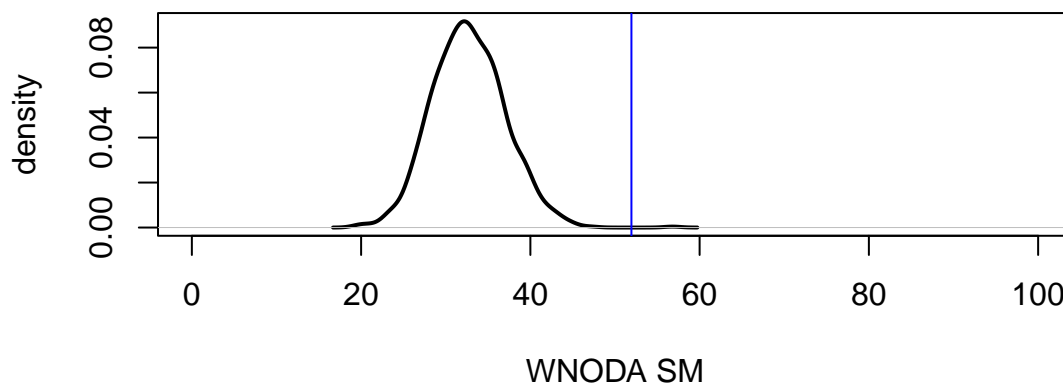


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 3.1
Nestedness between species in the same module 52
Nestedness between species in different modules 0.38

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.001

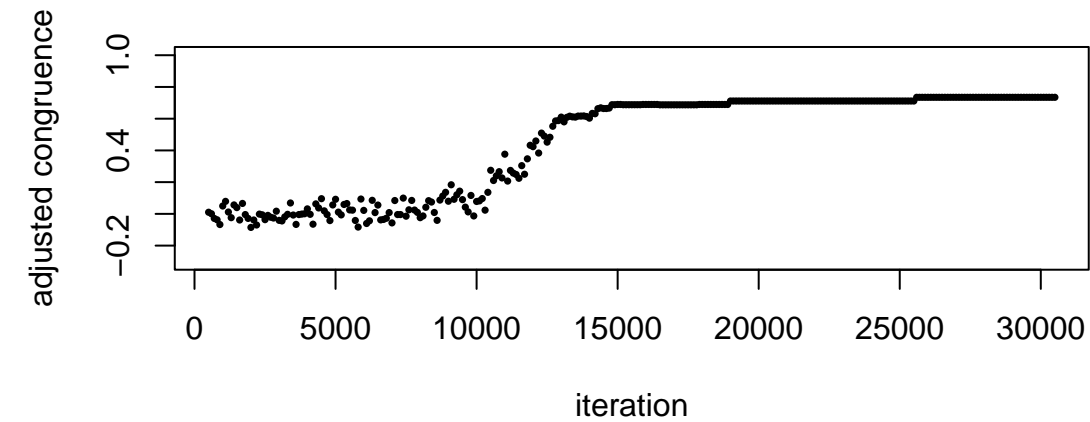
CONCLUSION: BN (B-C) has a compound topology

Bipartite Networks and Intercept

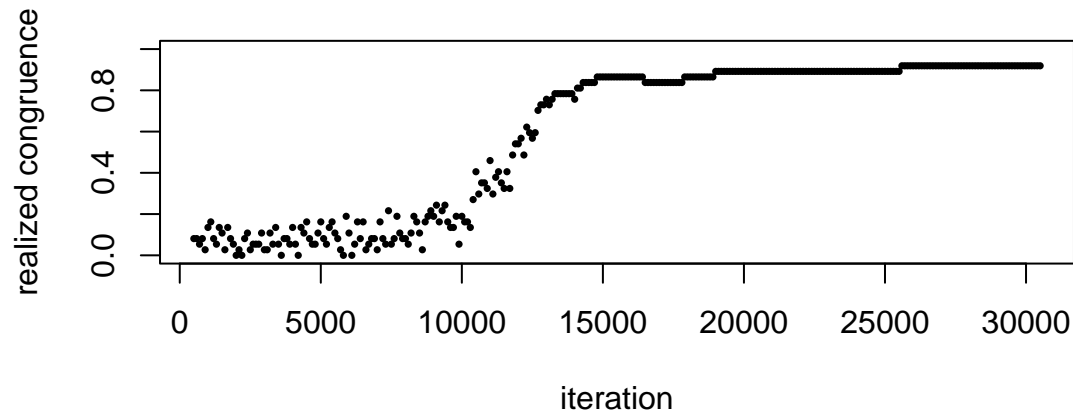
..
BN (A-B) Specialization (H2') 0.4
BN (A-B) Connectance 0.033
BN (B-C) Specialization (H2') 0.87
BN (B-C) Connectance 0.04
Plant richness in BN (A-B): 184
pulp.feeder richness in BN (A-B): 193
pulp.feeder richness in BN (B-C): 38
Parasitoid richness in BN (B-C): 51
Richness of shared pulp.feeders:38
Number of modules in BN (A-B) 29
Number of modules in BN (B-C) 20

Number of modules in BN (A-B) (only for shared species) 18
Number of modules in BN (B-C) (only for shared species) 20

Hipermodule Congruence
Optimization procedure

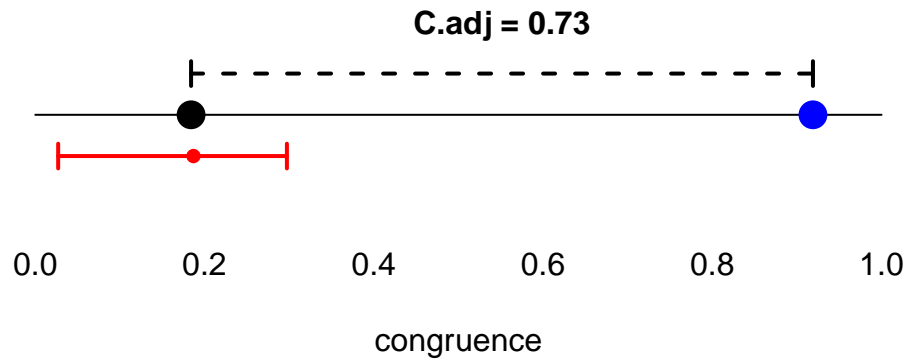


..



Adjusted Congruence: 0.73
Realized Congruence: 0.92
Hypermodularity: 0.64

Null Model 1

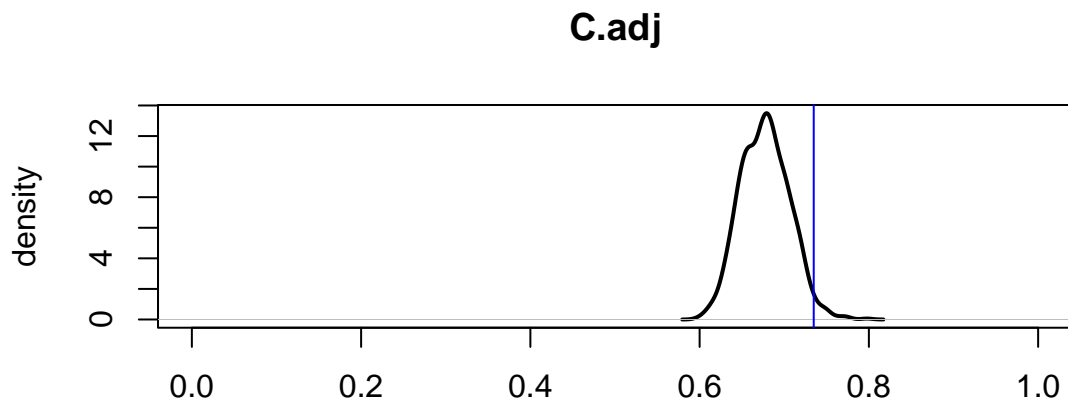


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.023

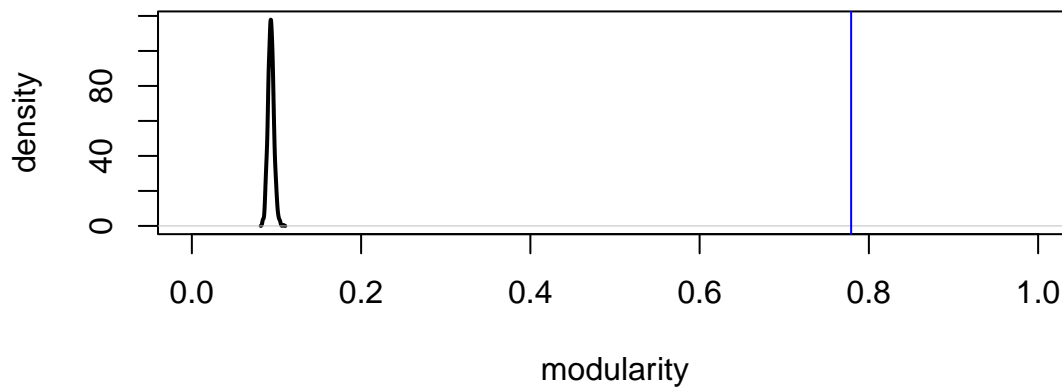
Dataset 40 : BASSET WAN

Topology BN (A-B): Plant - seed predator

Modularity

..
Observed Modularity: 0.78
Number of Modules: 21

Comparison between observed modularity (blue line) and proportional null model (density in black)

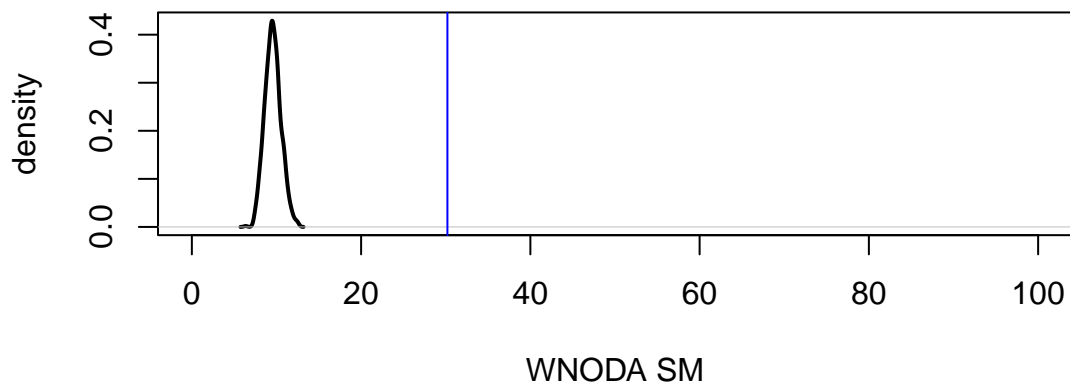


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 4
Nestedness between species in the same module: 30
Nestedness between species in different modules: 1.9

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0

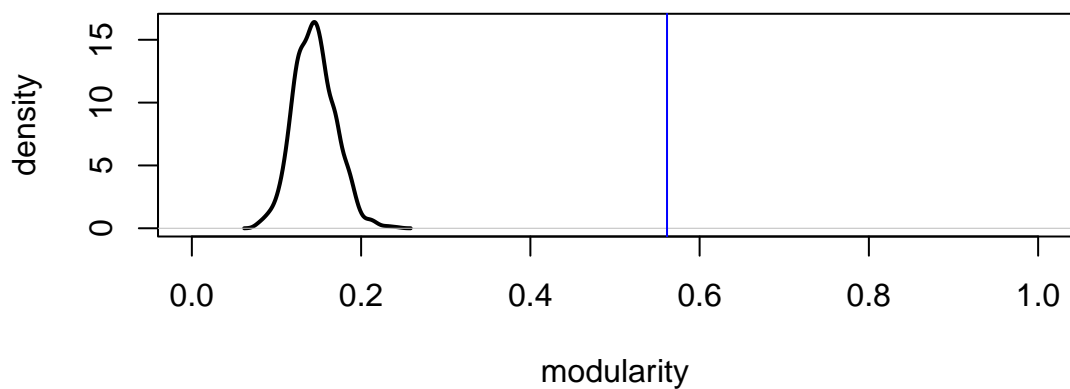
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): seed predator - Parasitoid

Modularity

..
Observed Modularity: 0.56
Number of Modules: 6

Comparison between observed modularity (blue line) and proportional null model (density in black)

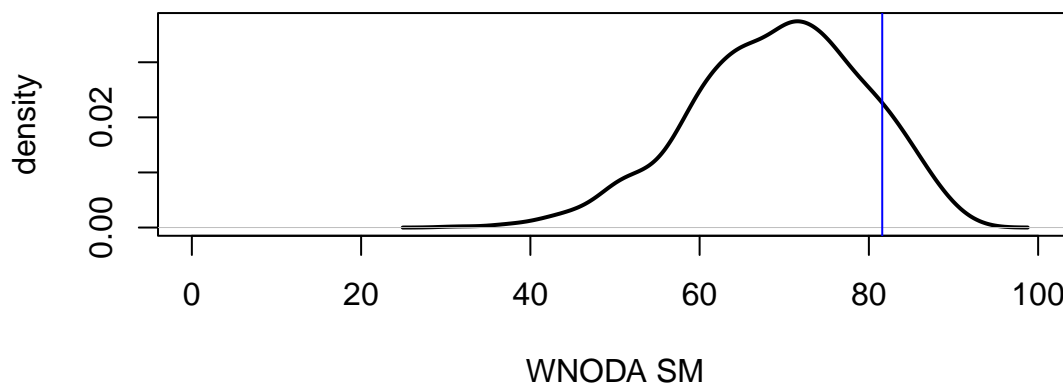


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 21
Nestedness between species in the same module 82
Nestedness between species in different modules 5.1

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.15

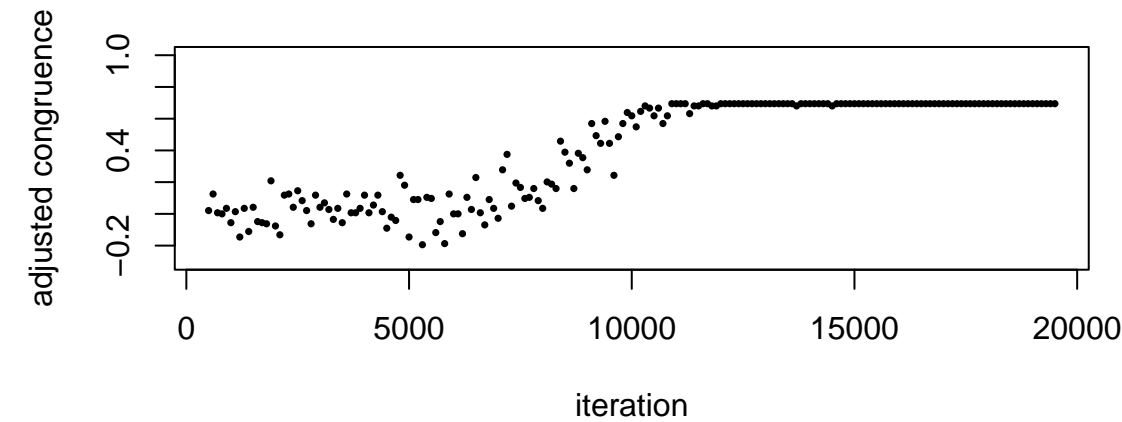
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

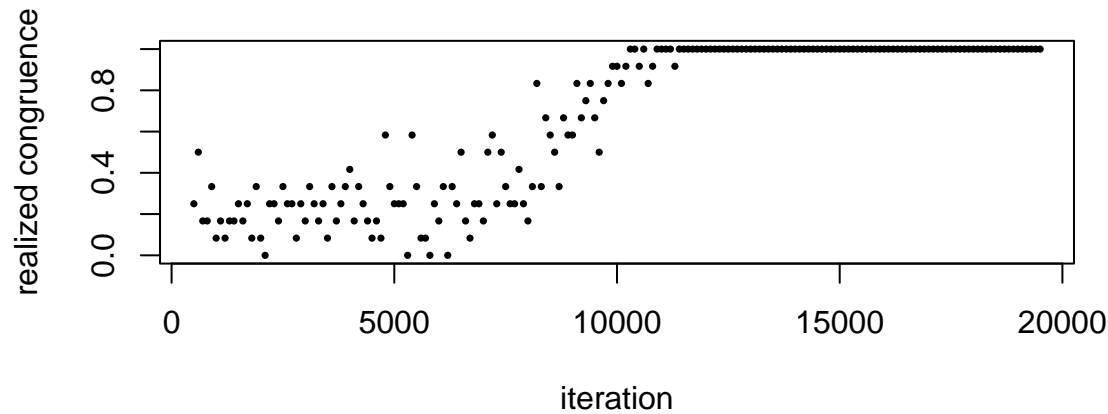
..
BN (A-B) Specialization (H2') 0.8
BN (A-B) Connectance 0.03
BN (B-C) Specialization (H2') 0.86
BN (B-C) Connectance 0.19
Plant richness in BN (A-B): 132
seed predator richness in BN (A-B): 77
seed predator richness in BN (B-C): 12
Parasitoid richness in BN (B-C): 8
Richness of shared seed predators: 12
Number of modules in BN (A-B) 21
Number of modules in BN (B-C) 6

Number of modules in BN (A-B) (only for shared species) 10
Number of modules in BN (B-C) (only for shared species) 6

Hipermodule Congruence
Optmization procedure

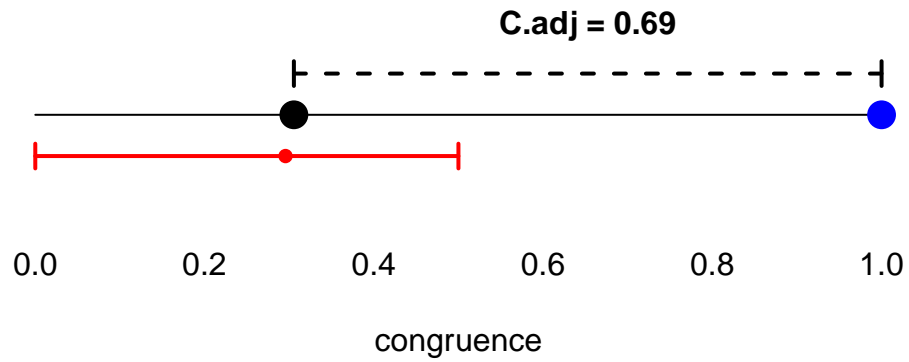


..



Adjusted Congruence: 0.69
Realized Congruence: 1
Hypermodularity: 0.56

Null Model 1

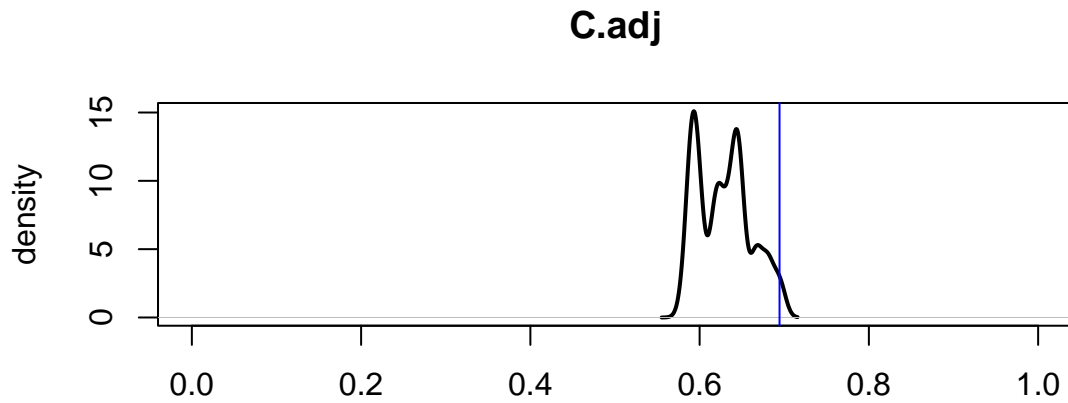


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.044

Dataset 41 : dattilo -REMOVED- BINARY DATASET

Topology BN (A-B): Seed disperser - Plant

Modularity

..
Observed Modularity: 0.48
Number of Modules: 7

Low-level nestedness

..
Nestedness in the entire matrix: 30
Nestedness between species in the same module: 57
Nestedness between species in different modules: 25

Topology BN (B-C): Plant - Pollinator

Modularity

..
Observed Modularity: 0.54
Number of Modules: 23

Low-level nestedness

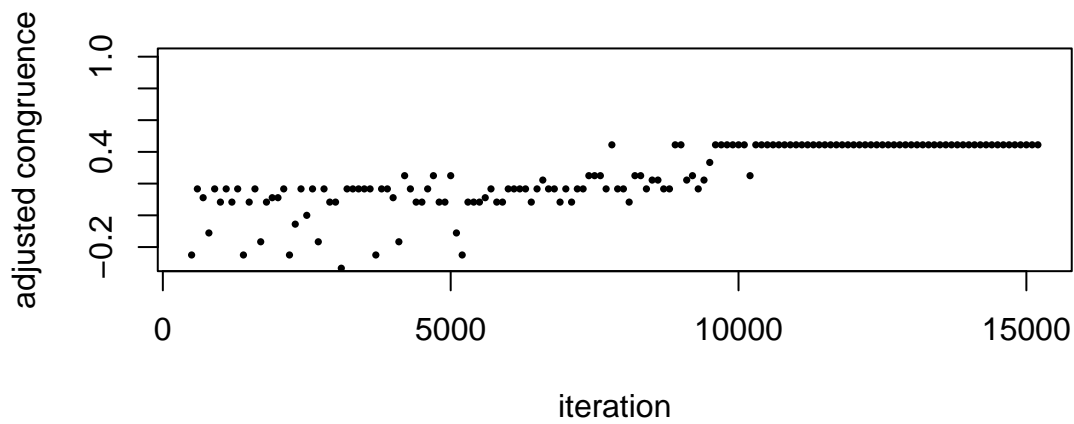
..
Nestedness in the entire matrix 7.9
Nestedness between species in the same module 33
Nestedness between species in different modules 6.7

Bipartite Networks and Intercept

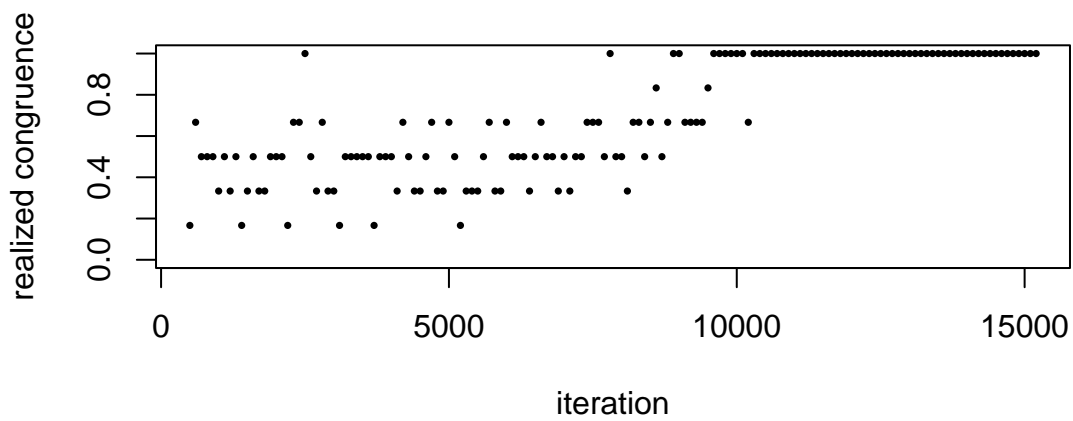
..
BN (A-B) Specialization (H2') NA
BN (A-B) Connectance 0.1
BN (B-C) Specialization (H2') NA
BN (B-C) Connectance 0.026
Seed disperser richness in BN (A-B): 46
Plant richness in BN (A-B): 27
Plant richness in BN (B-C): 93
Pollinator richness in BN (B-C): 173
Richness of shared Plants: 93
Number of modules in BN (A-B) 7
Number of modules in BN (B-C) 23
Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence

Optmization procedure



..



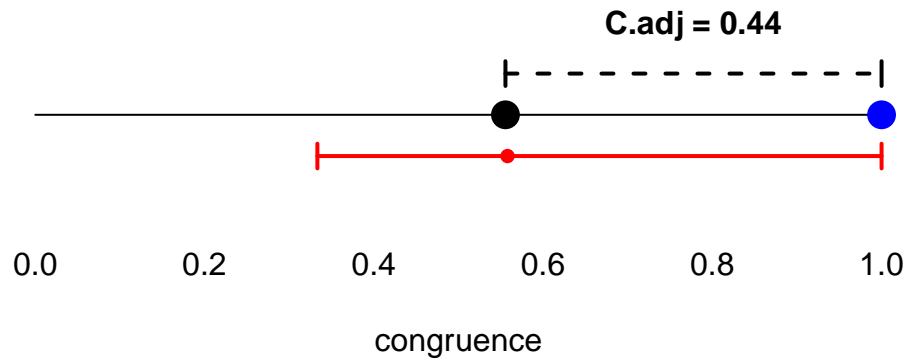
..

Adjusted Congruence: 0.44

Realized Congruence: 1

Hypermaturity: 0.26

Null Model 1

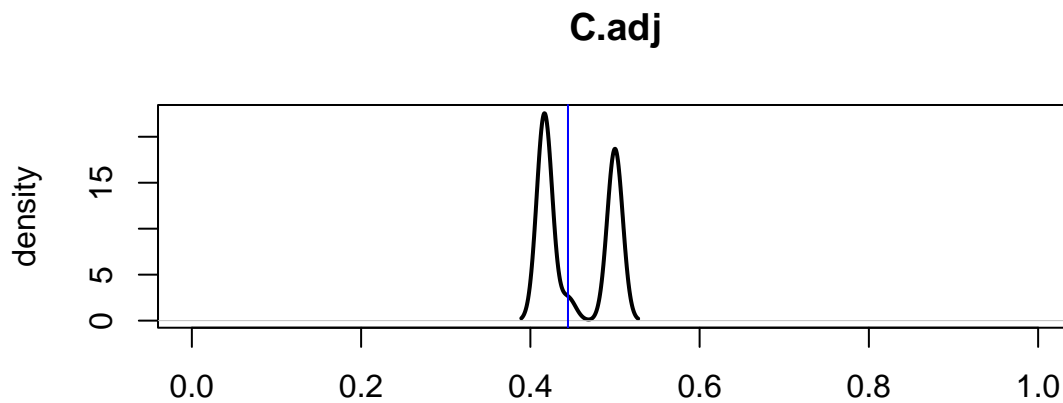


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.071

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 0.48

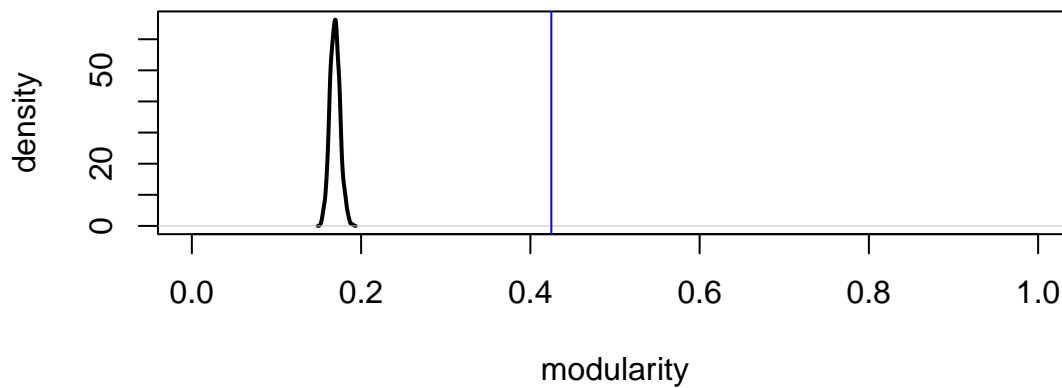
Dataset 42 : hackett HH -REMOVED-

Topology BN (A-B): Pollinator - Plant

Modularity

..
Observed Modularity: 0.42
Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

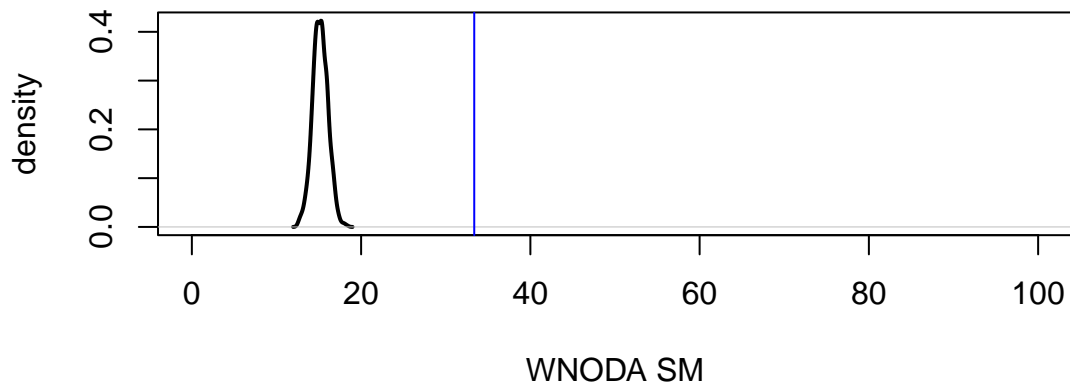


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 13
Nestedness between species in the same module: 33
Nestedness between species in different modules: 7.3

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

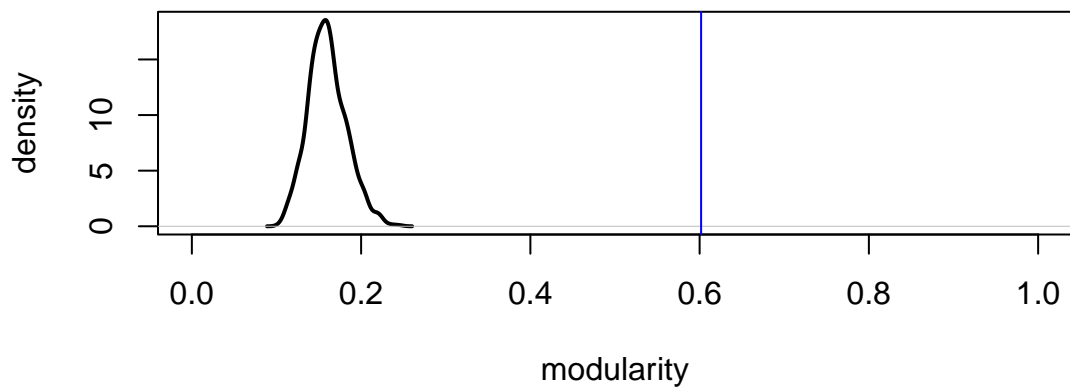
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Seed predator

Modularity

..
 Observed Modularity: 0.6
 Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

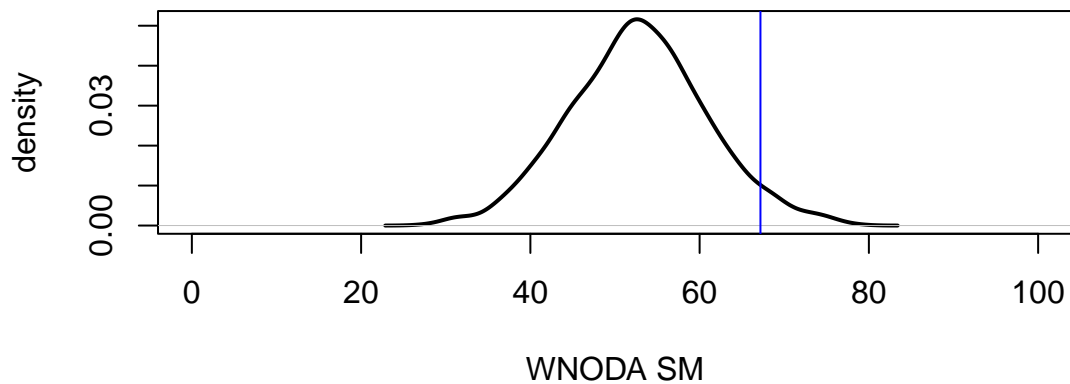


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 11
Nestedness between species in the same module 67
Nestedness between species in different modules 2.2

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.05

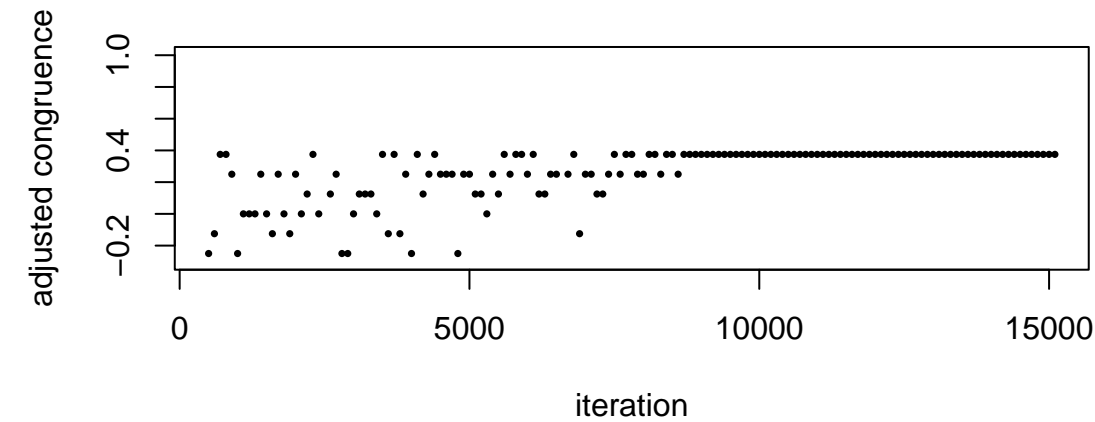
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

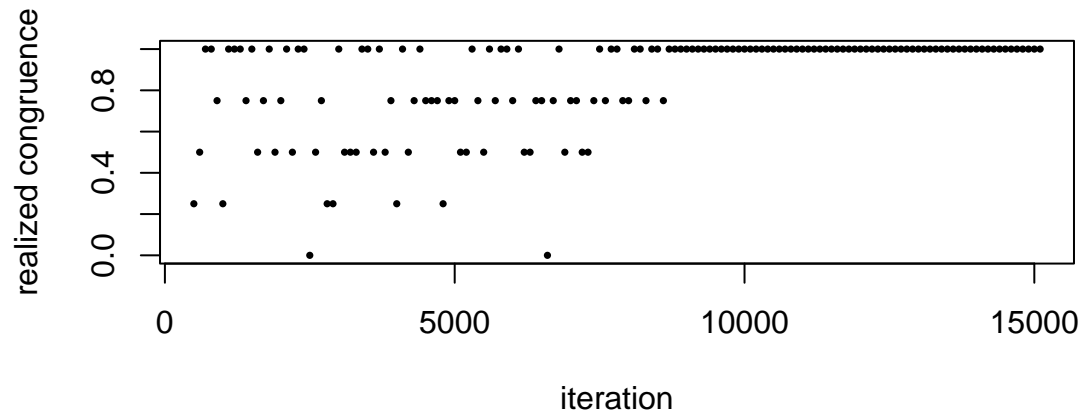
..
BN (A-B) Specialization (H2') 0.41
BN (A-B) Connectance 0.056
BN (B-C) Specialization (H2') 0.84
BN (B-C) Connectance 0.14
Pollinator richness in BN (A-B): 220
Plant richness in BN (A-B): 43
Plant richness in BN (B-C): 9
Seed predator richness in BN (B-C): 20
Richness of shared Plants:9
Number of modules in BN (A-B) 5
Number of modules in BN (B-C) 8

Number of modules in BN (A-B) (only for shared species) 2
Number of modules in BN (B-C) (only for shared species) 4

Hipermodule Congruence
Optmization procedure

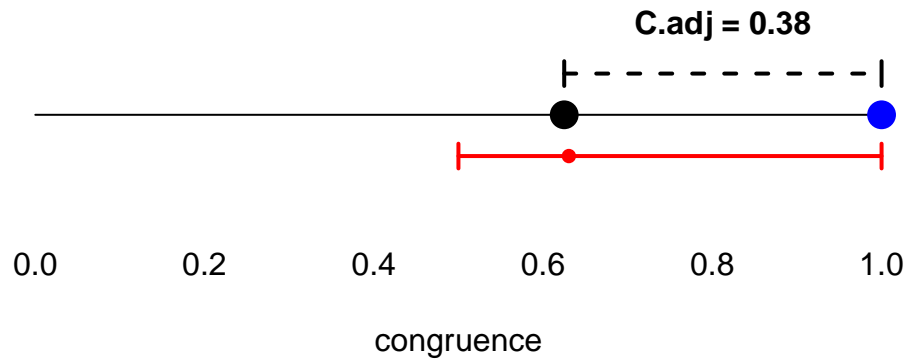


..



Adjusted Congruence: 0.38
Realized Congruence: 1
Hypermodularity: 0.36

Null Model 1

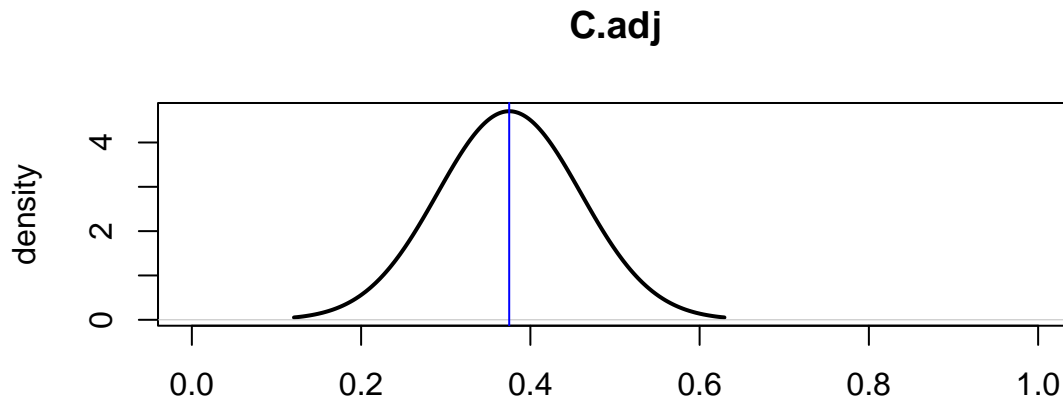


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.26

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

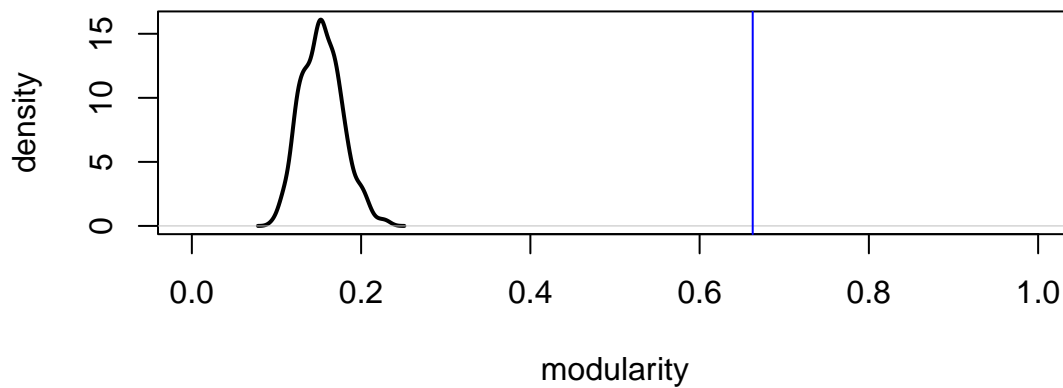
Dataset 43 : hackett HH -REMOVED-

Topology BN (A-B): Plant - seed predator

Modularity

..
Observed Modularity: 0.66
Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

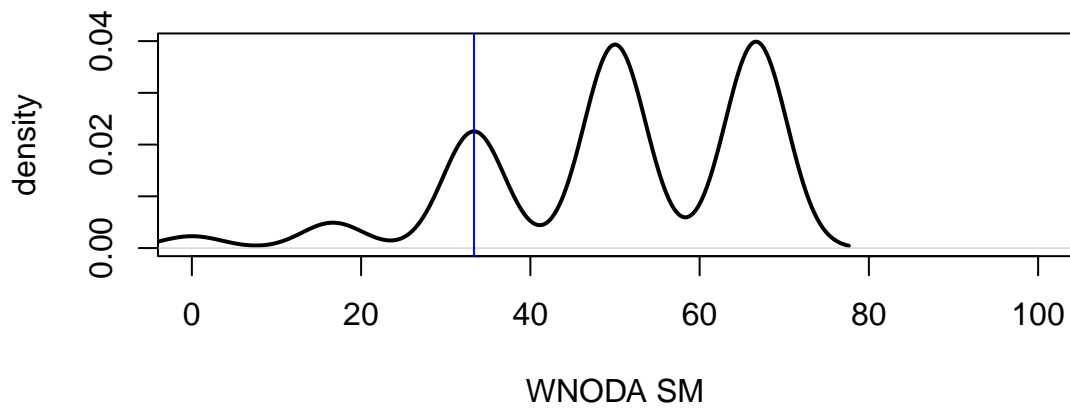


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 1.9
Nestedness between species in the same module: 33
Nestedness between species in different modules: 0.64

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.93

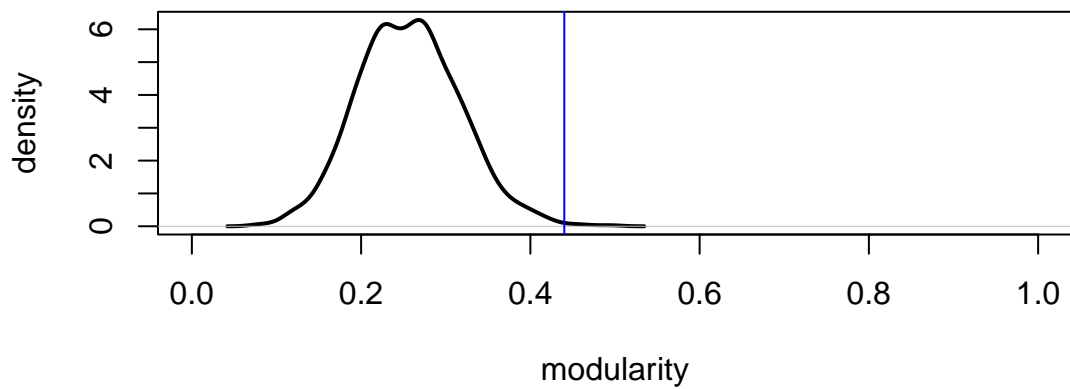
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): seed predator - Parasitoid

Modularity

..
 Observed Modularity: 0.44
 Number of Modules: 3

Comparison between observed modularity (blue line) and proportional null model (density in black)

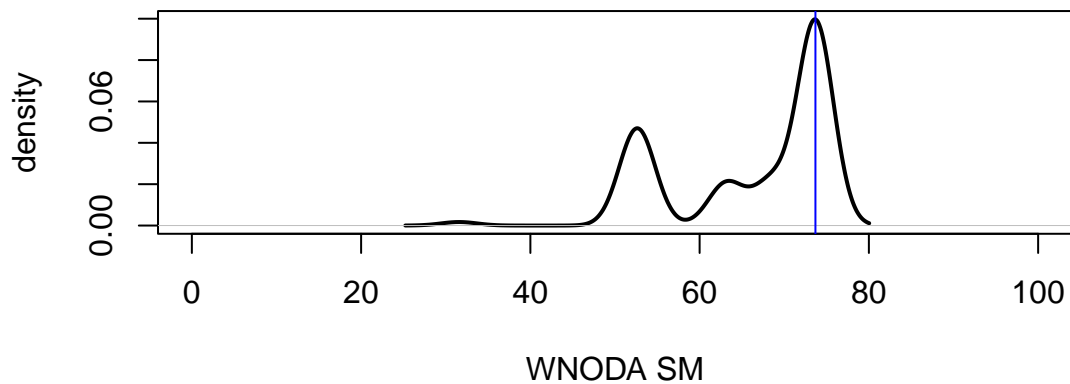


..
Number of Matrices in Null Model: 1000
P-Value: 0.003

Low-level nestedness

..
Nestedness in the entire matrix 24
Nestedness between species in the same module 74
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.52

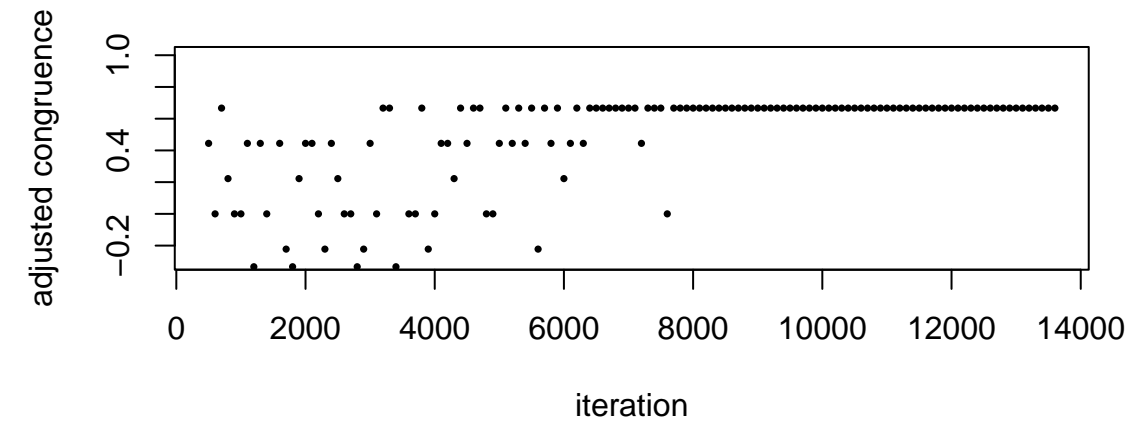
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

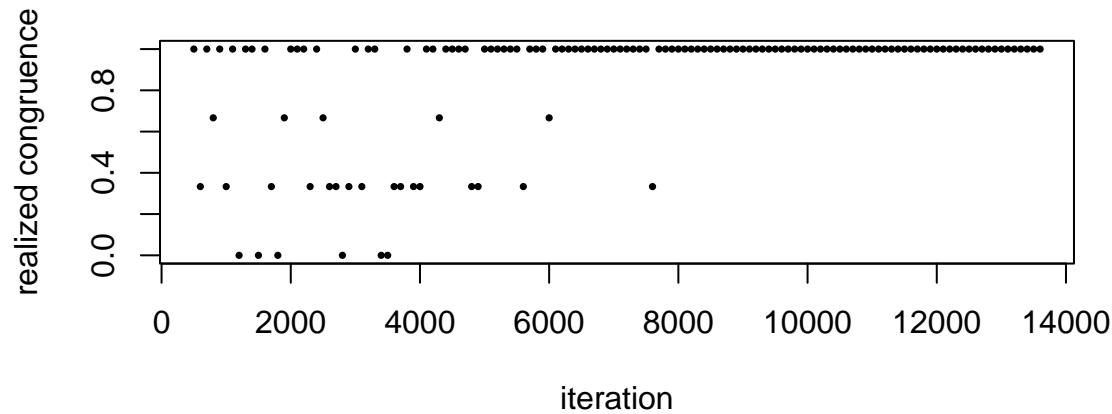
..
BN (A-B) Specialization (H2') 1
BN (A-B) Connectance 0.13
BN (B-C) Specialization (H2') 0.89
BN (B-C) Connectance 0.36
Plant richness in BN (A-B): 10
seed predator richness in BN (A-B): 9
seed predator richness in BN (B-C): 3
Parasitoid richness in BN (B-C): 11
Richness of shared seed predators: 3
Number of modules in BN (A-B) 8
Number of modules in BN (B-C) 3

Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 3

Hipermodule Congruence
Optimization procedure

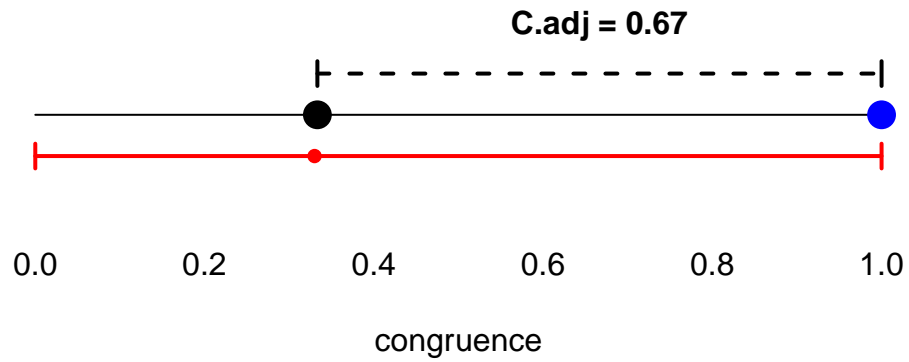


..



Adjusted Congruence: 0.67
Realized Congruence: 1
Hypermodularity: 0.5

Null Model 1

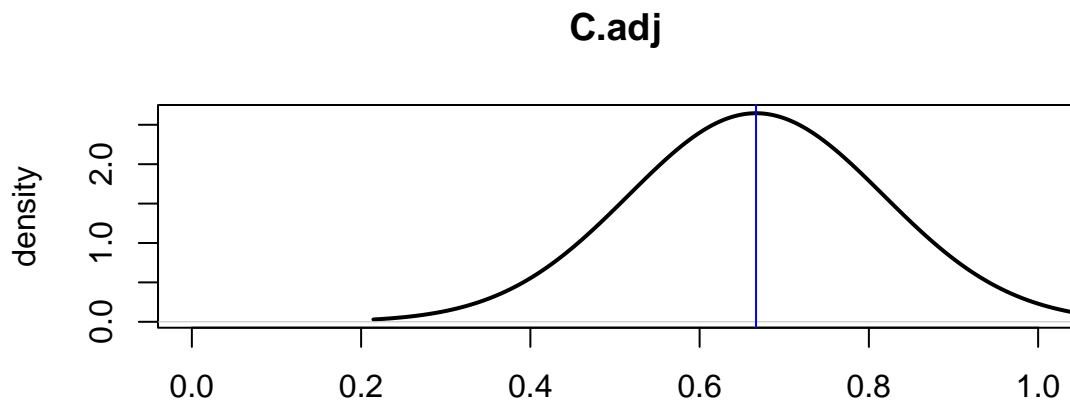


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.16

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

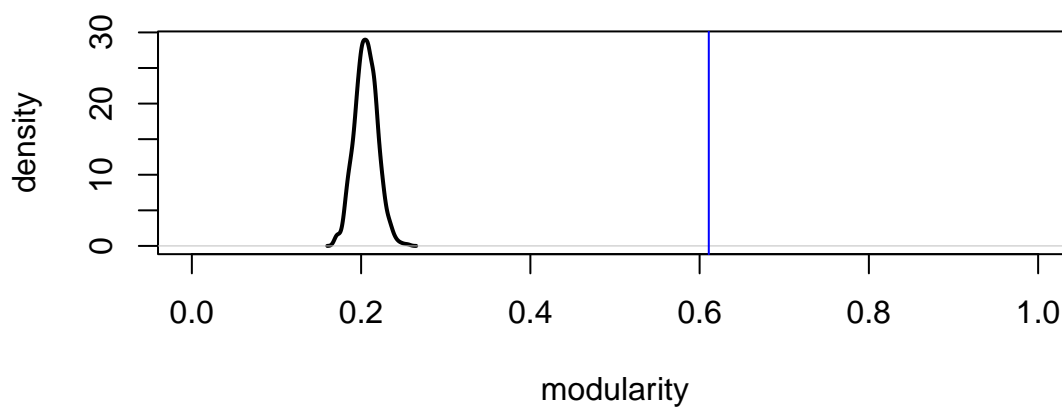
Dataset 44 : hackett TP -REMOVED-

Topology BN (A-B): Herbivore - Plant

Modularity

..
Observed Modularity: 0.61
Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

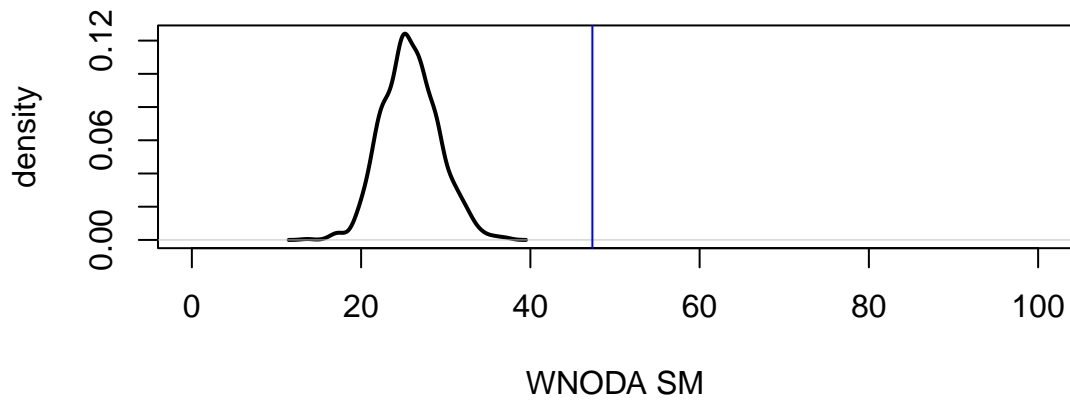


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 9
Nestedness between species in the same module: 47
Nestedness between species in different modules: 3.1

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

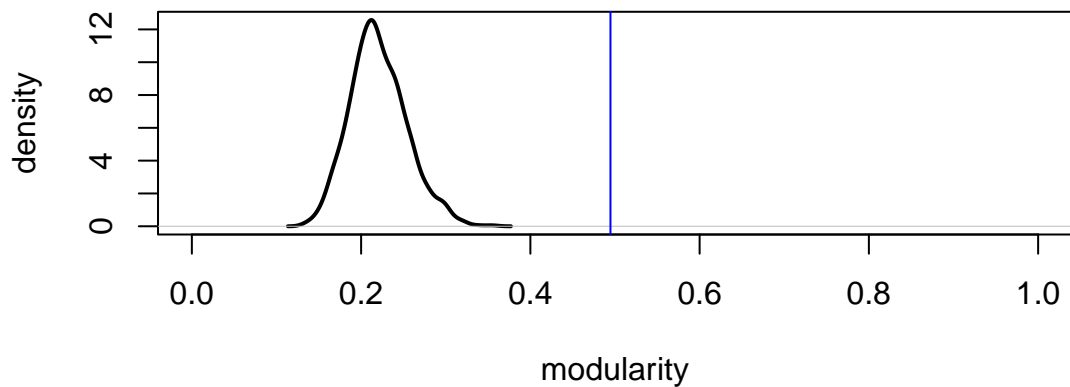
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): Plant - Pollinator

Modularity

..
 Observed Modularity: 0.49
 Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

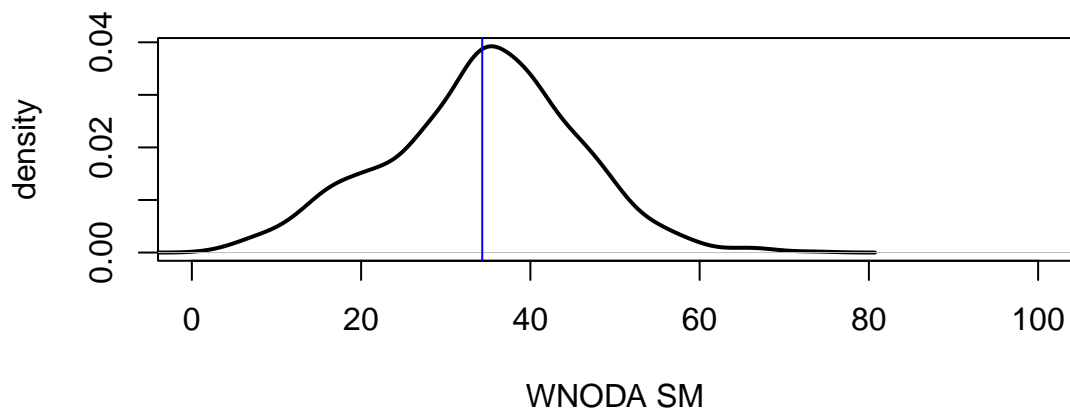


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 11
Nestedness between species in the same module 34
Nestedness between species in different modules 8.8

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.54

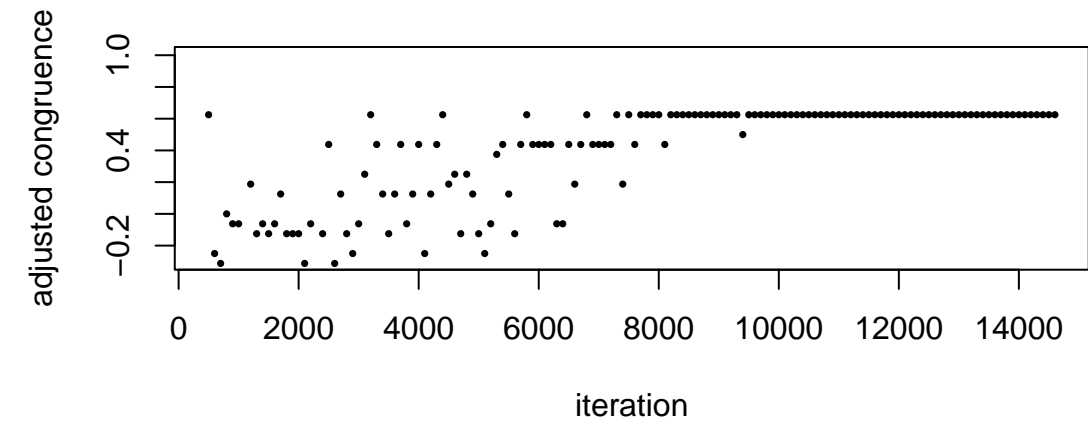
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

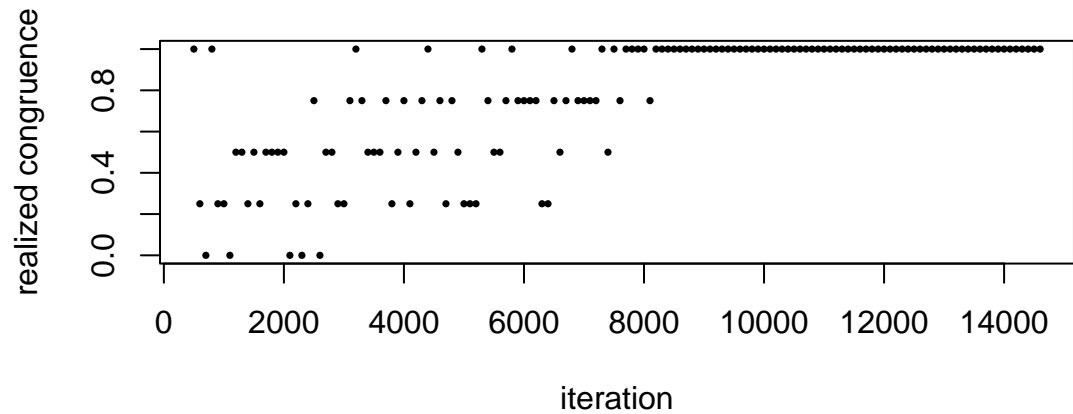
..
BN (A-B) Specialization (H2') 0.56
BN (A-B) Connectance 0.086
BN (B-C) Specialization (H2') 0.59
BN (B-C) Connectance 0.16
Herbivore richness in BN (A-B): 53
Plant richness in BN (A-B): 21
Plant richness in BN (B-C): 10
Pollinator richness in BN (B-C): 16
Richness of shared Plants:10
Number of modules in BN (A-B) 9
Number of modules in BN (B-C) 8

Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 4

Hipermodule Congruence
Optimization procedure

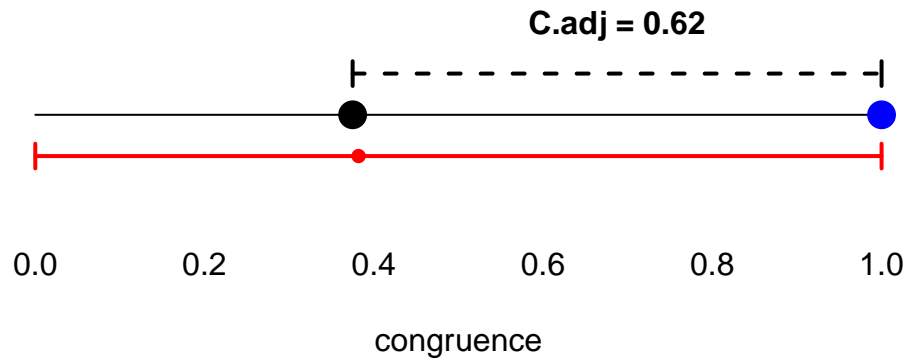


..



Adjusted Congruence: 0.62
Realized Congruence: 1
Hypermodularity: 0.22

Null Model 1

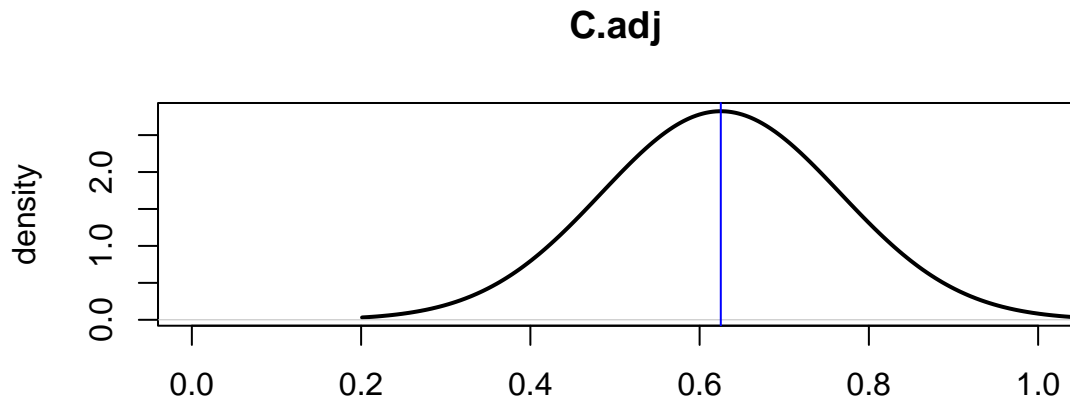


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.083

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

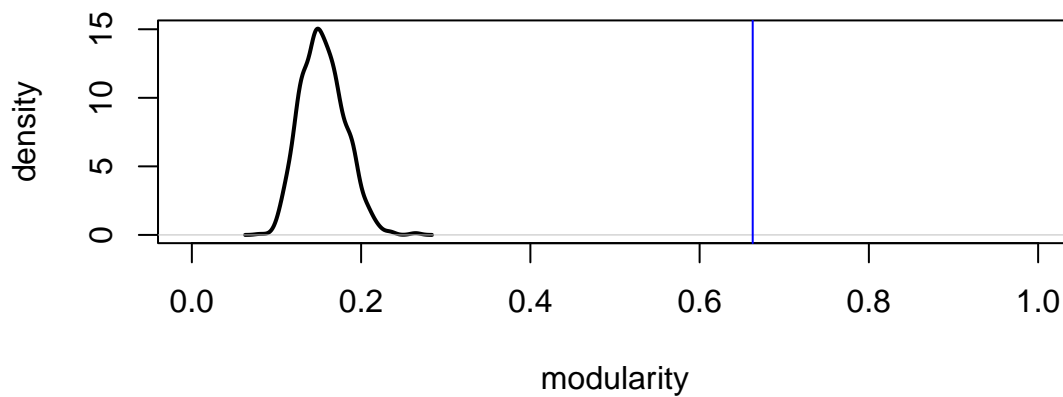
Dataset 45 : hackett TP -REMOVED-

Topology BN (A-B): Herbivore - Plant

Modularity

..
Observed Modularity: 0.66
Number of Modules: 8

Comparison between observed modularity (blue line) and proportional null model (density in black)

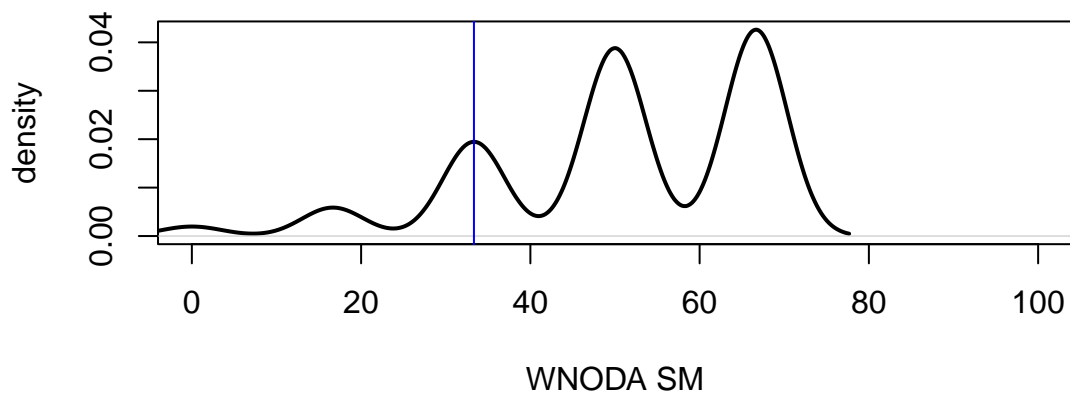


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 1.9
Nestedness between species in the same module: 33
Nestedness between species in different modules: 0.64

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.93

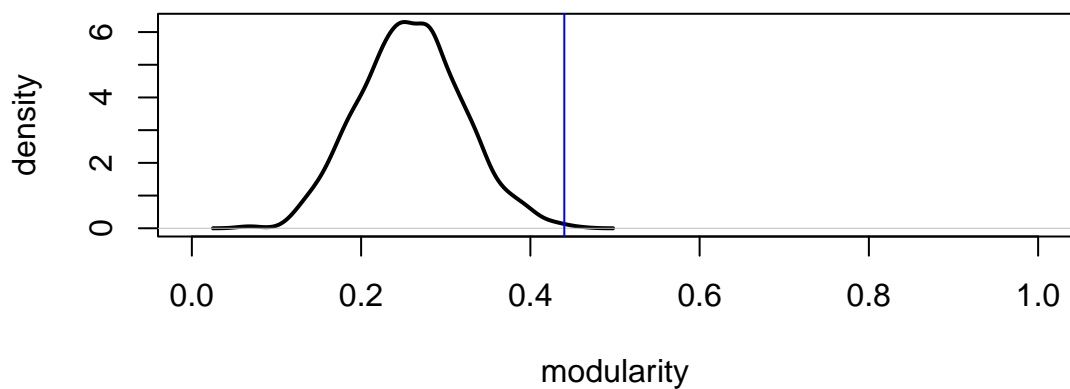
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Plant - Seed predator

Modularity

..
 Observed Modularity: 0.44
 Number of Modules: 3

Comparison between observed modularity (blue line) and proportional null model (density in black)

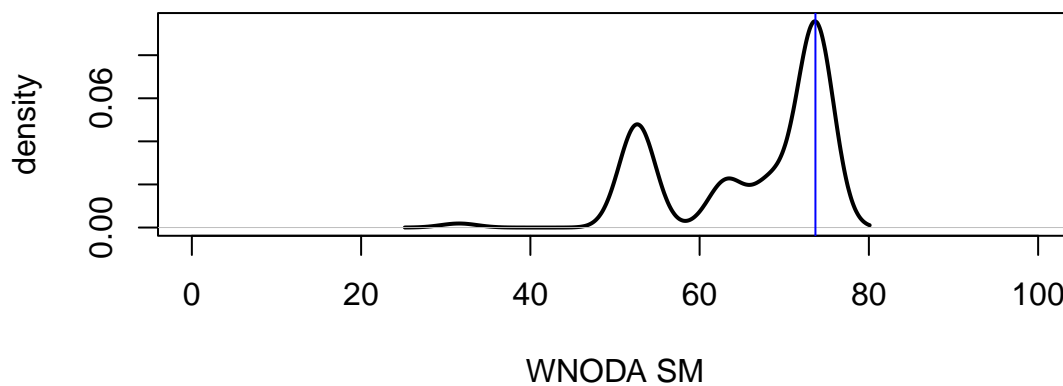


..
Number of Matrices in Null Model: 1000
P-Value: 0.001

Low-level nestedness

..
Nestedness in the entire matrix 24
Nestedness between species in the same module 74
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.51

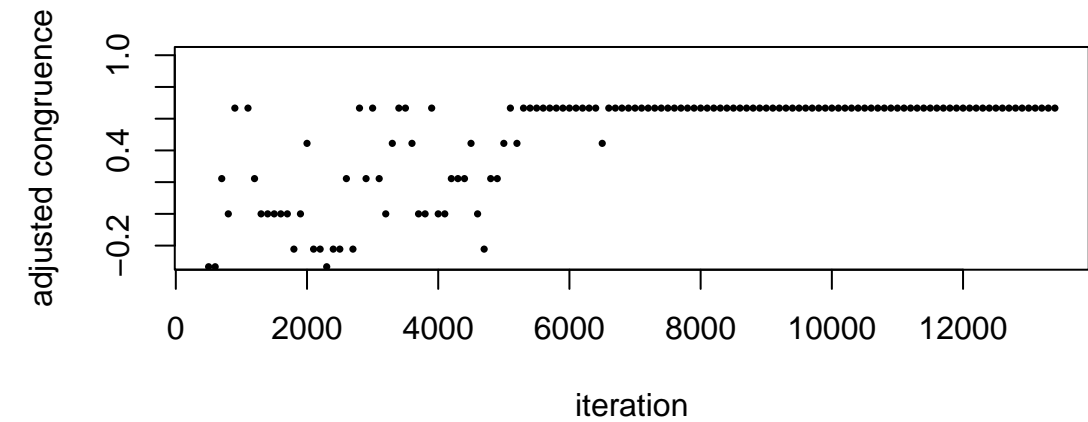
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

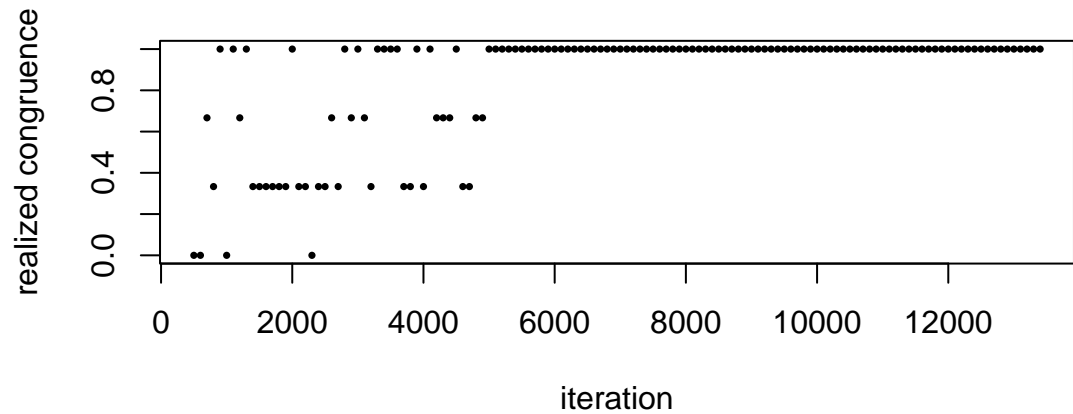
..
BN (A-B) Specialization (H2') 1
BN (A-B) Connectance 0.13
BN (B-C) Specialization (H2') 0.89
BN (B-C) Connectance 0.36
Herbivore richness in BN (A-B): 10
Plant richness in BN (A-B): 9
Plant richness in BN (B-C): 3
Seed predator richness in BN (B-C): 11
Richness of shared Plants:3
Number of modules in BN (A-B) 8
Number of modules in BN (B-C) 3

Number of modules in BN (A-B) (only for shared species) 3
Number of modules in BN (B-C) (only for shared species) 3

Hipermodule Congruence
Optmization procedure

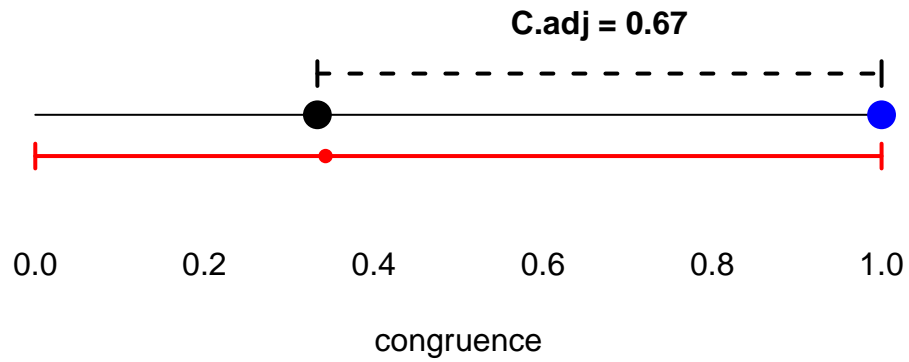


..



Adjusted Congruence: 0.67
Realized Congruence: 1
Hypermodularity: 0.5

Null Model 1

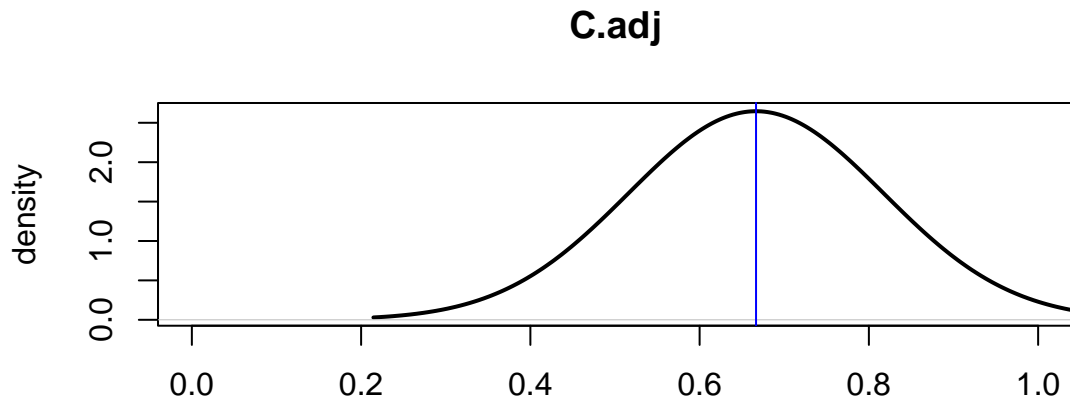


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.17

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

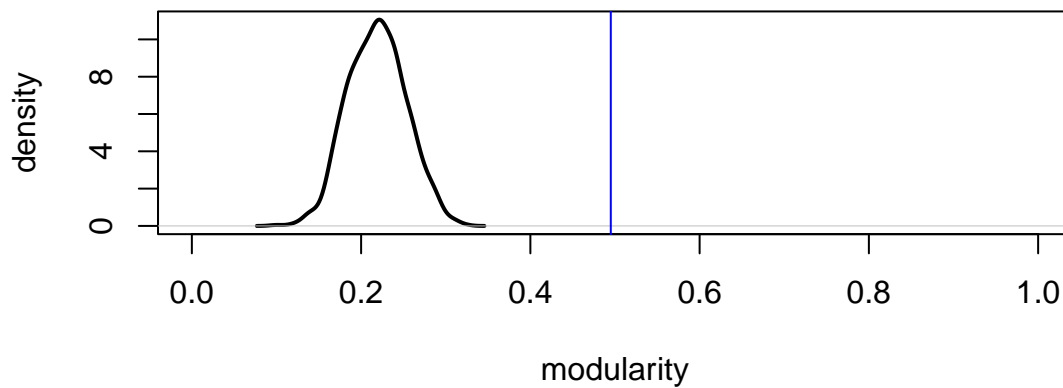
Dataset 46 : hackett TP -REMOVED-

Topology BN (A-B): Plant - Herbivore

Modularity

..
Observed Modularity: 0.5
Number of Modules: 9

Comparison between observed modularity (blue line) and proportional null model (density in black)

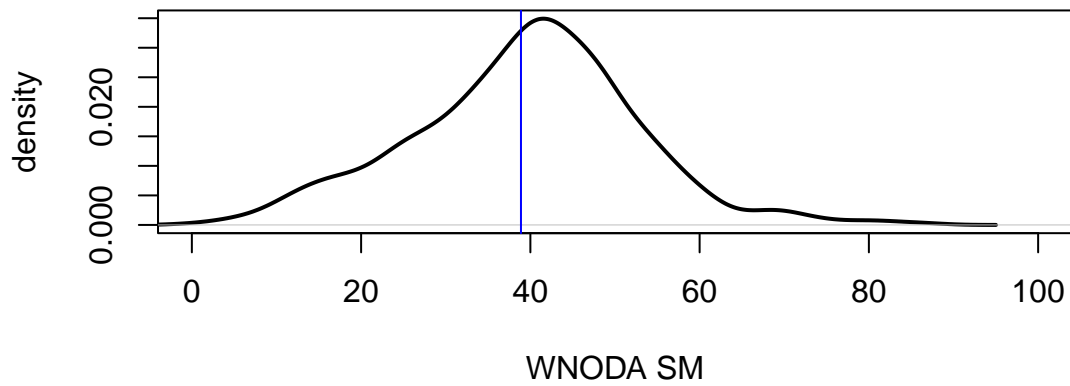


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 11
Nestedness between species in the same module: 39
Nestedness between species in different modules: 8.6

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0.57

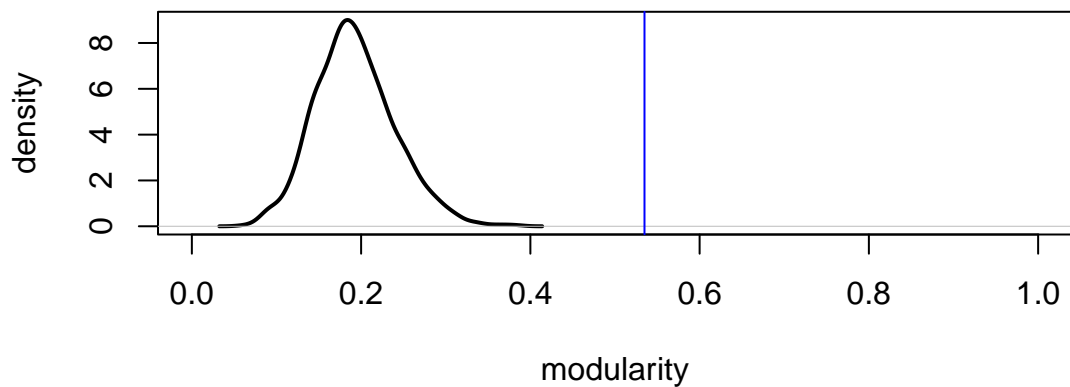
CONCLUSION: BN (A-B) has a purely modular topology

Topology BN (B-C): Herbivore - Parasitoid

Modularity

..
 Observed Modularity: 0.53
 Number of Modules: 4

Comparison between observed modularity (blue line) and proportional null model (density in black)

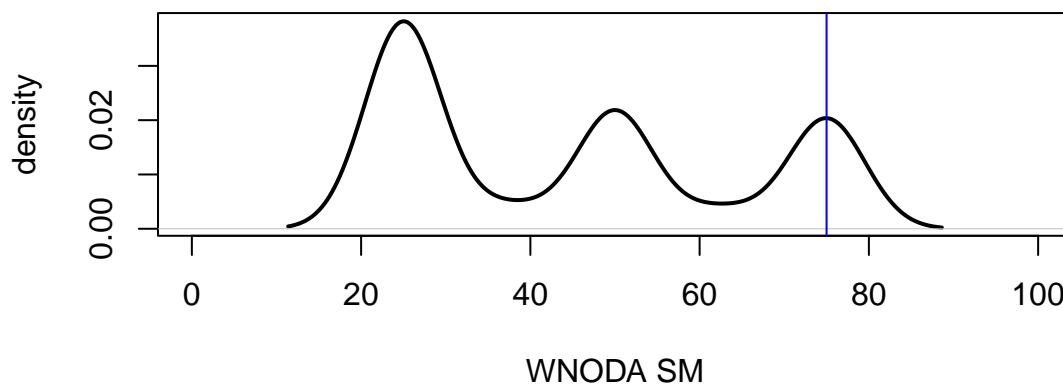


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 9.7
Nestedness between species in the same module 75
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 0.23

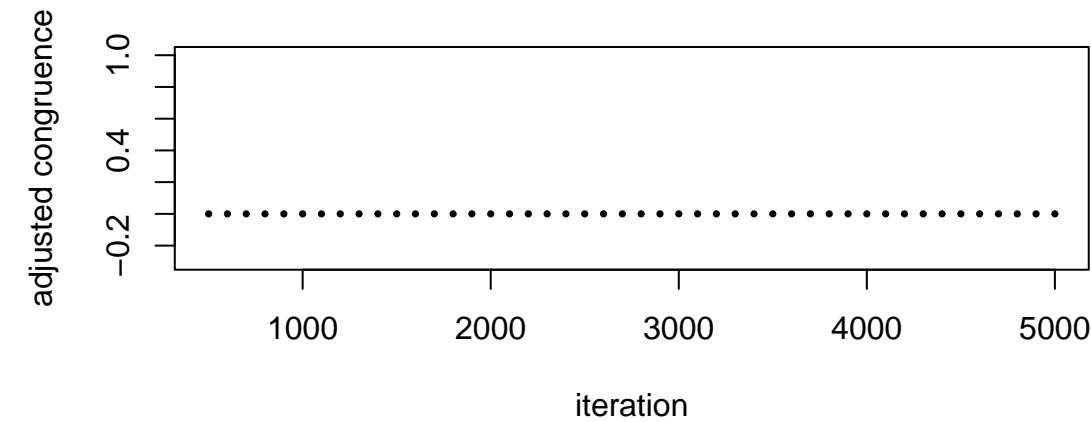
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

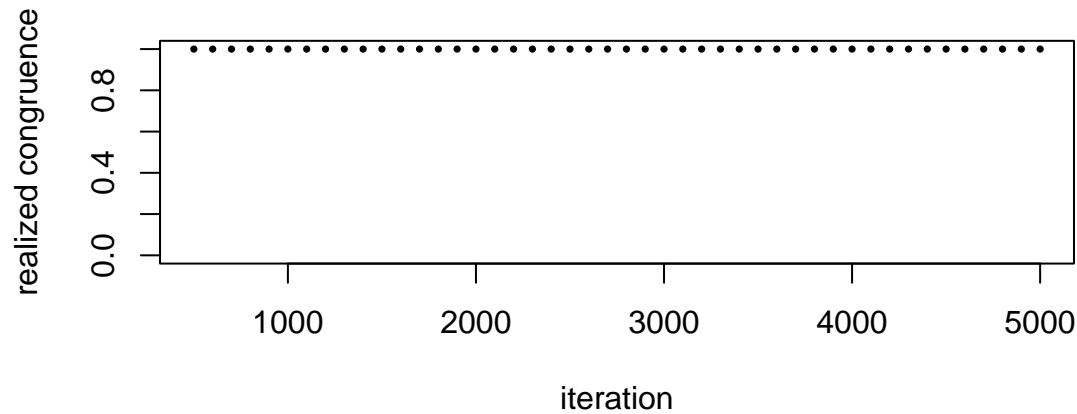
..
BN (A-B) Specialization (H2') 0.59
BN (A-B) Connectance 0.16
BN (B-C) Specialization (H2') 1
BN (B-C) Connectance 0.23
Plant richness in BN (A-B): 16
Herbivore richness in BN (A-B): 10
Herbivore richness in BN (B-C): 5
Parasitoid richness in BN (B-C): 7
Richness of shared Herbivores: 5
Number of modules in BN (A-B) 9
Number of modules in BN (B-C) 4

Number of modules in BN (A-B) (only for shared species) 2
Number of modules in BN (B-C) (only for shared species) 1

Hipermodule Congruence
Optmization procedure

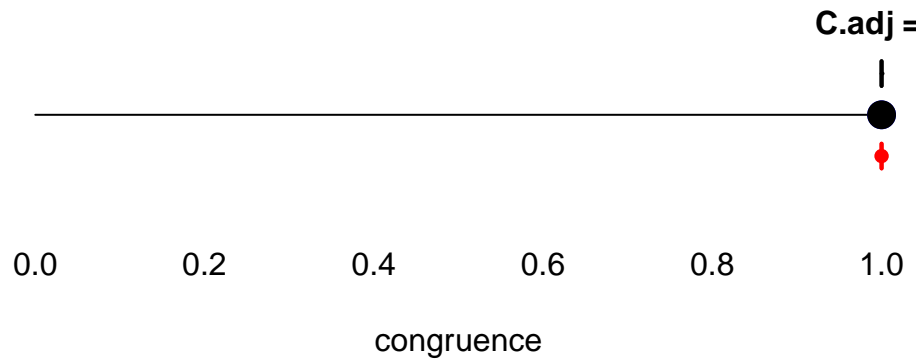


..



Adjusted Congruence: 0
Realized Congruence: 1
Hypermodularity: 0.00000000000000004

Null Model 1

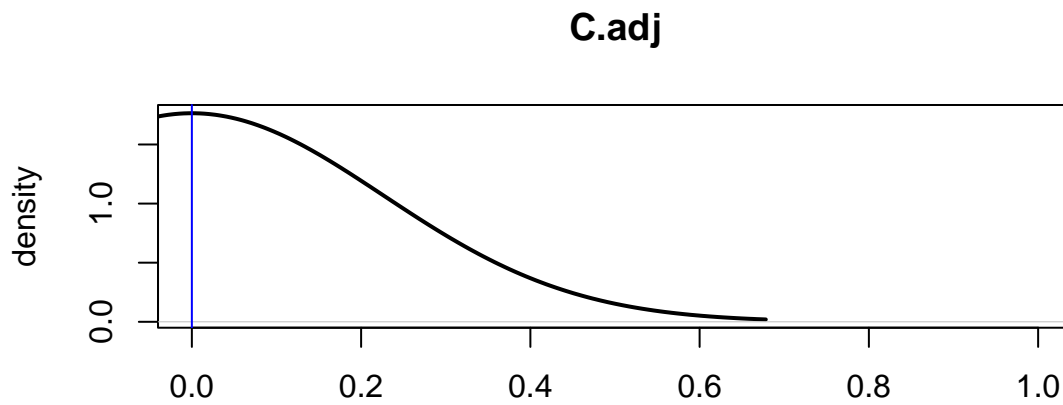


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 1

Null Model 2

Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

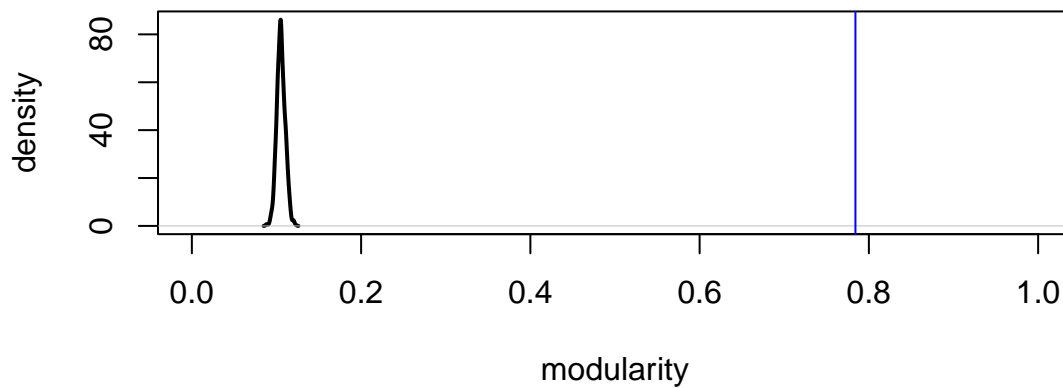
Dataset 47 : BASSET KHC -REMOVED-

Topology BN (A-B): Plant - seed predator

Modularity

..
Observed Modularity: 0.78
Number of Modules: 20

Comparison between observed modularity (blue line) and proportional null model (density in black)

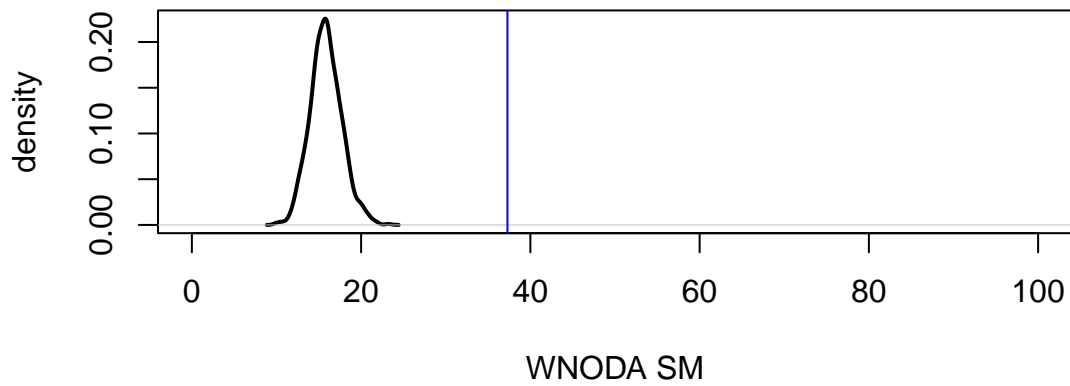


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix: 4.1
Nestedness between species in the same module: 37
Nestedness between species in different modules: 1.6

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
 Number of Matrices in Null Model: 1000
 P-Value: 0

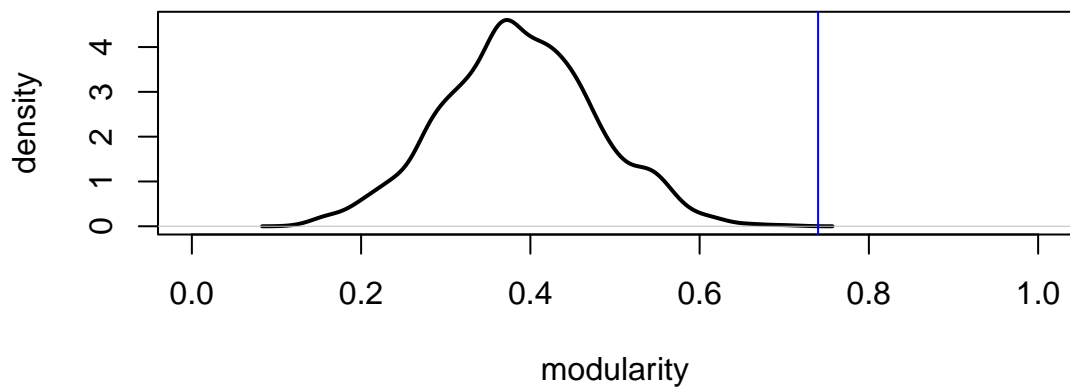
CONCLUSION: BN (A-B) has a compound topology

Topology BN (B-C): seed predator - Parasitoid

Modularity

..
 Observed Modularity: 0.74
 Number of Modules: 5

Comparison between observed modularity (blue line) and proportional null model (density in black)

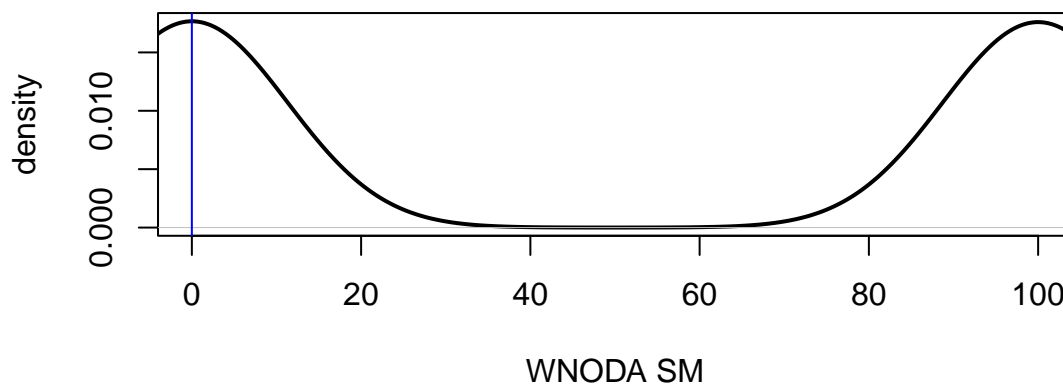


..
Number of Matrices in Null Model: 1000
P-Value: 0

Low-level nestedness

..
Nestedness in the entire matrix 0
Nestedness between species in the same module 0
Nestedness between species in different modules 0

Comparison between observed WNODA SM (blue line) and proportional null model (density in black)



..
Number of Matrices in Null Model: 1000
P-Value: 1

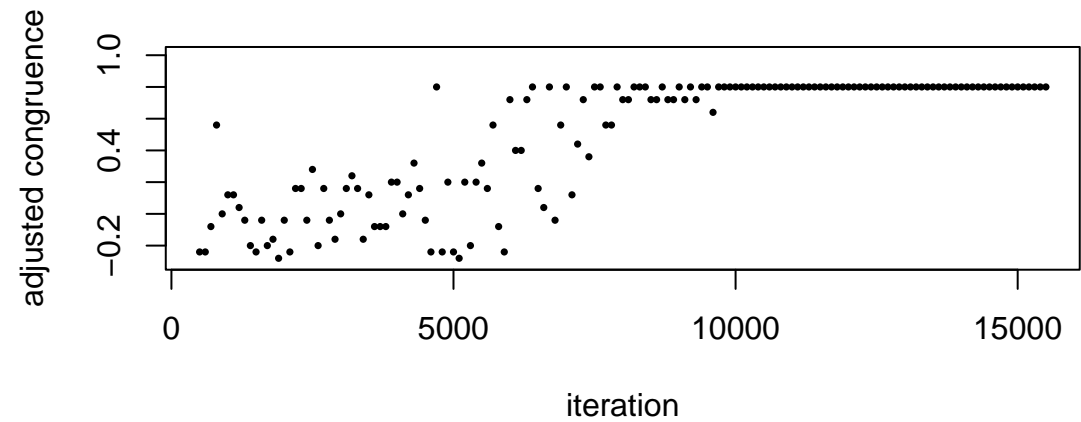
CONCLUSION: BN (B-C) has a purely modular topology

Bipartite Networks and Intercept

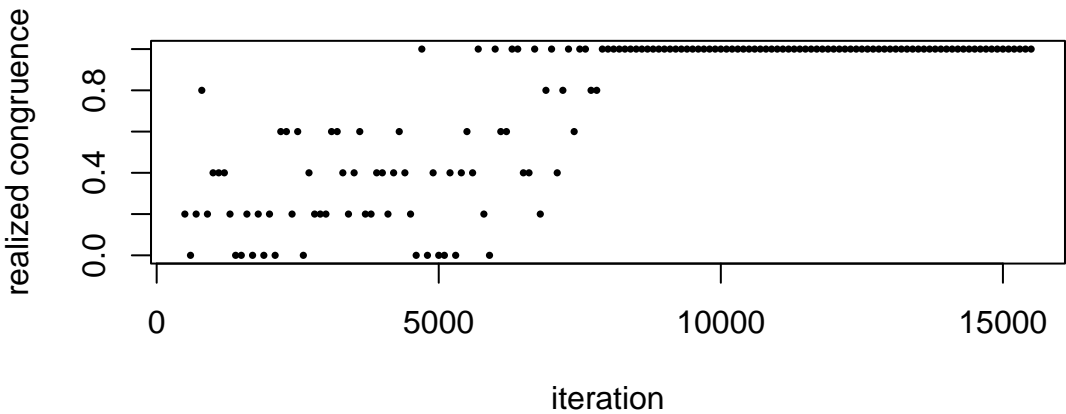
..
BN (A-B) Specialization (H2') 0.84
BN (A-B) Connectance 0.033
BN (B-C) Specialization (H2') 1
BN (B-C) Connectance 0.2
Plant richness in BN (A-B): 78
seed predator richness in BN (A-B): 57
seed predator richness in BN (B-C): 5
Parasitoid richness in BN (B-C): 6
Richness of shared seed predators:5
Number of modules in BN (A-B) 20
Number of modules in BN (B-C) 5

Number of modules in BN (A-B) (only for shared species) 5
Number of modules in BN (B-C) (only for shared species) 5

Hipermodule Congruence
Optmization procedure

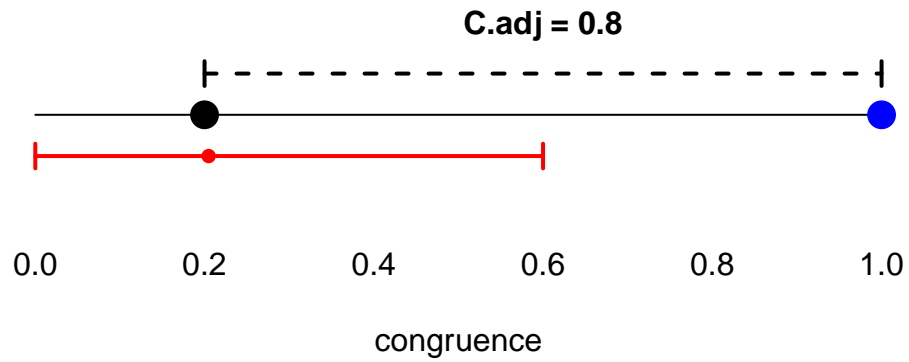


..



Adjusted Congruence: 0.8
Realized Congruence: 1
Hypermmodularity: 0.61

Null Model 1

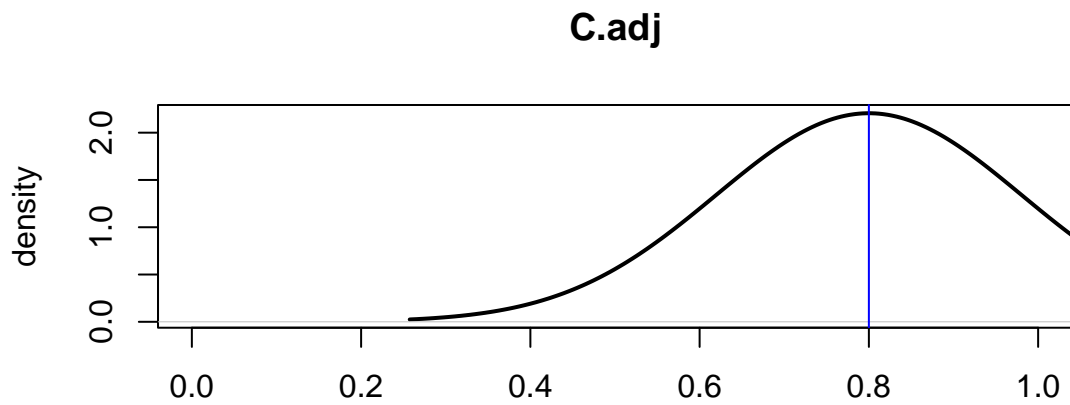


Blue point: realized congruence; Black point: baseline congruence; Red interval: .95 CI based on the null model.

..
Number of Matrices in Null Model 1: 1000
P-Value: 0.009

Null Model 2

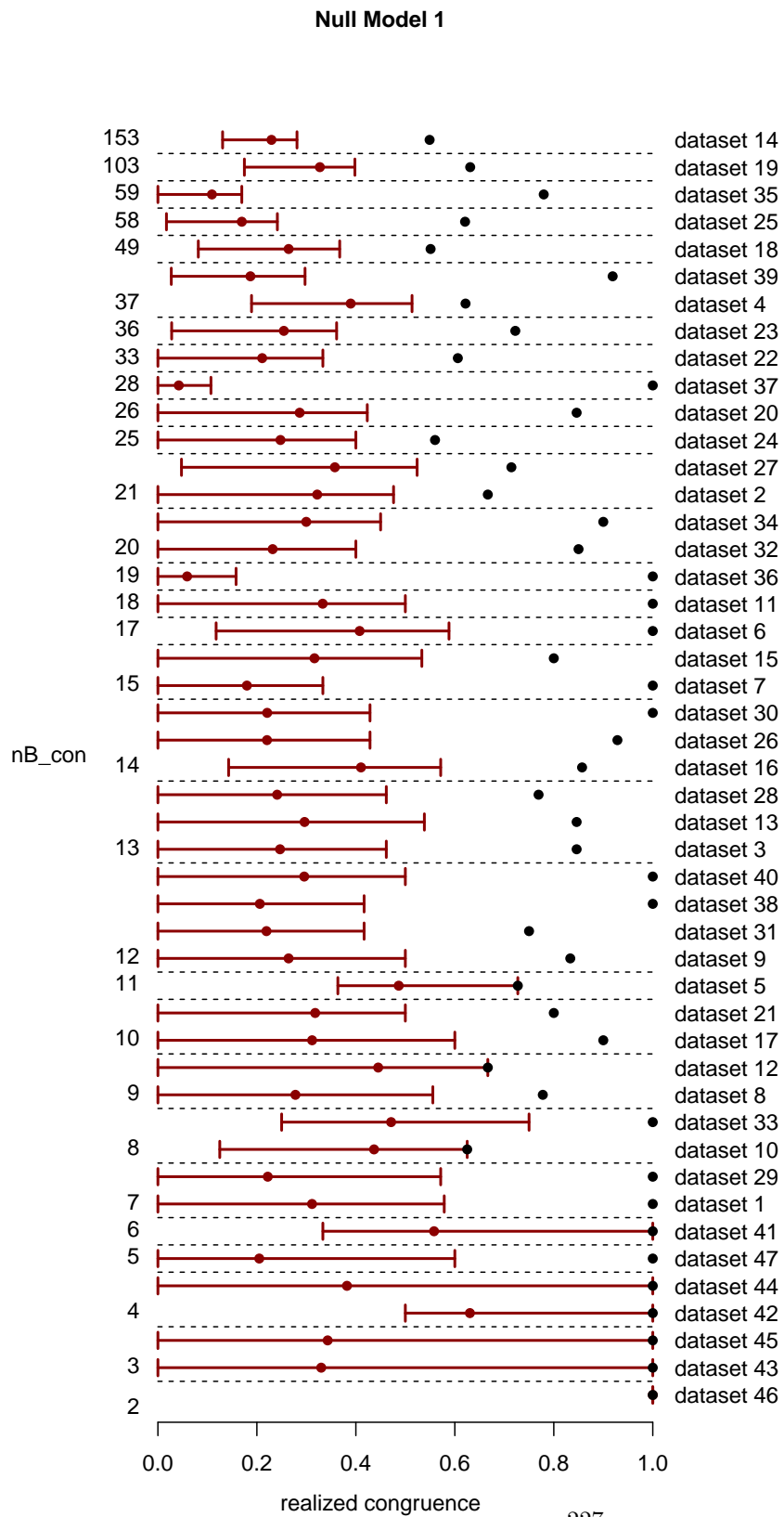
Comparison between observed adjusted congruence (blue line) and Null Model 2 (density in black)



..
Number of Matrices in Null Model 2: 1000
P-Value: 1

Summary of null model analysis

Null Model 1

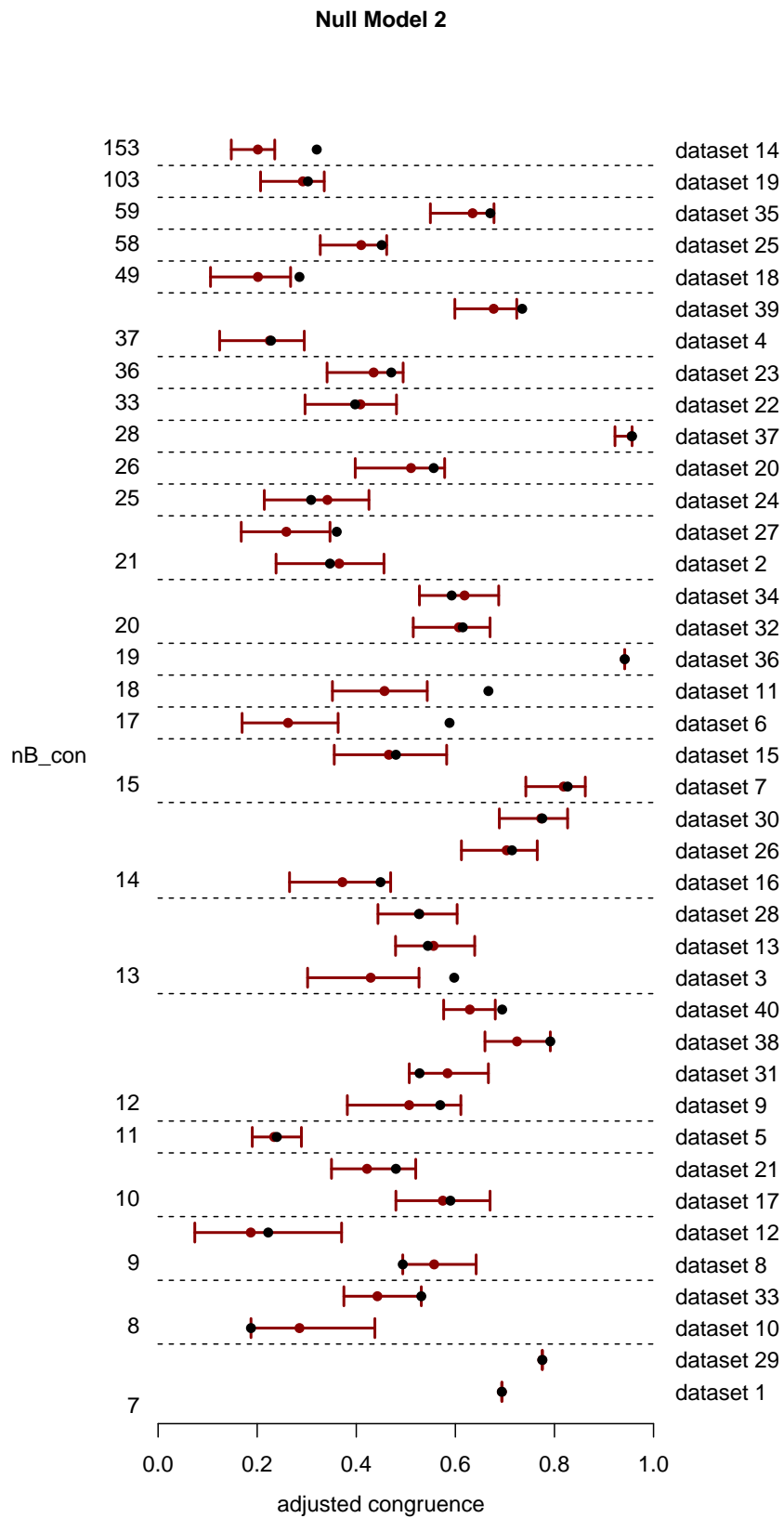


The inspection of these preliminary results reveals that in datasets with too few connector species, the distribution of congruence in the null model usually encompasses all the space for realized congruence (up to 1). Therefore, even a TN with maximal congruence would not be distinguished from the null expectation.

This complete lack of power is prevalent in datasets with less than 7 connector species, with only one exception (dataset 47), but does not occur for the remaining datasets.

These findings led to the selection criteria of at least 7 connector species for datasets, which we follow hereafter.

Null Model 2



Summary of structural analyses

Datasets Info

	A	B	C	nA	nB_con	nC	nB_AB	nB_BC	dt	tr
dataset 1	Pl	SD	Pa2	41	7	13	7	9	W	
dataset 2	He	Pl	SD	36	21	7	31	41	W	
dataset 3	Pl	He	Pa1	31	13	12	36	13	W	
dataset 4	SD	Pl	Po	21	37	212	84	110	W	2
dataset 5	Pl	He	Pa1	11	11	15	25	11	W	
dataset 6	Pl	He	Pa1	6	17	17	19	17	W	2
dataset 7	He	Pl	Po	28	15	241	30	47	W	2
dataset 8	Pl	He	Pa1	30	9	11	28	9	W	2
dataset 9	Pl	He	De	32	12	43	13	13	W	
dataset 10	Pl	SD	Pa2	29	8	6	15	18	W	
dataset 11	Pl	He	Pa1	22	18	40	31	18	W	1
dataset 12	Pl	Po	Pa1	4	9	11	9	9	W	
dataset 13	Pl	He	Pa1	32	13	7	28	13	W	
dataset 14	Pl	He	Pa1	139	153	192	357	157	W	
dataset 15	SD	Pl	Po	34	15	308	15	15	W	3
dataset 16	Pl	SD	Pa2	46	14	13	16	15	W	
dataset 17	My	Pl	SD	55	10	16	16	16	W	3
dataset 18	Pl	He	Pa1	75	49	60	90	49	W	
dataset 19	Pl	He	Pa1	111	103	232	131	103	W	
dataset 20	Pl	He	Pa1	109	26	27	85	27	W	
dataset 21	De	Pl	He	33	10	85	16	109	W	
dataset 22	Pl	He	Pr	109	33	23	85	33	W	
dataset 23	Pl	He	De	109	36	26	85	36	W	
dataset 24	De	He	En	26	25	50	37	40	W	
dataset 25	Pl	He	Pa1	37	58	102	58	58	B	
dataset 26	Pl	He	Pa1	21	14	18	14	14	B	
dataset 27	Pl	He	Pr	129	21	9	23	22	B	
dataset 28	De	Pl	Po	30	13	173	40	93	B	
dataset 29	He	Pl	Po	39	7	220	15	43	W	
dataset 30	Pl	He	Pa1	15	14	17	39	14	W	
dataset 31	Pl	He	De	120	12	10	97	19	B	
dataset 32	He	Pl	Po	93	20	52	58	48	W	
dataset 33	Po	Pl	SD	95	8	4	34	10	W	
dataset 34	Pl	He	De	41	20	35	24	20	W	
dataset 35	Pl	He	Pa1	44	59	68	80	59	W	
dataset 36	Pl	He	Pa1	157	19	30	214	19	W	
dataset 37	Pl	SP	Pa1	181	28	53	311	28	W	
dataset 38	Pl	He	Pa1	170	12	24	161	12	W	
dataset 39	Pl	He	Pa1	184	37	51	193	38	W	
dataset 40	Pl	SP	Pa1	132	12	8	77	12	W	

Only datasets with nB_con>=7. A,B,C= partitions; nA= number of species in partition A; nB_con= number of connector species; nC= number of species in partition C; nB_AB = number of species (connector and non-connector) in partition B of BN (A-B) ; nB_BC = number of species (connector and non-connector) in partition B of BN (B-C); dt= data type (binary= B, weighted= W); tr= data transformation (1= rounded to whole numbers, 2= log transformed and rounded, 3= rescaled and rounded). In A,B,C: De= Defenders, En= Enemies, He= Herbivores, My= Mycorrhizas, Pa1= Parasitoids, Pa2= Parasites, Pl= Plants, Po= Pollinators, Pr= Predators, SD= Seed Dispersers, SP= Seed Predator.

Bipartite networks

	dt	tr	M_AB	pM_AB	N_AB	pN_AB	T_AB	M_BC	pM_BC	N_BC	pN_BC	T_BC
dataset 1	W		0.34	0	57.3	0.00	C	0.80	0	100.0	0.92	M
dataset 2	W		0.49	0	66.4	0.00	C	0.34	0	61.4	0.00	C
dataset 3	W		0.49	0	68.4	0.00	C	0.61	0	47.8	0.01	C
dataset 4	W	2	0.53	0	51.3	0.00	C	0.34	0	26.6	0.00	C
dataset 5	W		0.30	0	57.2	0.00	C	0.47	0	61.6	0.00	C
dataset 6	W	2	0.62	0	86.3	0.66	M	0.52	0	40.7	0.02	C
dataset 7	W	2	0.87	0	36.0	0.87	M	0.50	0	58.1	0.00	C
dataset 8	W	2	0.87	0	36.0	0.54	M	0.48	0	52.8	0.24	M
dataset 9	W		0.55	0	39.9	0.00	C	0.36	0	47.0	0.00	C
dataset 10	W		0.27	0	71.1	0.00	C	0.12	0	63.7	0.00	C
dataset 11	W	1	0.19	0	92.9	0.03	C	0.46	0	33.4	0.00	C
dataset 12	W		0.13	0	93.2	0.00	C	0.06	0	65.7	0.00	C
dataset 13	W		0.47	0	51.1	0.00	C	0.34	0	67.7	0.00	C
dataset 14	W		0.54	0	29.0	0.00	C	0.22	0	9.6	0.00	C
dataset 15	W	3	0.34	0	55.7	0.00	C	0.39	0	41.1	0.00	C
dataset 16	W		0.52	0	62.1	0.00	C	0.46	0	75.5	0.00	C
dataset 17	W	3	0.40	0	48.5	0.00	C	0.34	0	71.8	0.00	C
dataset 18	W		0.42	0	31.2	0.00	C	0.58	0	33.7	0.00	C
dataset 19	W		0.89	0	38.9	0.00	C	0.55	0	14.4	0.00	C
dataset 20	W		0.63	0	50.3	0.00	C	0.56	0	34.0	0.00	C
dataset 21	W		0.23	0	67.6	0.00	C	0.63	0	43.1	0.00	C
dataset 22	W		0.63	0	36.9	0.00	C	0.39	0	30.9	0.00	C
dataset 23	W		0.63	0	47.8	0.00	C	0.33	0	41.6	0.00	C
dataset 24	W		0.33	0	44.4	0.00	C	0.44	0	20.3	0.00	C
dataset 25	B		0.91	-	5.9	0.00	-	0.61	-	24.3	0.00	-
dataset 26	B		0.78	-	0.0	0.00	-	0.55	-	67.8	0.00	-
dataset 27	B		0.40	-	66.7	0.00	-	0.22	-	65.4	0.00	-
dataset 28	B		0.29	-	59.8	0.00	-	0.54	-	26.3	0.00	-
dataset 29	W		0.82	0	80.3	0.37	M	0.43	0	43.7	0.00	C
dataset 30	W		0.82	0	80.3	0.33	M	0.79	0	45.5	0.73	M
dataset 31	B		0.78	-	18.6	0.33	-	0.63	-	32.1	0.73	-
dataset 32	W		0.73	0	42.7	0.00	C	0.40	0	50.8	0.00	C
dataset 33	W		0.48	0	30.0	0.00	C	0.48	0	68.9	0.04	C
dataset 34	W		0.72	0	72.5	0.00	C	0.10	0	68.3	0.00	C
dataset 35	W		0.95	0	83.9	0.12	M	0.48	0.015	8.9	0.01	C
dataset 36	W		0.86	0	29.9	0.00	C	0.87	0	53.3	0.86	M
dataset 37	W		0.91	0	35.7	0.00	C	0.86	0	82.4	0.90	M
dataset 38	W		0.62	0	29.1	0.00	C	0.57	0	65.5	0.00	C
dataset 39	W		0.29	0	32.5	0.00	C	0.81	0	51.9	0.00	C
dataset 40	W		0.78	0	30.2	0.00	C	0.56	0	81.6	0.15	M

A,B,C= partitions; dt= data type (binary= B, weighted= W); tr= data tranformation (1= rounded to whole numbers, 2= log transformed and rounded, 3= rescaled and rounded); M_AB/M_BC= modularity; pM_AB/pM_BC= P-value of modularity compared to null model; N_AB/N_BC= Nestedness SM; pN_AB/pN_BC= P-value of Nestedness SM compared to null model; T_AB/T_BC = Topology (M= purely modular, C= hierarchical compound). We applied NODF and WNODA to measure nestedness of, respectively, binary and weighted networks.

Tripartite networks

	A	B	C	SF	C.adj	C.r	H	p1	p2
dataset 1	Pl	SD	Pa2	S	0.69	1.00	0.48	0 *	1
dataset 2	He	Pl	SD	F	0.35	0.67	0.13	0 *	0.62
dataset 3	Pl	He	Pa1	S	0.60	0.85	0.48	0 *	0.01 *
dataset 4	SD	Pl	Po	F	0.23	0.62	0.19	0 *	0.44
dataset 5	Pl	He	Pa1	S	0.24	0.73	0.14	0.05	0.39
dataset 6	Pl	He	Pa1	S	0.59	1.00	0.52	0 *	0 *
dataset 7	He	Pl	Po	F	0.83	1.00	0.60	0 *	0.47
dataset 8	Pl	He	Pa1	S	0.49	0.78	0.48	0 *	1
dataset 9	Pl	He	De	S	0.57	0.83	0.32	0 *	0.18
dataset 10	Pl	SD	Pa2	S	0.19	0.62	0.07	0.35	1
dataset 11	Pl	He	Pa1	S	0.67	1.00	0.39	0 *	0 *
dataset 12	Pl	Po	Pa1	S	0.22	0.67	0.06	0.24	0.5
dataset 13	Pl	He	Pa1	S	0.54	0.85	0.12	0 *	0.55
dataset 14	Pl	He	Pa1	S	0.32	0.55	0.27	0 *	0 *
dataset 15	SD	Pl	Po	F	0.48	0.80	0.27	0 *	0.35
dataset 16	Pl	SD	Pa2	S	0.45	0.86	0.34	0 *	0.11
dataset 17	My	Pl	SD	F	0.59	0.90	0.44	0 *	0.38
dataset 18	Pl	He	Pa1	S	0.29	0.55	0.32	0 *	0.02 *
dataset 19	Pl	He	Pa1	S	0.30	0.63	0.12	0 *	0.33
dataset 20	Pl	He	Pa1	S	0.56	0.85	0.39	0 *	0.12
dataset 21	De	Pl	He	F	0.48	0.80	0.26	0 *	0.14
dataset 22	Pl	He	Pr	S	0.40	0.61	0.16	0 *	0.59
dataset 23	Pl	He	De	S	0.47	0.72	0.28	0 *	0.16
dataset 24	De	He	En	F	0.31	0.56	0.08	0 *	0.73
dataset 25	Pl	He	Pa1	S	0.45	0.62	0.42	0 *	0.09
dataset 26	Pl	He	Pa1	S	0.71	0.93	0.55	0 *	0.42
dataset 27	Pl	He	Pr	S	0.36	0.71	0.17	0 *	0.03 *
dataset 28	De	Pl	Po	F	0.53	0.77	0.24	0 *	0.5
dataset 29	He	Pl	Po	F	0.78	1.00	0.58	0 *	1
dataset 30	Pl	He	Pa1	S	0.78	1.00	0.72	0 *	0.53
dataset 31	Pl	He	De	S	0.53	0.75	0.37	0 *	0.91
dataset 32	He	Pl	Po	F	0.62	0.85	0.47	0 *	0.41
dataset 33	Po	Pl	SD	F	0.53	1.00	0.41	0 *	0.11
dataset 34	Pl	He	De	S	0.59	0.90	0.30	0 *	0.72
dataset 35	Pl	He	Pa1	S	0.67	0.78	0.51	0 *	0.08
dataset 36	Pl	He	Pa1	S	0.94	1.00	0.83	0 *	1
dataset 37	Pl	SP	Pa1	S	0.96	1.00	0.81	0 *	0.91
dataset 38	Pl	He	Pa1	S	0.79	1.00	0.54	0 *	0.06
dataset 39	Pl	He	Pa1	S	0.73	0.92	0.64	0 *	0.02 *
dataset 40	Pl	SP	Pa1	S	0.69	1.00	0.56	0 *	0.04 *

A,B,C= partitions; S/F= stacked or forked TN; dt= data type (binary= B, weighted= W); tr= data tranformation (1= rounded to whole numbers, 2= log transformed and rounded, 3= rescaled and rounded); C.adj= adjusted congruence; C.r= realized congruence; H= hypermodularity; p1= P-value of adjusted congruence compared to null model 1; p2= P-value of adjusted congruence compared to null model 2. In A,B,C: De= Defenders, En= Enemies, He= Herbivores, My= Mycorrhizas, Pa1= Parasitoids, Pa2= Parasites, Pl= Plants, Po= Pollinators, Pr= Predators, SD= Seed Dispersers, SP= Seed Predator.

Forked vs. Stacked

Realized Congruence

```
## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): não é
## possível computar o valor de p exato com o de desempate

##
## Wilcoxon rank sum test with continuity correction
##
## data: x2_2$C.r by x2_2$SF
## W = 160, p-value = 1
## alternative hypothesis: true location shift is not equal to 0
```

Adjusted Congruence

```
## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): não é
## possível computar o valor de p exato com o de desempate

##
## Wilcoxon rank sum test with continuity correction
##
## data: x2_2$C.adj by x2_2$SF
## W = 148, p-value = 0.8
## alternative hypothesis: true location shift is not equal to 0
```

Hypermodularity

```
##
## Wilcoxon rank sum exact test
##
## data: x2_2$H by x2_2$SF
## W = 134, p-value = 0.5
## alternative hypothesis: true location shift is not equal to 0
```

Mechanism Testing (Mantel tests)

DATASET3

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.049

P-Value: [1] 0.82

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.14

P-Value: [1] 1

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.27

P-Value: [1] 0.55

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.035

P-Value: [1] 0.55

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel(xdis = TAXODIST, ydis = HYPERMOD_DIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.013

P-Value: [1] 0.82

Permutations: [1] 10

DATASET14

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.052

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.011

P-Value: [1] 0.27

Permutations: [1] 10

Partition B

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.039

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.031

P-Value: [1] 1

Permutations: [1] 10

DATASET18

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.091

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.038

P-Value: [1] 0.18

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.032

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.018

P-Value: [1] 0.45

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0056

P-Value: [1] 0.55

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0018

P-Value: [1] 0.55

Permutations: [1] 10

DATASET19

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.1

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.04

P-Value: [1] 1

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.25

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0046

P-Value: [1] 0.45

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.00029

P-Value: [1] 0.55

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.033

P-Value: [1] 0.091

Permutations: [1] 10

DATASET20

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.014

P-Value: [1] 1

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0019

P-Value: [1] 0.64

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: `mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.3

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: `mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.031

P-Value: [1] 0.45

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: `mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.18

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: `mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.063

P-Value: [1] 0.91

Permutations: [1] 10

DATASET21

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.11

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.028

P-Value: [1] 0.18

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.18

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.14

P-Value: [1] 0.91

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.019

P-Value: [1] 0.18

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0025

P-Value: [1] 0.55

Permutations: [1] 10

DATASET22

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.013

P-Value: [1] 0.64

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.022

P-Value: [1] 1

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0038

P-Value: [1] 0.45

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.059

P-Value: [1] 0.091

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.029

P-Value: [1] 0.36

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.0063

P-Value: [1] 0.27

Permutations: [1] 10

DATASET23

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.014

P-Value: [1] 0.27

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.011

P-Value: [1] 0.45

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.017

P-Value: [1] 0.91

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.038

P-Value: [1] 0.27

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.095

P-Value: [1] 0.18

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.016

P-Value: [1] 0.73

Permutations: [1] 10

DATASET24

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.00013

P-Value: [1] 0.36

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.0031

P-Value: [1] 0.64

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.089

P-Value: [1] 0.18

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.032

P-Value: [1] 0.55

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.036

P-Value: [1] 0.18

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.017

P-Value: [1] 0.55

Permutations: [1] 10

DATASET29

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.25

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.45

P-Value: [1] 0.091

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.1

P-Value: [1] 0.27

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.18

P-Value: [1] 0.18

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.018

P-Value: [1] 0.18

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.18

P-Value: [1] 0.091

Permutations: [1] 10

DATASET30

Partition A

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.076

P-Value: [1] 0.82

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.29

P-Value: [1] 0.091

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: `mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.28

P-Value: [1] 0.091

Permutations: [1] 10

Distribution x Hypermodules

Call: `mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.23

P-Value: [1] 0.091

Permutations: [1] 10

Partition C

Taxonomy x Hypermodules

Call: `mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.16

P-Value: [1] 1

Permutations: [1] 10

Distribution x Hypermodules

Call: `mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)`

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.3

P-Value: [1] 0.091

Permutations: [1] 10

DATASET32

Partition A

Distribution x Hypermodules

Call: mantel(xdis = GEODIST, ydis = HYPERMOD_DIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.056

P-Value: [1] 0.091

Permutations: [1] 10

Partition B

Taxonomy x Hypermodules

Call: mantel.partial(xdis = TAXODIST, ydis = HYPERMOD_DIST, zdis = GEODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] -0.079

P-Value: [1] 0.91

Permutations: [1] 10

Distribution x Hypermodules

Call: mantel.partial(xdis = GEODIST, ydis = HYPERMOD_DIST, zdis = TAXODIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.086

P-Value: [1] 0.36

Permutations: [1] 10

Partition C

Distribution x Hypermodules

Call: mantel(xdis = GEODIST, ydis = HYPERMOD_DIST, method = "spearman", permutations = 10)

Method: [1] "Spearman's rank correlation rho"

Statistic: [1] 0.03

P-Value: [1] 0.18

Permutations: [1] 10