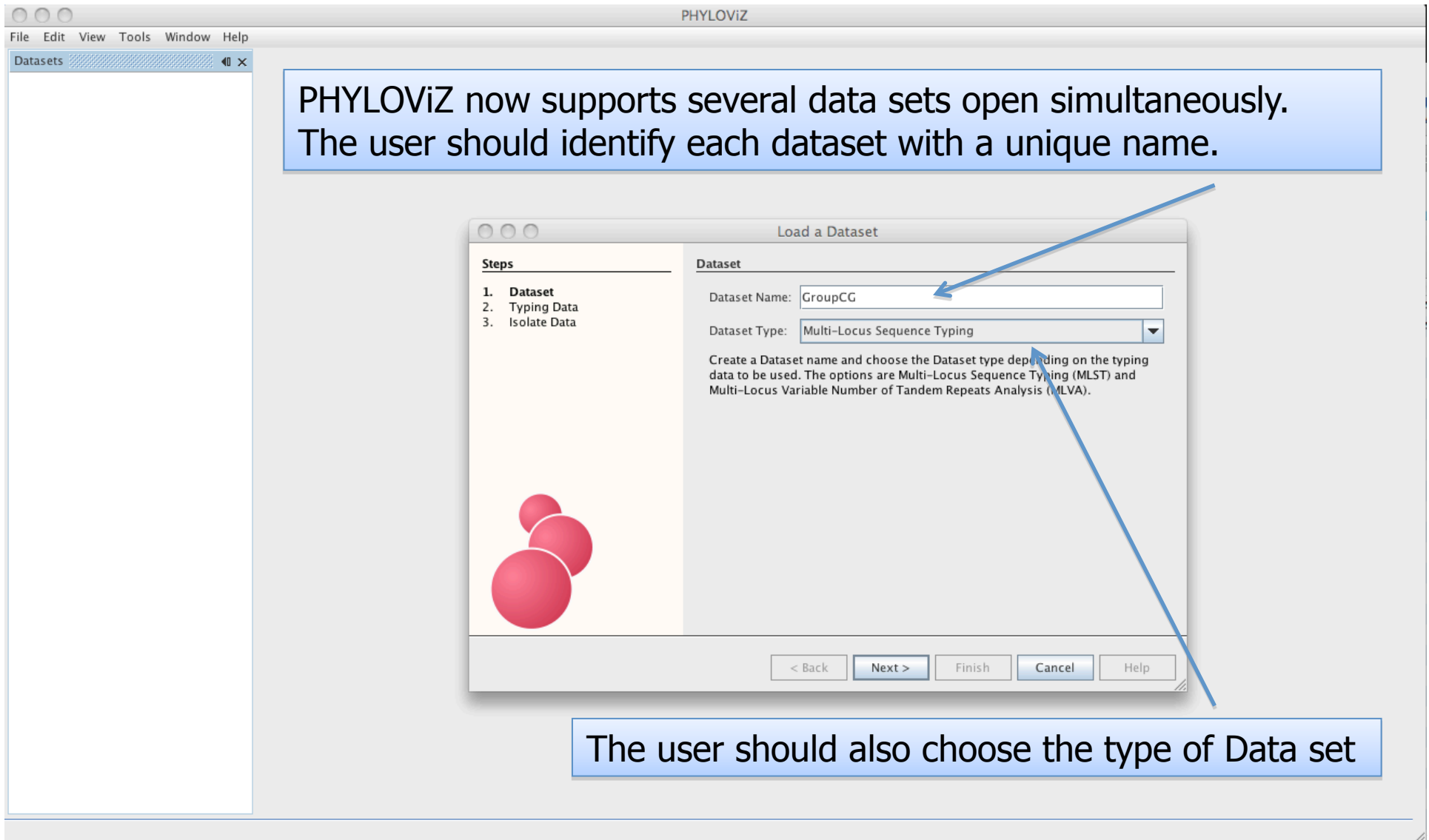


PHYLOViZ tutorial

The objective of this tutorial is providing the user with a visual guide to PHYLOViZ features, and with a quick How-to guide to the analysis and visualization of data sets composed of allelic profiles as well as additional information for a strain collection.

The first step is to Load the data set to be analyzed. Select File > Load Dataset



ST	gki	gtr	murI	mutS	recP	xpt	ygiZ	Strain	emm type	Group	carbohydrate	ST	Location	Collection
1	10	6	6	6	12	13	8	168554	stG485	G	47	Portugal	UL	
2	5	4	4	1	2	15	2	171712	stG480	G	38	Portugal	UL	
3	5	3	4	1	6	2	1	220269	stG2078	G	15	Portugal	UL	
4	2	2	4	1	8	7	2	223754	stC839	C	3	Portugal	UL	
5	2	2	4	1	12	12	7	230631	stG480	G	8	Portugal	UL	
6	1	3	1	1	1	1	4	231995	stC74a	G	29	Portugal	UL	
7	1	1	1	1	1	1	3	241940	stC36	C	50	Portugal	UL	
8	1	1	1	1	1	1	4	273600	stG166b	G	65	Portugal	UL	
9	1	1	1	1	1	1	2	299298	stG643	G	8	Portugal	UL	
10	10	4	7	7	12	13	8	313247	stG6	G	25	Portugal	UL	
11	11	3	4	1	2	7	5	363962	stG2078	G	17	Portugal	UL	
12	4	4	5	2	17	6	2	378119	stC839	G	15	Portugal	UL	
13	10	5	6	6	12	13	9	380870	stG480	G	41	Portugal	UL	
14	10	4	7	6	12	13	8	386041	stC839	C	3	Portugal	UL	
15	3	3	2	2	9	8	2	394314	stG2078	G	72	Portugal	UL	
16	4	4	1	2	17	1	2	423738	stG62647	C	20	Portugal	UL	
17	4	4	4	2	17	6	3	450784	stG10	G	15	Portugal	UL	
18								460800	stG10	G	15	Portugal	UL	
19								493188	stG485	C	69	Portugal	UL	
20								542567	stG6	G	62	Portugal	UL	
21								618280	emm57	G	57	Portugal	UL	
22								SH00						
23								SH00						
24								SH00						
25								SH01						
26	3	2	1	1	7	10	2	SH01						
27	2	2	4	1	13	12	7	SH01						
28	3	3	4	2	16	14	2	SH01						
29	3	2	4	2	7	1	3	SH01						
30	3	2	4	1	7	10	2	SH01						
31	3	2	4	1	8	7	2	SH0218	stG245	G	15	Portugal	UL	
32	3	2	4	1	4	10	5	SH0254	stG485	C	69	Portugal	UL	
33	3	8	2	8	9	6	6	SH0257	stC6979	C	80	Portugal	UL	
34	3	7	4	1	14	15	10	SH0259	stG652	G	71	Portugal	UL	
35	3	7	4	1	14	15	2	SH0275	stG485	G	55	Portugal	UL	
36	4	4	1	2	17	6	3	SH0330	stC36	C	49	Portugal	UL	
37	3	2	1	1	4	1		SH0336	stG5420	G	25	Portugal	UL	
38	1	1	1	1	1	1						Australia	QIMR	
39	1	1	1	1	1	21						Australia	QIMR	
40	1	1	1	4	1	1						46	Australia	QIMR
41	1	1	1	9	1	1						20	Australia	QIMR
42	1	1	4	1	1	1						20	Australia	QIMR
43	2	2	4	1	1	1						Australia	QIMR	
44	2	2	4	2	3	7						Australia	QIMR	
45	2	2	4	10	8	19						Australia	QIMR	
46	2	4	4	1	19	17						29	Australia	QIMR
47	3	2	1	1	20	1						12	Australia	QIMR
48	3	2	1	2	10	4	2	GG5120	stG4831	G	74	Australia	QIMR	
49	3	2	3	1	5	5	2	GG519	stC1400	G	64	Australia	QIMR	

The input data for the analysis consists of a tab separated file with the allelic profiles and...

...a file (also tab separated) with ancillary information about the isolates.

Tab separated files can be easily exported from Excel using "Save as" and choosing "Tab delimited text"

File Edit View Tools Window Help

Datasets

sampleAPfile.txt

ST	gki	gtr	murI	mutS	recP	xpt	yqiZ
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4	2	2	4	1	8	7	2
5	2	2	4	1	12	12	7
6	1	3	1	1	1	1	4
7	1	1	1	1	1	1	3
8	1	1	1	1	1	1	4
9	1	1	1	1	1	1	2
10	10	4	7	7	12	13	8
11	11	3	4	1	2	7	5
12	4	4	5	2	17	6	2
13	10	5	6	6	12	13	9
14	10	4	7	6	12	13	8
15	3	3	2	2	9	8	2
16	4	4	1	2	17	1	2
17	4	4	1	2	17	6	2
18	4	2	4	1	8	7	2
19	3	8	4	1	8	7	2
20	3	3	2	8	9	6	6
21	3	8	2	2	9	8	2
22	3	3	2	8	1	11	6
23	3	3	4	1	3	1	1
24	3	2	1	5	15	4	3
25	3	2	1	5	7	4	3
26	3	2	1	1	7	10	2
27	2	2	4	1	13	12	7
28	3	3	4	2	16	14	2
29	3	2	4	2	7	1	3
30	3	2	4	1	7	10	2
31	3	2	4	1	8	7	2
32	3	2	4	1	4	10	5
33	3	8	2	8	9	6	6
34	3	7	4	1	14	15	10
35	3	7	4	1	14	15	2
36	4	4	1	2	17	6	3
37	3	2	1	1	4	1	3
38	1	1	1	1	1	1	1
39	1	1	1	1	1	21	4
40	1	1	1	4	1	1	4
41	1	1	1	9	1	1	1
42	1	1	4	1	1	1	4
43	2	2	4	1	1	1	2
44	2	2	4	2	3	7	1
45	2	2	4	10	8	19	2
46	2	4	4	1	19	17	6
47	3	2	1	1	20	1	3
48	3	2	1	2	10	4	4
49	3	2	3	1	5	5	2
50	3	2	3	1	5	18	2
51	3	2	4	1	11	1	2
52	3	2	4	1	11	3	5

Load a Dataset

Steps

1. Dataset
2. Typing Data
3. Isolate Data

Typing Data

File:

Load a tab separated file with the first row containing column headers (field names). The first column should be a Sequence Identifier, such as the ST for MLST data. Other columns should be the different loci used in the typing scheme. Example of a MLST dataset for *Streptococcus dysgalactiae subspecies equisimilis*.

ST	gki	gtr	murI	mutS	recP	xpt	yqiZ
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4	2	2	4	1	8	7	2
5	2	2	4	1	12	12	7
6	1	3	1	1	1	1	4

The Typing Data file should contain the allelic profiles for MLST, MLVA or SNP data. The first column should be a unique identifier such as the "sequence type" in case of MLST.

sampleADfile.txt

Strain	emm type	Group	carbohydrate	ST	Location	Collection
168854	stG485	G	47	Portugal	UL	
171712	stG480	G	38	Portugal	UL	
229269	stG2078	G	15	Portugal	UL	
223754	stC839	C	3	Portugal	UL	
238631	stG480	G	8	Portugal	UL	
231995	stC74a	G	29	Portugal	UL	
241940	stC36	C	58	Portugal	UL	
273690	stG166b	G	65	Portugal	UL	
299298	stG643	G	8	Portugal	UL	
313247	stG6	G	25	Portugal	UL	
363962	stG2078	G	17	Portugal	UL	
378119	stC839	G	15	Portugal	UL	
388070	stG480	G	41	Portugal	UL	
386941	stC839	C	3	Portugal	UL	
394314	stG2078	G	72	Portugal	UL	
423738	stG62647	C	20	Portugal	UL	
458784	stG10	G	15	Portugal	UL	
468880	stG18	G	15	Portugal	UL	
493188	stG485	C	69	Portugal	UL	
542567	stG6	G	62	Portugal	UL	
618280	emm57	G	57	Portugal	UL	
SH0004	stG6792	G	4	Portugal	UL	
SH0015	stG6	G	25	Portugal	UL	
SH0032	stG166b	G	15	Portugal	UL	
SH0102	stG2078	G	17	Portugal	UL	
SH0107	stG643	G	52	Portugal	UL	
SH0110	stG6	G	25	Portugal	UL	
SH0113	stG6792	G	4	Portugal	UL	
SH0124	stG6792	G	4	Portugal	UL	
SH0210	stG245	G	15	Portugal	UL	
SH0254	stG485	C	69	Portugal	UL	
SH0257	stC6979	C	88	Portugal	UL	
SH0259	stG652	G	71	Portugal	UL	
SH0275	stG485	G	55	Portugal	UL	
SH0330	stC36	C	49	Portugal	UL	
SH0336	stG5420	G	25	Portugal	UL	
G121	stC74a	G	29	Australia	QIMR	
G122	stC74a	G	29	Australia	QIMR	
GCS18128	stC1400	C	46	Australia	QIMR	
GC32816	stG62647	C	20	Australia	QIMR	
GC36894	stG62647	C	20	Australia	QIMR	
GC36929	stG62647	C	20	Australia	QIMR	
GC8075	stG166b	G	56	Australia	QIMR	
GC8101	stG643	G	12	Australia	QIMR	
GC810b	stG6	G	44	Australia	QIMR	
GC81172	stC74a	G	29	Australia	QIMR	
GC811543	stG643	G	12	Australia	QIMR	
GC8120	stC4831	G	74	Australia	QIMR	
GC819	stC1400	G	64	Australia	QIMR	
GC82	stG10	G	15	Australia	QIMR	
GC824	stG6	G	44	Australia	QIMR	
GC8430	stG643	G	12	Australia	QIMR	

Load a Dataset

Steps

1. Dataset
2. Typing Data
3. Isolate Data

Isolate Data

File:

Key:

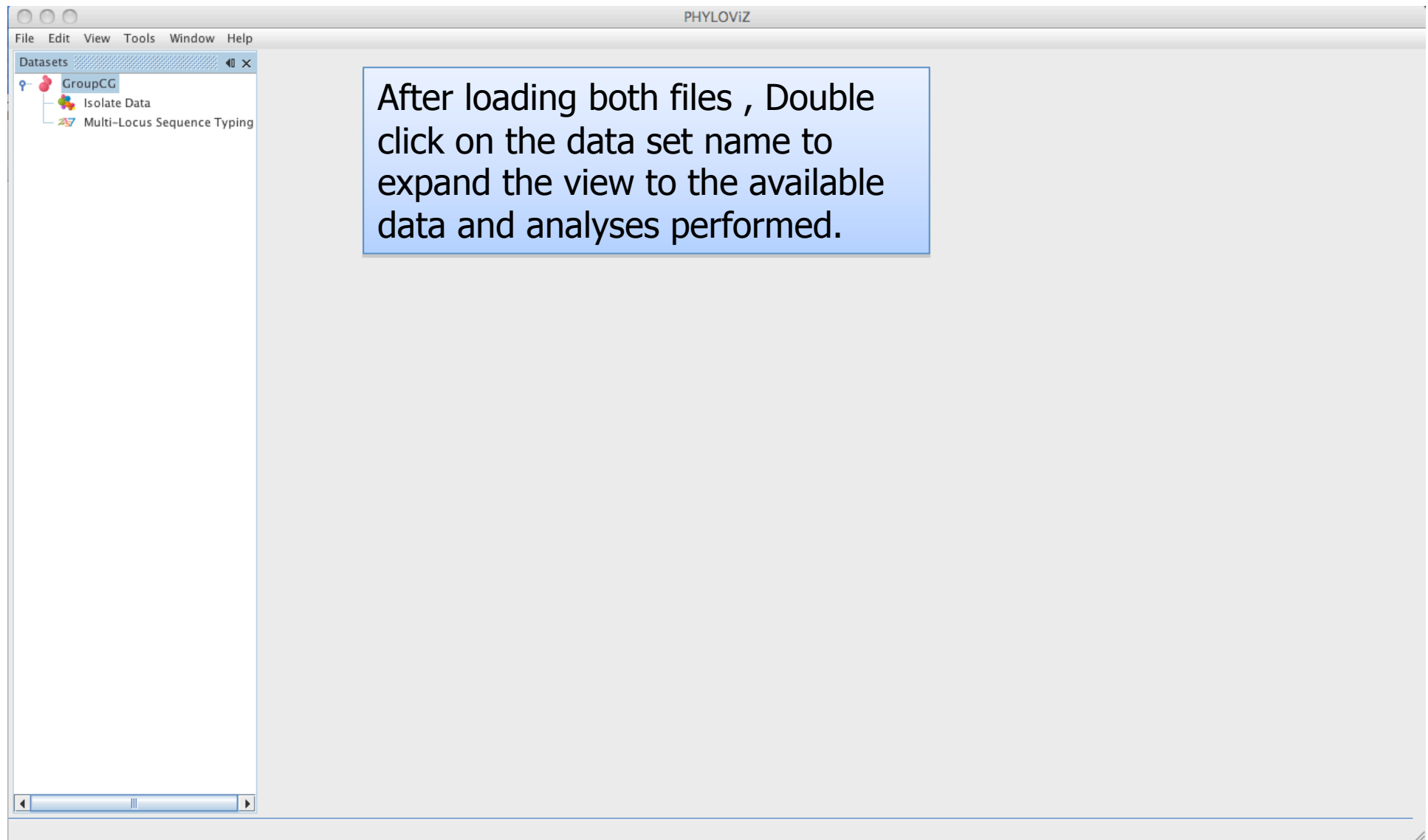
If you inform absent algorithm header choice

Strain
emm type
Group carbohydrate
ST
Location
Collection

phic
ene presence
it on the
with column
entifier.
ata to the

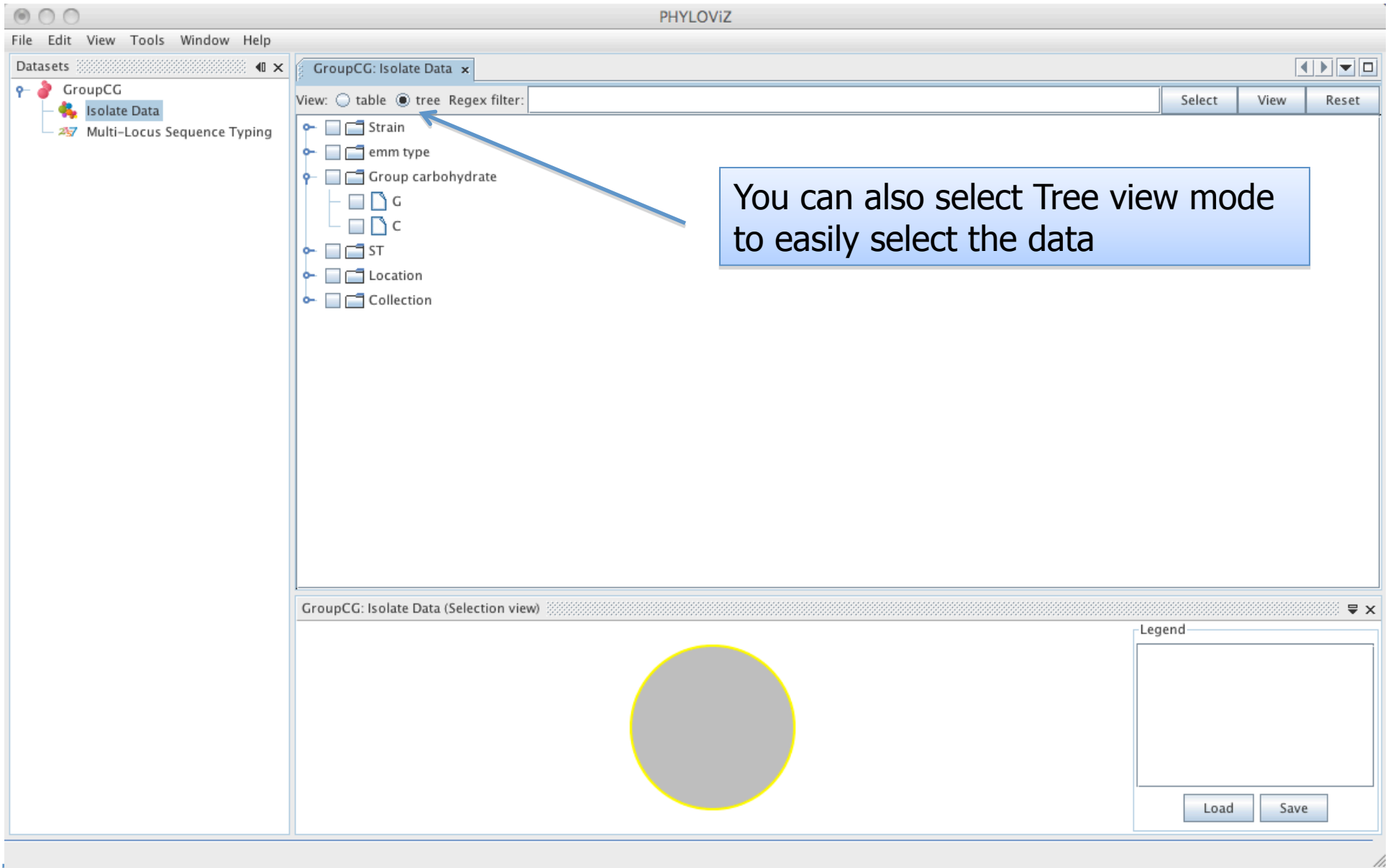
allelic prone data. If the new does not appear in the drop down menu press the Update button. If you don't have any available data or don't wish do load any leave this fields blank an press Finish.

The Isolate Data file contains the ancillary data about the isolates. The key is the field that connects the data to the Sequence Type identifier of the Typing Data file.



Strain	emm type	Group carb...	ST	Location	Collection
168554	stG485	G	47	Portugal	UL
171712	stG485	G	38	Portugal	UL
220269	stG2078	G	15	Portugal	UL
223754	stC839	C	3	Portugal	UL
230631	stG480	G	8	Portugal	UL
231995	stC74a	G	29	Portugal	UL
241940	stC36	C	50	Portugal	UL
273600	stG166b	G	65	Portugal	UL
299298	stG643	G	8	Portugal	UL
313247	stG6	G	25	Portugal	UL
363962	stG2078	G	17	Portugal	UL
378119	stC839	G	15	Portugal	UL
380870	stG480	G	41	Portugal	UL
386041	stC839	C	3	Portugal	UL
394314	stG2078	G	72	Portugal	UL
423738	stG62647	C	20	Portugal	UL
450784	stG10	G	15	Portugal	UL
460880	stG10	G	15	Portugal	UL
493188	stG485	C	69	Portugal	UL
542567	stG6	G	62	Portugal	UL
618280	emm57	G	57	Portugal	UL
SH0004	stG6792	G	4	Portugal	UL
SH0015	stG6	G	25	Portugal	UL
SH0032	stG166b	G	15	Portugal	UL
SH0102	stG2078	G	17	Portugal	UL
SH0107	stG643	G	52	Portugal	UL
SH0110	stG6	G	25	Portugal	UL
SH0113	stG6792	G	4	Portugal	UL
SH0124	stG6792	G	4	Portugal	UL
SH0218	stG245	G	15	Portugal	UL
SH0254	stG485	C	69	Portugal	UL

Double clicking on the Isolate Data displays it in the Table view mode



PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG Isolate Data Multi-Locus Sequence Typing

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x

View: table tree Regex filter: [] [Select View Reset]

	ST	gki	gtr	murl	mutS	recr	xpt	yqiZ
1	10	6	6	6	6	12	13	8
2	5	4	4	4	1	2	15	2
3	5	3	4	4	1	6	2	1
4	2	2	4	4	1	8	7	2
5	2	2	4	4	1	12	12	7
6	1	3	1	1	1	1	1	4
7	1	1	1	1	1	1	1	3
8	1	1	1	1	1	1	1	4
9	1	1	1	1	1	1	1	2
10	10	4	7	7	7	12	13	8
11	11	3	4	4	1	2	7	5
12	4	4	5	5	2	17	6	2
13	10	5	6	6	6	12	12	6
14	10	4	7	7	6	12	12	6
15	3	3	2	2	2	9	9	3
16	4	4	1	1	2	17	17	3
17	4	4	1	1	2	17	17	3
18	4	2	4	4	1	8	8	3
19	3	8	4	4	1	8	8	3
20	3	3	2	2	8	9	9	3
21	3	8	2	2	2	9	9	3
22	3	3	2	2	8	1	11	6
23	3	3	4	4	1	3	1	1
24	3	2	1	1	5	15	4	3
25	3	2	1	1	5	7	4	3
26	3	2	1	1	1	7	10	2
27	2	2	4	4	1	13	12	7
28	3	3	4	4	2	16	14	2
29	3	2	4	4	2	7	1	3
30	3	2	4	4	1	7	10	2
31	3	2	4	4	1	8	7	2

GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus Sequence Typing (Selection view)

Legend

Load Save

Opened data and analyses files are organized in Tabs

Double clicking on the Typing Data also displays it in the Table view mode

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG Isolate Data Multi-Locus Sequence Typing

View: table tree Regex filter:

ST	gki	gtr	murl	mutS	recP	xpt	ygiz
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4		2	4	1	8	7	2
5		2	4	1	12	12	7
6		3	1	1	1	1	4
7	1	1	1	1	1	1	3
8	1	1	1	1	1	1	4
9	1	1	1	1	1	1	2
10	10	4	7	7	12	13	8
11	11	3	4	1	2	7	5
12	4	4	5	2	17	6	2
13	10	5	6	6	12	13	9
14	10	4	7	6	12	13	8
15	3	3	2	2	9	8	2
16	4	4	1	2	17	1	2
17	4	4	1	2	17	6	2
18							
19							
20							
21							
22							
23							
24							
25							
26							
27							
28							
29							
30							
31							
32							
33							
34							
35							
36							
37							
38							
39							
40							
41							
42							
43							
44							
45							
46							
47							
48							
49							
50							
51							
52							
53							
54							
55							
56							
57							
58							
59							
60							
61							
62							
63							
64							
65							
66							
67							
68							
69							
70							
71							
72							
73							
74							
75							
76							
77							
78							
79							
80							
81							
82							
83							
84							
85							
86							
87							
88							
89							
90							
91							
92							
93							
94							
95							
96							
97							
98							
99							
100							

Select View Reset

Compute

View

Save

goeBURST

goeBURST Full MST

GroupCG: Multi-Locus Sequence Typing (Selection view)

Legend

Load Save

To analyze the data just click the right mouse button in the Typing Data and select Compute. You can then choose from using the goeBURST algorithm or to create a Minimum Spanning Tree using an expanded version of the goeBURST rules.

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG Isolate Data Multi-Locus Sequence Typing

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x

View: table tree Regex filter:

ST	gki	gtr	murl	mutS	recP	xpt	yqiZ
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4	2	2	4	1	8	7	2
5	2	2	4	1	12	12	7
6	1	3	1	1	1	1	4
7	1	1					
8	1	1					
9	1	1					
10	10	4					
11	11	3					
12	4	4					
13	10	5					
14	10	4					
15	3	3					
16	4	4					
17	4	4					
18	4	2					
19	3	8					
26	3	2					
27	2	2					
28	3	3					
29	3	2					
30	3	2					
31	3	2					

goeBURST Configuration

Steps

1. Distance
2. Level

Distance

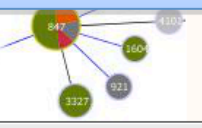
Distance: eBURST Distance

This list contains only distances compatible with the current dataset.

< Back Next > Finish Cancel Help

Legend

Load Save



If you choose the goeBURST algorithm you then choose the eBURST Distance ...

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x

View: table tree Regex filter: [] Select View Reset

ST	gki	gtr	murl	mutS	recP	xpt	yqiZ
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4	2	2	4	1	8	7	2
5	2	2	4	1	12	12	7
6	1	3	1	1	1	1	4
7	1	1					
8	1	1					
9	1	1					
10	10	4					
11	11	3					
12	4	4					
13	10	5					
14	10	4					
15	3	3					
16	4	4					
17	4	4					
18	4	2					
19	3	8					
20							
21							
22							
23							
24							
25							
26	3	2					
27	2	2					
28	3	3					
29	3	2					
30	3	2					
31	3	7					

goeBURST Configuration

Steps

- Distance
- Level

Level

Level: SLV DLV TLV

The SLV (level 1) is the default level.

< Back Next > Finish Cancel Help

Legend

Load Save

... and then you can choose to define groups at SLV , DLV or TLV Level

SLV – Single Locus Variant
DLV – Double Locus Variant
TLV – Triple Locus Variant

PHYLOViZ

File Edit View Tools Window Help

Datasets GroupCG Isolate Data Multi-Locus Sequence Typing goeBURST (Level 1)

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x

View: table tree Regex filter: [] Select View Reset

ST	gki	gtr	murl	mutS	recP	xpt	ygiz
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4	2	2	4	1	8	7	2
5	2	2	4	1	12	12	7
6	1	3	1	1	1	1	4
7	1	1	1	1	1	1	3
8	1	1	1	1	1	1	4
9	1	1	1	1	1	1	2
10	10	4	7	7	12	13	8
11	11	3	4	1	2	7	5
12	4	4	5	2	17	6	2
13	10	5	6	6	12	13	9
14	10	4	7	6	12	13	8

GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus Sequence Typing (Selection view) GroupCG: goeBURST Output

```
[Fri Mar 25 11:22:20 WET 2011] goeBURST started
goeBURST algorithm: computing groups...

[Fri Mar 25 11:22:20 WET 2011] goeBURST algorithm: integrating data...

#CC = 42

CC 0 has 9 STs:
ST 38 (2) 4 4 0 0 (4 4 0 72)
ST 9 (0) 3 5 0 0 (3 5 1 71)
ST 7 (0) 3 5 0 0 (3 5 2 70)
ST 8 (6) 7 1 0 0 (7 1 0 72) *
ST 39 (1) 1 6 1 0 (1 6 1 72)
ST 40 (1) 1 7 0 0 (1 7 0 72)
ST 41 (1) 1 4 3 0 (1 4 3 72)
ST 42 (1) 1 6 1 0 (1 6 2 71)
ST 6 (0) 1 6 1 0 (1 6 1 72)

CC 0 has 8/11 selected edges:
8 - 38
7 - 8
8 - 9
8 - 40
8 - 39
8 - 42
6 - 8
38 - 41
```

The algorithm runs and you can see the total text output in the Output window. Next you can double click on the goeBURST output to visualize the resulting goeBURST trees

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (L

Groups at SLV:

- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26

Options > || animation speed >> 50 search >>

GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus Sequence Typing (Selection view) GroupCG: goeBURST Output

```
[Fri Mar 25 11:22:20 WET 2011] goeBURST started
goeBURST algorithm: computing groups...

[Fri Mar 25 11:22:20 WET 2011] goeBURST algorithm: integrating data...

#CC = 42

CC 0 has 9 STs:
ST 38 (2) 4 4 0 0 (4 4 0 72)
ST 9 (0) 3 5 0 0 (3 5 1 71)
ST 7 (0) 3 5 0 0 (3 5 2 70)
ST 8 (6) 7 1 0 0 (7 1 0 72) *
ST 39 (1) 1 6 1 0 (1 6 1 72)
ST 40 (1) 1 7 0 0 (1 7 0 72)
ST 41 (1) 1 4 3 0 (1 4 3 72)
ST 42 (1) 1 6 1 0 (1 6 2 71)
```

The total resulting groups (Clonal complexes) are displayed. You can visualize several groups simultaneously by selecting them while pressing CTRL key or Shift key for multiple selection (see next slide).

PHYLOViZ

File Edit View Tools Window Help

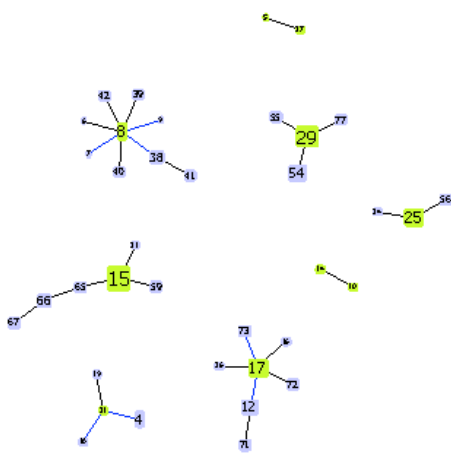
Datasets GroupCG: Isolate Data GroupCG: Multi-Locus Sequence Typing GroupCG: goeBURST (Level 1)

GroupCG
Isolate Data
Multi-Locus Sequence Typing
goeBURST (Level 1)

Groups at SLV:
0
1
2
3
4

The Options button activates several features:

- Info** – displays a new window with information about the groups, STs and links when you click on them.
- High Level Edges** – Draws the links at DLV or TLV level in the goeBURST algorithm result if these were computed when the analysis was performed.
- Linear Nodes** – The node size varies linearly with the number of isolates of a given ST. Default is a logarithmic scale.
- High Quality** – activates Higher quality graphics, recommended for publication.
- Control** – Display optimization options.
- Export** – Exports the current display as images.



Options
 Groups
 Info
 High Level Edges
 Linear Nodes
 High Quality
Control
Export

50

search >>

GroupCG: Multi-Locus Sequence Typing (Selection view) GroupCG: goeBURST Output

goeBURST started groups...
goeBURST algorithm: integrating data...

PHYLOViZ

File Edit View Tools Window Help

Datasets GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

Groups at SLV:

- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14
- 15
- 16
- 17
- 18
- 19
- 20
- 21
- 22
- 23
- 24
- 25
- 26
- 27
- 28

Info window

Info:

- # tiebreaks by FRQ = 0
- # tiebreaks by ID = 0
- Group(s): 1
- # STs = 7
- # isolates = 11
- # edges = 7 [7 0 0]
- # forest edges = 6 [6 0 0]
- # edges without ties = 4
- # tiebreaks by SLV = 2
- # tiebreaks by DLV = 0
- # tiebreaks by TLV = 0
- # tiebreaks by FRQ = 0
- # tiebreaks by ID = 0
- Group(s): 0
- # STs = 9
- # isolates = 12
- # edges = 11 [11 0 0]
- # forest edges = 8 [8 0 0]
- # edges without ties = 5
- # tiebreaks by SLV = 3
- # tiebreaks by DLV = 0
- # tiebreaks by TLV = 0
- # tiebreaks by FRQ = 0
- # tiebreaks by ID = 0

search >>

(Sele... GroupCG: goeBURST Output GroupCG: goeBURST Full MST Output

4 -- 31 (level: 1)
31 -- 18 (level: 1)
31 -- 19 (level: 1)

When you hover the mouse cursor on a given node, the SLV nodes are highlighted in orange and the DLV nodes are highlighted in yellow

PHYLOViZ

File Edit View Tools Window Help

Datasets GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

View: table tree Regex filter:

Strain	emm type	Group carb...	ST	Location	Collection	goeBURST[0]
G121	stC74a	G	29	Australia	QIMR	4
G122	stC74a	G	29	Australia	QIMR	4
GCS10128	stC1400	C	46	Australia	QIMR	27
GCS2816	stG62647	C	20	Australia	QIMR	9
GCS6894	stG62647	C	20	Australia	QIMR	9
GCS6929	stG62647	C	20	Australia	QIMR	9
GG5075	stG166b	G	56	Australia	QIMR	5
GG5101	stG643	G	12	Australia	QIMR	1
GG510b	stG6	G	44	Australia	QIMR	13
GG511172	stC74a	G	29	Australia	QIMR	4
GG511543	stG643	G	12	Australia	QIMR	1
GG5120	stG4831	G	74	Australia	QIMR	15
GG519	stC1400	G	64	Australia	QIMR	35
GG52	stG10	G	15	Australia	QIMR	2
GG524	stG6	G	44	Australia	QIMR	13
GG5430	stG643	G	12	Australia	QIMR	1
GG5463	stG10	G	15	Australia	QIMR	2
GG5539813	stC74a	G	29	Australia	QIMR	4
GG5540048	stG485	G	29	Australia	QIMR	4
GG5545448	stG10	G	15	Australia	QIMR	2
GG5569	stC6979	G	54	Australia	QIMR	4
GG5592	stG480	G	8	Australia	QIMR	0
GG59225	stC74a	G	29	Australia	QIMR	4
GG5985	stC1400	G	66	Australia	QIMR	2
GG5SRHD	stG480	G	39	Australia	QIMR	0
MD01	stG11	G	8	Australia	QIMR	0

GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus Sequence Typing (Sele...)

[Fri Mar 25 11:26:09 WET 2011] MST algorithm has started
MST algorithm: computing nodes...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: computing LVs...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: sorting nodes...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: computing tree edges...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: printing edges...
46 -- 4 (level: 1)
4 -- 31 (level: 1)
31 -- 18 (level: 1)
31 -- 19 (level: 1)

Select View Reset

To visualize the isolate data directly onto the result of any algorithm, select the data on the Isolate data and press the **Select** button and then the **View** button. You can use the right mouse button on the column header to select an entire column. Clicking on a column header also sorts the column data alphabetically.

PHYLOViZ

File Edit View Tools Window Help

Datasets: GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

View: table tree Regex filter:

Strain	emm type	Group carb...	ST	Location	Collection	goeBURST[0]
G121	stC74a	G	29	Australia	QIMR	4
G122	stC74a	G	29	Australia	QIMR	4
GCS10128	stC1400	C	46	Australia	QIMR	27
GCS2816	stG62647	C	20	Australia	QIMR	9
GCS6894	stG62647	C	20	Australia	QIMR	9
GCS6929	stG62647	C	20	Australia	QIMR	9
GGS075	stG166b	G	56	Australia	QIMR	5
GGS101	stG643	G	12	Australia	QIMR	1
GGS10b	stG6	G	44	Australia	QIMR	13
GGS11172	stC74a	G	29	Australia	QIMR	4
GGS11543	stG643	G	12	Australia	QIMR	1
GGS120	stG4831	G	74	Australia	QIMR	15
GGS19	stC1400	G	64	Australia	QIMR	35
GGS2	stG10	G	15	Australia	QIMR	2
GGS24	stG6	G	44	Australia	QIMR	13
GGS430	stG643	G	12	Australia	QIMR	1
GGS463	stG10	G	15	Australia	QIMR	2
GGS539813	stC74a	G	29	Australia	QIMR	4
GGS540048	stG485	G	29	Australia	QIMR	4
GGS545448	stG10	G	15	Australia	QIMR	2
GGS569	stC6979	G	54	Australia	QIMR	4
GGS592	stG480	G	8	Australia	QIMR	0
GGS9225	stC74a	G	29	Australia	QIMR	4
GGS985	stC1400	G	66	Australia	QIMR	2
GGSRHD	stG480	G	39	Australia	QIMR	0
MD01	stG11	G	8	Australia	QIMR	0

Select View Reset

GroupCG: Isolate Data (Selection view) x GroupCG: Multi-Locus Sequence Typing (Sele... GroupCG: goeBURST Output GroupCG: goeBURST Full MST Output

Legend

- Location:Australia (n = 55, 80.01%)
- Location:Portugal (n = 36, 30.77%)
- Location:Other (n = 15, 12.82%)
- Location:USA (n = 11, 9.4%)

Load Save

After pressing the **View** button you have access to a pie chart that will be the color legend of the analysis graphs. In the legend you will also find some basic statistics of the data selected.

Note that the results of the analyses and the pie charts are organized in Tabs at the bottom of the screen

PHYLOViZ

File Edit View Tools Window Help

Datasets GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

View: table tree Regex filter:

Strain	emm type	Group carb...	ST	Location	Collection	goeBURST[0]
G121	stC74a	G	29	Australia	QIMR	4
G122	stC74a	G	29	Australia	QIMR	4
GCS10128	stC1400	C	46	Australia	QIMR	27
GCS2816	stG62647	C	20	Australia		
GCS6894	stG62647	C	20	Australia		
GCS6929	stG62647	C	20	Australia		
GGS075	stG166b	G	56	Australia		
GGS101	stG643	G	12	Australia		
GGS10b	stG6	G	44	Australia		
GGS11172	stC74a	G	29	Australia		
GGS11543	stG643	G	12	Australia		
GGS120	stG4831	G	74	Australia		
GGS19	stC1400	G	64	Australia		
GGS2	stG10	G	15	Australia		
GGS24	stG6	G	44	Australia		
GGS430	stG643	G	12	Australia		
GGS463	stG10	G	15	Australia		
GGS539813	stC74a	G	29	Australia		
GGS540048	stG485	G	29	Australia		
GGS545448	stG10	G	15	Australia		
GGS569	stC6979	G	54	Australia		
GGS592	stG480	G	8	Australia		
GGS9225	stC74a	G	29	Australia		
GGS985	stC1400	G	66	Australia		
GGSRHD	stG480	G	39	Australia		
MD01	stG11	G	8	Australia		

Colors

Swatches HSB RGB

Recent:

Preview

Change Cancel

GroupCG: Multi-Locus Sequence Typing (Sele... | GroupCG: goeBURST Output

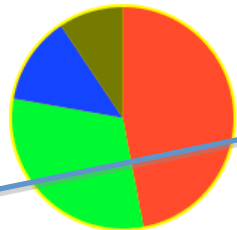
GroupCG: goeBURST Full MST Output

Legend

- Location:Australia (n = 55, 47.01%
- Location:Portugal (n = 36, 30.77%
- Location:Other (n = 15, 12.82%)
- Location:USA (n = 11, 9.4%)

Load Save

You can change the colors directly on the legend by clicking with the right mouse button on the color you want to change



PHYLOViZ

File Edit View Tools Window Help

Datasets GroupCG: Isolate Data GroupCG: Multi-Locus Sequence Typing GroupCG: goeBURST (Level 1) GroupCG: goeBURST Full MST

GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

-Groups at SLV:

0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28

Options animation speed >> 50

search >>

GroupCG: Multi-Locus Sequence Typing (Sele... GroupCG: goeBURST Output GroupCG: goeBURST Full MST Output

Legend

- Location:Australia (n = 55, 47.01%
- Location:Portugal (n = 36, 30.77%
- Location:Other (n = 15, 12.82%)
- Location:USA (n = 11, 9.4%)

Load Save

Info:

```
# tiebreaks by FRQ = 0
# tiebreaks by ID = 0

Group(s): 1
# STs = 7
# isolates = 11
# edges = 7 [ 7 0 0]
# forest edges = 6 [ 6 0 0]
# edges without ties = 4
# tiebreaks by SLV = 2
# tiebreaks by DLV = 0
# tiebreaks by TLV = 0
# tiebreaks by FRQ = 0
# tiebreaks by ID = 0

Group(s): 0
# STs = 9
# isolates = 12
# edges = 11 [ 11 0 0]
# forest edges = 8 [ 8 0 0]
# edges without ties = 5
# tiebreaks by SLV = 3
# tiebreaks by DLV = 0
# tiebreaks by TLV = 0
# tiebreaks by FRQ = 0
# tiebreaks by ID = 0
```

To visualize the algorithm result with the selected data over imposed on it, double click on it. You can still drag around the nodes.

PHYLOVIZ

File Edit View Tools Window Help

Datasets

- GroupCG
 - Isolate Data
 - Multi-Locus Sequence Typing
 - goeBURST (Level 1)
 - goeBURST Full MST

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

View: table tree Regex filter:

ST	gki	gtr	murI	mutS	recP	xpt	yqiZ
1	10	6	6	6	12	13	8
2	5	4	4	1	2	15	2
3	5	3	4	1	6	2	1
4	2	2	4	1	8	7	2
5	2	2	4	1	12	12	7
6	1	3	1	1	1	1	4
7	1	1	1	1	1	1	3
8	1	1	1	1	1	1	4
9	1	1	1	1	1	1	2
10	10	4	7	7	12	13	8
11	11	3	4	1	2	7	5
12	4	4	5	2	17	6	2
13	10	5	6	6	12	13	9
14	10	4	7	6	12	13	8
15	3	3	2	2	9	8	2
16	4	4	1	2	17	1	2
17	4	4	1	2	17	6	2
18	4	2	4	1	8	7	2
19	3	8	4	1	8	7	2
20	3	3	2	8	9	6	6
21	3	8	2	2	9	8	2
22	3	3	2	8	1	11	6
23	3	3	4	1	3	1	1
24	3	2	1	5	15	4	3
25	3	2	1	5	7	4	3
26	3	2	1	1	7	10	2

Select View Reset

You can combine multiple column results automatically and show it on the graph. Just select multiple columns and press **Select** then **View** and all combinations are displayed.

GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus Sequence Typin... GroupCG: goeBURST Output GroupCG: goeBURST Full MST Output

Legend

- murI:4 mutS:2 (n = 28, 23.93%)
- murI:4 mutS:1 (n = 24, 20.51%)
- murI:2 mutS:2 (n = 16, 13.68%)
- murI:1 mutS:1 (n = 12, 10.26%)
- murI:1 mutS:2 (n = 8, 6.84%)
- murI:1 mutS:5 (n = 6, 5.13%)
- murI:2 mutS:8 (n = 6, 5.13%)
- murI:5 mutS:2 (n = 4, 3.42%)
- murI:2 mutS:1 (n = 3, 2.56%)

Load Save

You can also display typing information onto the analyses results. In this case we are displaying combinations of the *murI* and *mutS* alleles

PHYLOViZ

File Edit View Tools Window Help

Datasets: GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

Groups at SLV:

0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28

Options > || animation speed >> 50

Info:

```
# S1s = 9
# isolates = 12
# edges = 11 [ 11 0 0]
# forest edges = 8 [ 8 0 0]
# edges without ties = 5
# tiebreaks by SLV = 3
# tiebreaks by DLV = 0
# tiebreaks by TLV = 0
# tiebreaks by FRQ = 0
# tiebreaks by ID = 0

ST: 8 Profile: 1 1 1 1 1 1 4# SLVs =
# DLVs = 1 ( 1)
# TLVs = 0 ( 0)
# SAT = 0 ( 72)
# isolates = 6
Chart details:
+ muri:1 mutS:1 100%

ST: 41 Profile: 1 1 1 9 1 1 1# SLVs =
# DLVs = 4 ( 4)
# TLVs = 3 ( 3)
# SAT = 0 ( 72)
# isolates = 1
Chart details:
+ muri:1 mutS:9 100%
```

search >>

GroupCG: Multi-Locus Sequence Typin... x GroupCG: goeBURST Output GroupCG: goeBURST Full MST Output

Legend

- muri:4 mutS:2 (n = 28, 23.93%
- muri:4 mutS:1 (n = 24, 20.51%
- muri:2 mutS:2 (n = 16, 13.68%
- muri:1 mutS:1 (n = 12, 10.26%
- muri:1 mutS:2 (n = 8, 6.84%
- muri:1 mutS:5 (n = 6, 5.13%
- muri:2 mutS:8 (n = 6, 5.13%
- muri:5 mutS:2 (n = 4, 3.42%
- muri:2 mutS:1 (n = 3, 2.50%

Load Save

Double clicking again in the algorithm displays the new selected elements.

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG: Isolate Data GroupCG: Multi-Locus Sequence Typing GroupCG: goeBURST (Level 1) GroupCG: goeBURST Full MST

GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

-Groups at SLV:

0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16

Info:

```
# tiebreaks by FRQ = 0
# tiebreaks by ID = 0

Group(s): 1
# STs = 7
# isolates = 11
# edges = 7 [ 7 0 0]
# forest edges = 6 [ 6 0 0]
# edges without ties = 4
# tiebreaks by SLV = 2
# tiebreaks by DLV = 0
# tiebreaks by TLV = 0
# tiebreaks by FRQ = 0
# tiebreaks by ID = 0

Group(s): 0 1
# STs = 16
# isolates = 23
# edges = 18 [ 18 0 0]
# forest edges = 14 [ 14 0 0]
# edges without ties = 9
```

Export view as ...

/Users/jcarrico/export.eps

Encapsulated PostScript (.eps, .epi, .epsi, .epsf)

Encapsulated PostScript (.eps, .epi, .epsi, .epsf)

MacroMedia Flash File Format (.swf)

Portable Document Format (.pdf)

PostScript (.ps)

Scalable Vector Graphics (.svg, .svgz)

Windows Enhanced Metafile (.emf)

Bitmap Formats

FreeHEP Graphics Interchange Format (.gif)

FreeHEP RAW Image Format (.raw)

FreeHEP UNIX Portable PixMap Format (.ppm)

Standard BMP Image Writer (.bmp)

Standard JPEG Image Writer (.jpg, .jpeg)

Standard PNG image writer (.png)

Standard WBMP Image Writer (.wbmp)

Other

Java Source File (for Testing) (.java)

50

Remember that you can export the final graphs with the annotations in a variety of graphical formats by pressing the **Options** and selecting Export. We recommend eps format for publication quality and png format for quick preview.

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG Isolate Data Multi-Locus Sequence Typing goeBURST (Level 1)

Groups at SLV: 0 1 2 3 goeBURST goeBURST Full MST 7 8 9 10 11 12 13 14 15 16 17 18

View Save Compute

Options animation speed >> 50 search >>

GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus Sequence Typing (Selection view) GroupCG: goeBURST Output

[Fri Mar 25 11:22:20 WET 2011] goeBURST started
goeBURST algorithm: computing groups...

[Fri Mar 25 11:22:20 WET 2011] goeBURST algorithm: integrating data...

To create a Minimum Spanning Tree (MST) using an extension of the goeBURST rules just click the Right Mouse button on the Typing Data and select Compute. You can then choose "goeBURST Full MST" algorithm

PHYLOViZ

File Edit View Tools Window Help

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x

Datasets

- GroupCG
 - Isolate Data
 - Multi-Locus Sequence Typing
 - goeBURST (Level 1)

Groups at SLV:

0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38

Options > || animation speed >>

GroupCG: Isolate Data (Selection view)

[Fri Mar 25 11:22:20 WET 2011] goeBURST started
goeBURST algorithm: computing groups...

[Fri Mar 25 11:22:20 WET 2011] goeBURST algorithm: integrating data...

MST Algorithm Configuration

Distance

Distance: eBURST Distance

This list contains only distances compatible with the current dataset.

< Back Next > Finish Cancel Help

PHYLOVIZ

File Edit View Tools Window Help

Datasets GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST

Groups

1

Level: 6

Get Groups

Save Groups

Options animation speed >>

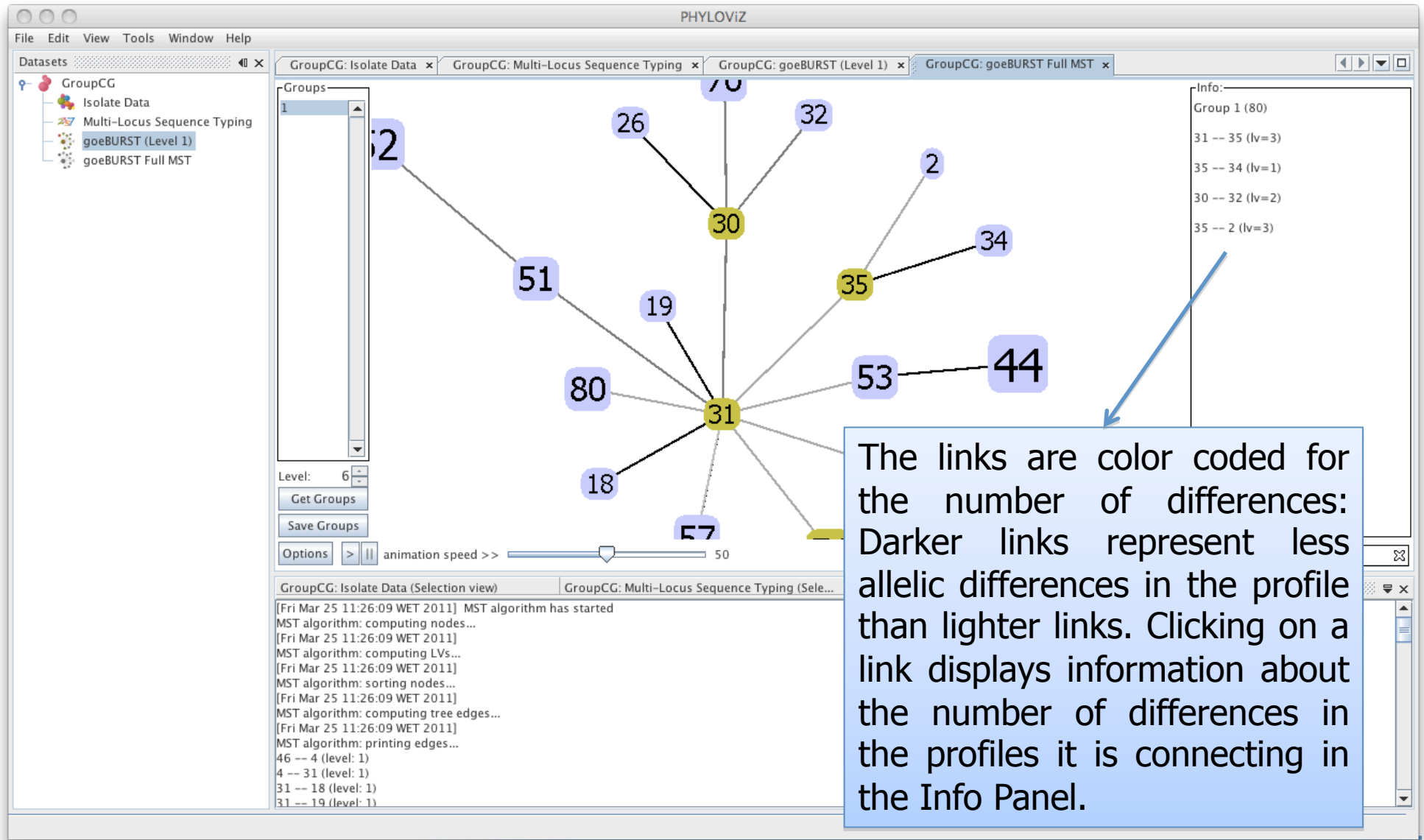
GroupCG: Isolate Data (Selection view) GroupCG: Multi-Locus

[Fri Mar 25 11:26:09 WET 2011] MST algorithm has started
MST algorithm: computing nodes...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: computing LVs...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: sorting nodes...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: computing tree edges...
[Fri Mar 25 11:26:09 WET 2011]
MST algorithm: printing edges...
46 -- 4 (level: 1)
4 -- 31 (level: 1)
31 -- 18 (level: 1)
31 -- 19 (level: 1)

BURST Full MST Output

...and Double Click on goeBURST Full MST to display the result

You can divide the MST in groups by keeping only links up to a determined level. Click the **Get Groups** button to divide the MST into different groups. Clicking on the **Save Groups** button, a column is added to the Isolate Data file identifying the group that each ST belongs at the defined level.



PHYLOVIZ

File Edit View Tools Window Help

Datasets

- GroupCG
 - Isolate Data
 - Multi-Locus Sequence Typing
 - goeBURST (Level 1)
 - goeBURST Full MST
 - goeBURST (Level 3)

Groups

1

Level: 6

Get Groups

Save Group

Options > animation speed > 50

search >>

GroupCG: Isolate Data (Selection v...)

CC 4 has 1 STs:
ST 57 (1) 0 0 0 0 (0 0 0 80) *

CC 4 has 0/0 selected edges

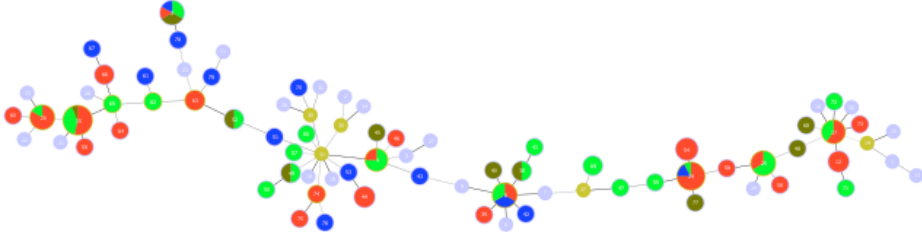
CC 5 has 1 STs:
ST 68 (1) 0 0 0 0 (0 0 0 80) *

CC 5 has 0/0 selected edges

[Fri Mar 25 11:40:41 WET 2011] goeB
[Fri Mar 25 11:40:41 WET 2011] goeB

GroupCG: goeBURST Full MST Output

GroupCG: goeBURST Output



The goeBURST Full MST algorithm also allows the visual exploration of how the Minimum Spanning Tree was constructed and how it could be subdivided by removing links

The **Level** box can be altered to only allow links between two nodes of distances equal or less than the number it indicates. This means that allows links to be drawn if the differences are 6 or less.

PHYLOVIZ

File Edit View Tools Window Help

Datasets

- GroupCG
 - Isolate Data
 - Multi-Locus Sequence Typing
 - goeBURST (Level 1)
 - goeBURST Full MST
 - goeBURST (Level 3)

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

Groups

1

Level: 5

Get Groups

Save Groups

Options > || animation speed >> 50

search >>

GroupCG: Isolate Data (Selection v... GroupCG: Mu

CC 4 has 1 STs:
ST 57 (1) 0 0 0 0 (0 0 0 80) *

CC 4 has 0/0 selected edges

CC 5 has 1 STs:
ST 68 (1) 0 0 0 0 (0 0 0 80) *

CC 5 has 0/0 selected edges

[Fri Mar 25 11:40:41 WET 2011] goeBURST algorithm
[Fri Mar 25 11:40:41 WET 2011] goeBURST algorithm

CG: goeBURST Full MST Output GroupCG: goeBURST Output

In the dataset used in this example lowering the level to 5, you can see a group detaching. This means that the connection between the two nodes had at least 6 differences

PHYLOVIZ

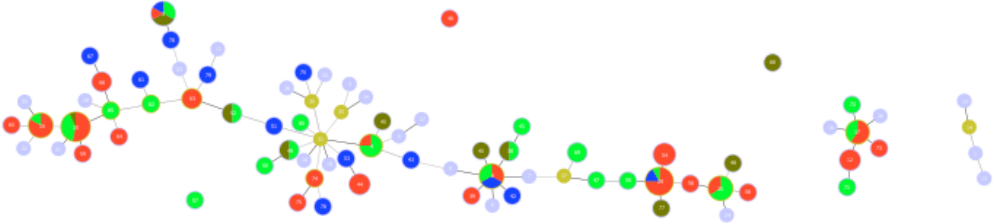
File Edit View Tools Window Help

Datasets GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

- GroupCG
 - Isolate Data
 - Multi-Locus Sequence Typing
 - goeBURST (Level 1)
 - goeBURST Full MST
 - goeBURST (Level 3)

-Groups-

1



Level: 3

Get Groups

Save Groups

Options > animation s

GroupCG: Isolate Data (Select output GroupCG: goeBURST Full MST Output GroupCG: goeBURST Output x

search >>

CC 4 has 1 STs:
ST 57 (1) 0 0 0 0 (0 0 0 80) *

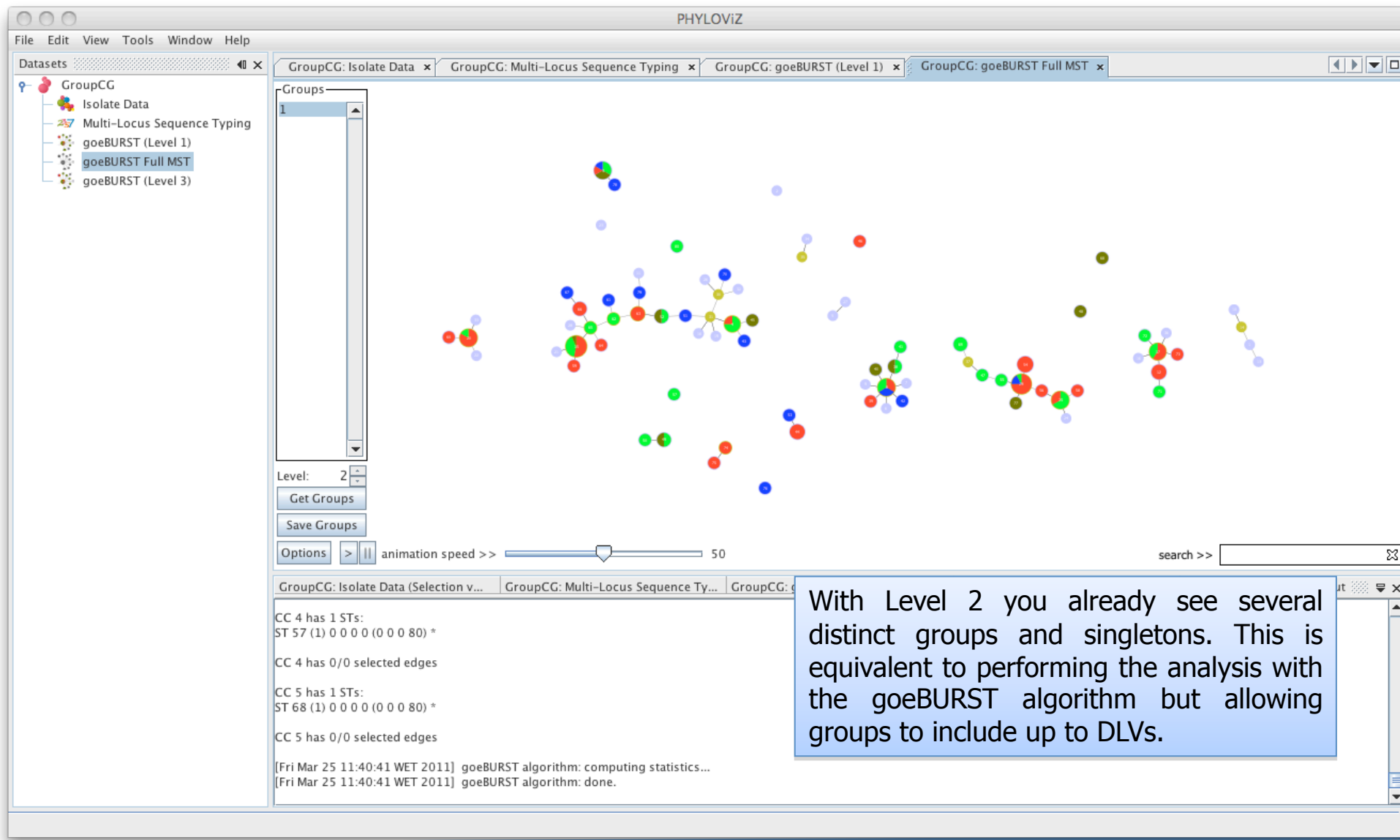
CC 4 has 0/0 selected edges

CC 5 has 1 STs:
ST 68 (1) 0 0 0 0 (0 0 0 80) *

CC 5 has 0/0 selected edges

[Fri Mar 25 11:40:41 WET 2011] goeBURST algorithm: computing statistics...
[Fri Mar 25 11:40:41 WET 2011] goeBURST algorithm: done.

With Level 3 you already see 3 distinct groups and 3 singletons appearing. This is running goeBURST algorithm allowing groups to include up to TLVs.



PHYLOViZ

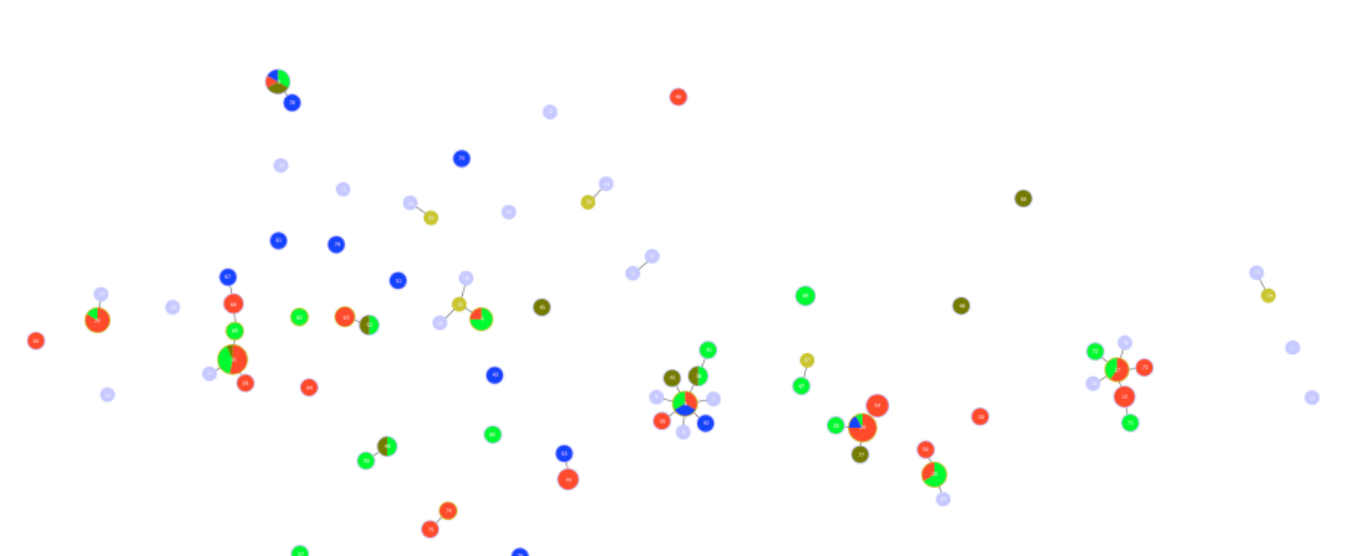
File Edit View Tools Window Help

Datasets: GroupCG

- Isolate Data
- Multi-Locus Sequence Typing
- goeBURST (Level 1)
- goeBURST Full MST
- goeBURST (Level 3)

GroupCG: Isolate Data x GroupCG: Multi-Locus Sequence Typing x GroupCG: goeBURST (Level 1) x GroupCG: goeBURST Full MST x

Groups: 1



Level: 1

Get Groups

Save Groups

Options animation speed >> 50

GroupCG: Isolate Data (Selection v... GroupCG: Multi-Locus Sequence Ty... GroupCG: goeBURST Output

CC 4 has 1 STs:
ST 57 (1) 0 0 0 0 (0 0 0 80) *

CC 4 has 0/0 selected edges

CC 5 has 1 STs:
ST 68 (1) 0 0 0 0 (0 0 0 80) *

CC 5 has 0/0 selected edges

[Fri Mar 25 11:40:41 WET 2011] goeBURST algorithm: computing statistics...
[Fri Mar 25 11:40:41 WET 2011] goeBURST algorithm: done.

Output

With Level 1 you already see the equivalent of running the goeBURST algorithm with the default parameter (allowing groups to include only SLVs). Pressing the **Get Groups** button would divide the observed groups allowing for separate manipulation.