NetRAX Experiment Evaluation

February 10, 2021

[1]:

```
%matplotlib inline
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
sns.set(style="darkgrid")
```

[2]:

```
def bic_stats(df):
    print("Inferred BIC better or equal: " + str(len(df[df['bic_inferred'] <=␣
 ↪df['bic_true']])))
    print("Inferred BIC worse: " + str(len(df[df['bic_inferred'] >␣
 ↪df['bic_true']])))
    df['bic_diff'].plot.hist(bins=100, alpha=0.5, title='(bic_true -␣
 ↪bic_inferred) / bic_true\n value >0 means inferred BIC was better')

def logl_stats(df):
    print("Inferred loglh better or equal: " + str(len(df[df['logl_inferred']␣
 ↪>= df['logl_true']])))
    print("Inferred loglh worse: " + str(len(df[df['logl_inferred'] <␣
 ↪df['logl_true']])))
    df['logl_diff'].plot.hist(bins=100, alpha=0.5, title='(logl_true -␣
 ↪logl_inferred) / logl_true\n value <0 means inferred logl was better')

def reticulation_stats(df):
    print("Inferred n_reticulations less: " +␣
 ↪str(len(df[df['n_reticulations_inferred'] < df['n_reticulations']])))
    print("Inferred n_reticulations equal: " +␣
 ↪str(len(df[df['n_reticulations_inferred'] == df['n_reticulations']])))
    print("Inferred n_reticulations more: " +␣
 ↪str(len(df[df['n_reticulations_inferred'] > df['n_reticulations']])))

def weirdness_stats(df):
    df['true_network_weirdness'].plot.hist(bins=10, alpha=0.5, range=(0,1),␣
 ↪title='True network weirdness')

def zero_branches_stats(df):
    df['near_zero_branches_raxml'].plot.hist(bins=10, alpha=0.5,␣
 ↪title='Near-zero branches raxml')
```

```
def distances(df):
    fig, axes = plt.subplots(3, 2, constrained_layout=True)
    df['hardwired_cluster_distance'].plot.hist(bins=10, alpha=0.5,␣
 ↪title='Hardwired cluster distance', ax=axes[0,0])
    df['softwired_cluster_distance'].plot.hist(bins=10, alpha=0.5,␣
 ↪title='Softwired cluster distance', ax=axes[0,1])
    df['displayed_trees_distance'].plot.hist(bins=10, alpha=0.5,␣
 ↪title='Displayed trees distance', ax=axes[1,0])
    df['tripartition_distance'].plot.hist(bins=10, alpha=0.5,␣
 ↪title='Tripartition distance', ax=axes[1,1])
    df['nested_labels_distance'].plot.hist(bins=10, alpha=0.5, title='Nested␣
 ↪labels distance', ax=axes[2,0])
    df['path_multiplicity_distance'].plot.hist(bins=10, alpha=0.5, title='Path␣
 ↪multiplicity distance', ax=axes[2,1])

def build_stats(df):
    plt.figure(0)
    bic_stats(df)
    print("")
    plt.figure(1)
    logl_stats(df)
    print("")
    plt.figure(2)
    reticulation_stats(df)
    print("")
    plt.figure(3)
    weirdness_stats(df)
    print("")
    plt.figure(4)
    zero_branches_stats(df)
    print("")
    plt.figure(5)
    distances(df)
```

Load the result CSV:

[3]:

```
df = pd.read_csv('small_network_results.csv')
#df = pd.read_csv('medium_network_norandom_results.csv')
#df = pd.read_csv('small_network_uniform_results.csv')
#df = pd.read_csv('medium_network_norandom_uniform_results.csv')

df['bic_diff'] = (df['bic_true'] - df['bic_inferred']) / df['bic_true']
df['logl_diff'] = (df['logl_true'] - df['logl_inferred']) / df['logl_true']
```

[4]:

```
pd.set_option('display.max_columns', None)
df.head()
```

[4]:

```
                                                name  n_taxa  n_trees  \
0  datasets_small_network_0_0/0_9_taxa_1_reticula…      9        2
1  datasets_small_network_0_0/0_9_taxa_1_reticula…      9        2
2  datasets_small_network_0_0/0_9_taxa_1_reticula…      9        2
3  datasets_small_network_0_0/0_9_taxa_1_reticula…      9        2
4  datasets_small_network_0_0/0_9_taxa_1_reticula…      9        2

   n_reticulations  msa_size     sampling_type simulation_type  \
0                1       101  PERFECT_SAMPLING          CELINE
1                1       101  PERFECT_SAMPLING          CELINE
2                1       101  PERFECT_SAMPLING          CELINE
3                1       101  PERFECT_SAMPLING          CELINE
4                1       201  PERFECT_SAMPLING          CELINE

                                       celine_params  \
0  {'to': 0.29257489911596035| 'lambda': 13.92596…
1  {'to': 0.29257489911596035| 'lambda': 13.92596…
2  {'to': 0.29257489911596035| 'lambda': 13.92596…
3  {'to': 0.29257489911596035| 'lambda': 13.92596…
4  {'to': 0.29257489911596035| 'lambda': 13.92596…

                   seqgen_params  near_zero_branches_raxml  \
0  -mHKY -t3.0 -f0.3|0.2|0.2|0.3                         1
1  -mHKY -t3.0 -f0.3|0.2|0.2|0.3                         1
2  -mHKY -t3.0 -f0.3|0.2|0.2|0.3                         1
3  -mHKY -t3.0 -f0.3|0.2|0.2|0.3                         1
4  -mHKY -t3.0 -f0.3|0.2|0.2|0.3                         0

   n_equal_tree_pairs  true_network_weirdness  \
0                   0                       0
1                   0                       0
2                   0                       0
3                   0                       0
4                   0                       0

                                   true_network_path  \
0  datasets_small_network_0_0/0_9_taxa_1_reticula…
1  datasets_small_network_0_0/0_9_taxa_1_reticula…
2  datasets_small_network_0_0/0_9_taxa_1_reticula…
3  datasets_small_network_0_0/0_9_taxa_1_reticula…
4  datasets_small_network_0_0/0_9_taxa_1_reticula…

                               inferred_network_path likelihood_type  \
0  datasets_small_network_0_0/0_9_taxa_1_reticula…         AVERAGE
1  datasets_small_network_0_0/0_9_taxa_1_reticula…         AVERAGE
2  datasets_small_network_0_0/0_9_taxa_1_reticula…            BEST
3  datasets_small_network_0_0/0_9_taxa_1_reticula…            BEST
```

```
4  datasets_small_network_0_0/0_9_taxa_1_reticula…         AVERAGE

  brlen_linkage_type  start_type  timeout  n_random_start_networks  \
0             LINKED  FROM_RAXML        0                        0
1             LINKED      RANDOM        0                        5
2             LINKED  FROM_RAXML        0                        0
3             LINKED      RANDOM        0                        5
4             LINKED  FROM_RAXML        0                        0

   n_parsimony_start_networks  runtime_inference  n_reticulations_inferred  \
0                           0            403.473                         0
1                           5           4479.135                         0
2                           0            112.167                         0
3                           5           1381.504                         0
4                           0            191.855                         0

      bic_true   logl_true  bic_inferred  logl_inferred    bic_raxml  \
0  1161.790768 -451.460827   1139.928369    -454.154318  1139.928108
1  1161.790768 -451.460827   1139.927152    -454.153709  1139.928108
2  1161.778885 -451.454886   1139.928369    -454.154318  1139.928108
3  1161.778885 -451.454886   1139.941146    -454.160706  1139.928108
4  2046.490494 -880.735187   2035.762447    -890.372222  2035.762098

   logl_raxml  rf_absolute_raxml  rf_relative_raxml  rf_absolute_inferred  \
0 -454.154187                 -1                 -1                    -1
1 -454.154187                 -1                 -1                    -1
2 -454.154187                 -1                 -1                    -1
3 -454.154187                 -1                 -1                    -1
4 -890.372048                 -1                 -1                    -1

   rf_relative_inferred  hardwired_cluster_distance  \
0                    -1                         4.0
1                    -1                         4.0
2                    -1                         4.0
3                    -1                         4.0
4                    -1                         4.0

   softwired_cluster_distance  displayed_trees_distance  \
0                         5.5                       1.5
1                         5.5                       1.5
2                         5.5                       1.5
3                         4.5                       1.5
4                         6.5                       1.5

   tripartition_distance  nested_labels_distance  path_multiplicity_distance  \
0                    5.5                     7.0                         6.0
1                    5.5                     7.0                         6.0
```

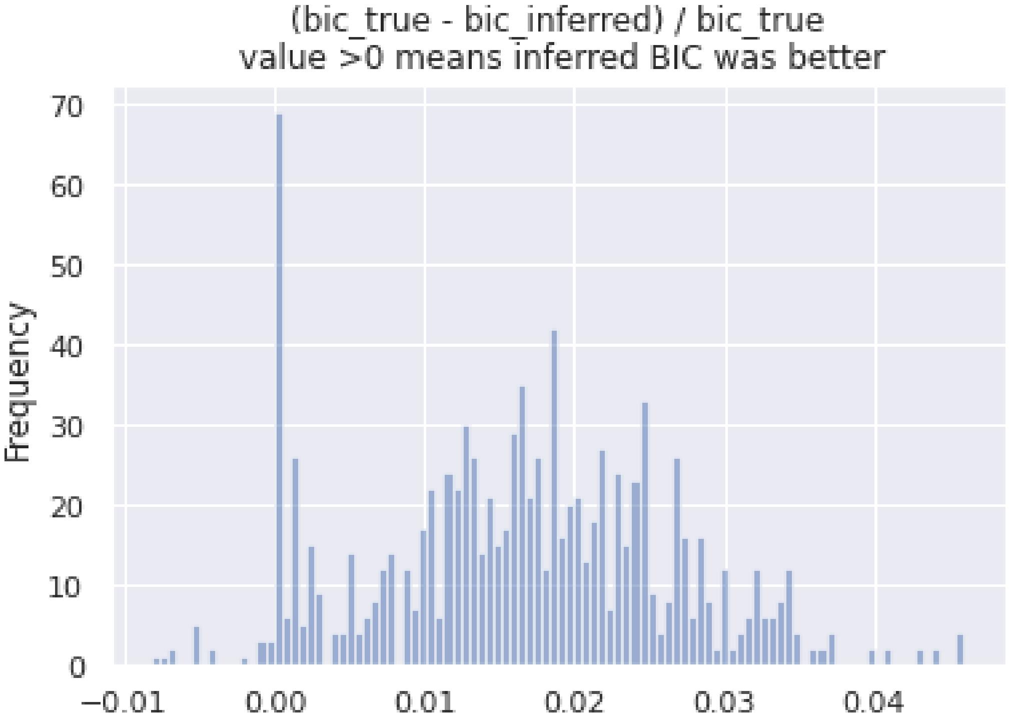
```
2                    5.5                     7.0                          6.0
3                    5.5                     7.0                          6.0
4                    5.5                     7.0                          6.0

   bic_diff  logl_diff
0  0.018818  -0.005966
1  0.018819  -0.005965
2  0.018808  -0.005979
3  0.018797  -0.005994
4  0.005242  -0.010942
```

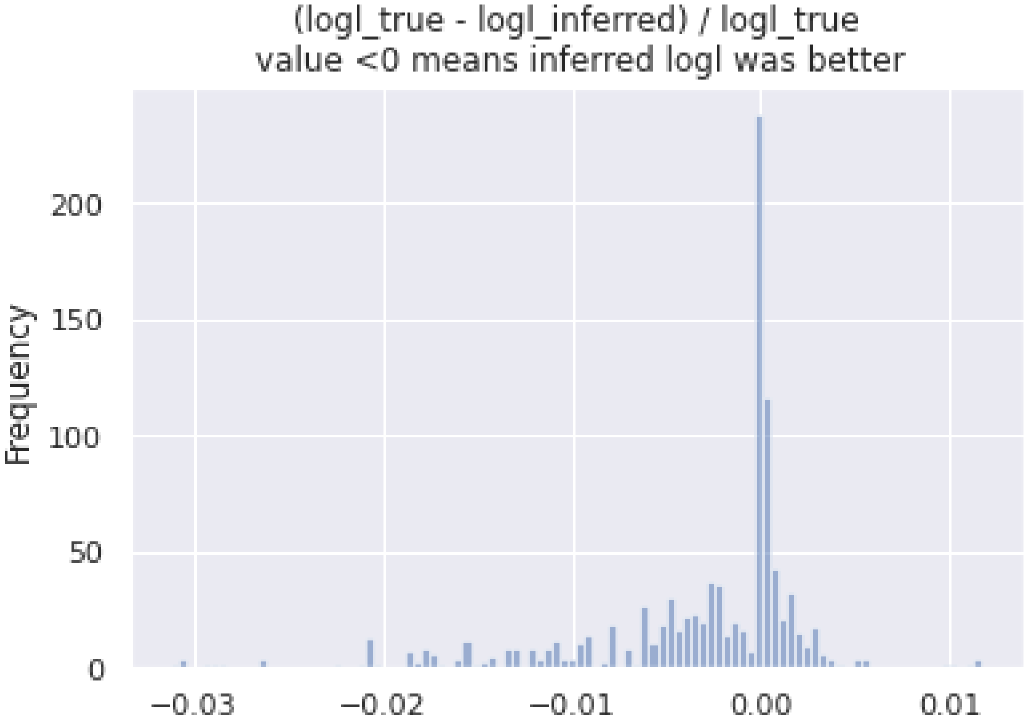
[5]:
```
df.columns
```

[5]:
```
Index(['name', 'n_taxa', 'n_trees', 'n_reticulations', 'msa_size',
       'sampling_type', 'simulation_type', 'celine_params', 'seqgen_params',
       'near_zero_branches_raxml', 'n_equal_tree_pairs',
       'true_network_weirdness', 'true_network_path', 'inferred_network_path',
       'likelihood_type', 'brlen_linkage_type', 'start_type', 'timeout',
       'n_random_start_networks', 'n_parsimony_start_networks',
       'runtime_inference', 'n_reticulations_inferred', 'bic_true',
       'logl_true', 'bic_inferred', 'logl_inferred', 'bic_raxml', 'logl_raxml',
       'rf_absolute_raxml', 'rf_relative_raxml', 'rf_absolute_inferred',
       'rf_relative_inferred', 'hardwired_cluster_distance',
       'softwired_cluster_distance', 'displayed_trees_distance',
       'tripartition_distance', 'nested_labels_distance',
       'path_multiplicity_distance', 'bic_diff', 'logl_diff'],
      dtype='object')
```

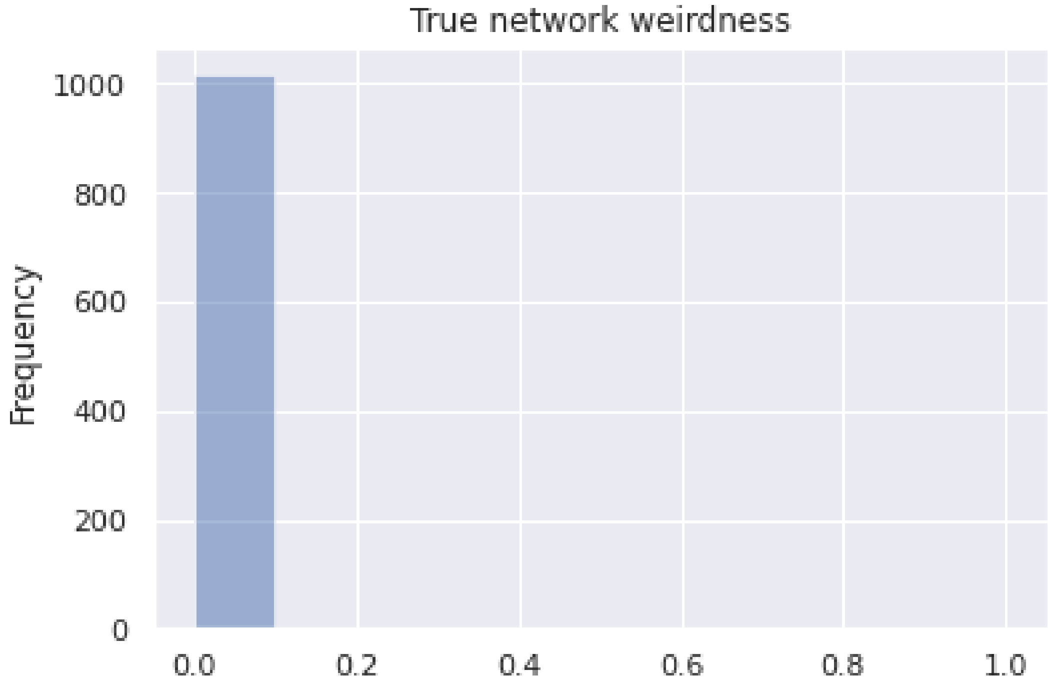
[6]:
```
build_stats(df)
```

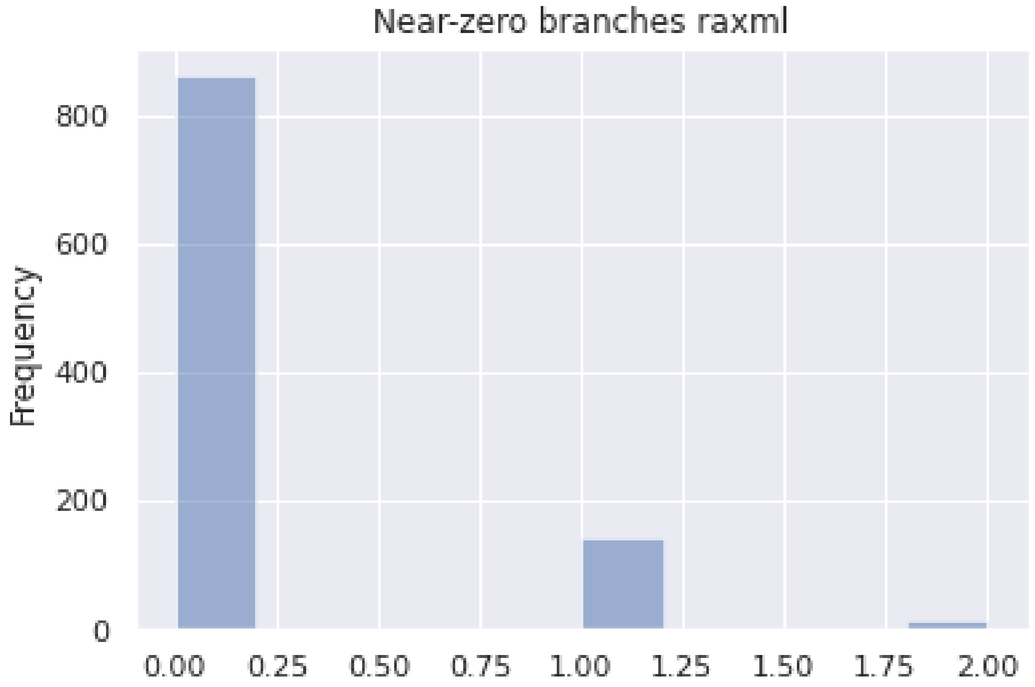
```
Inferred BIC better or equal: 977
Inferred BIC worse: 39

Inferred loglh better or equal: 452
Inferred loglh worse: 564

Inferred n_reticulations less: 912
Inferred n_reticulations equal: 104
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
10
20
30
40
50
60
70
−0.01
0.00
0.01
0.02
0.03
0.04

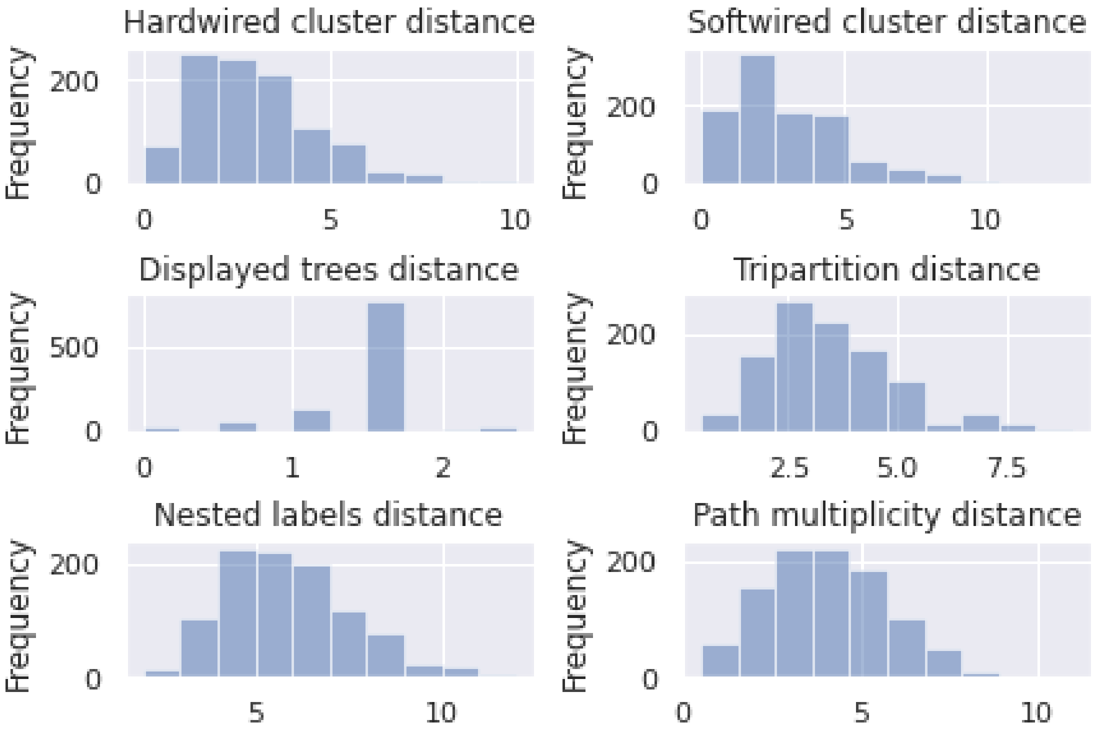

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
50
100
150
200
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
1000
800
600
400
200
0
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
800
600
400
200
0
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

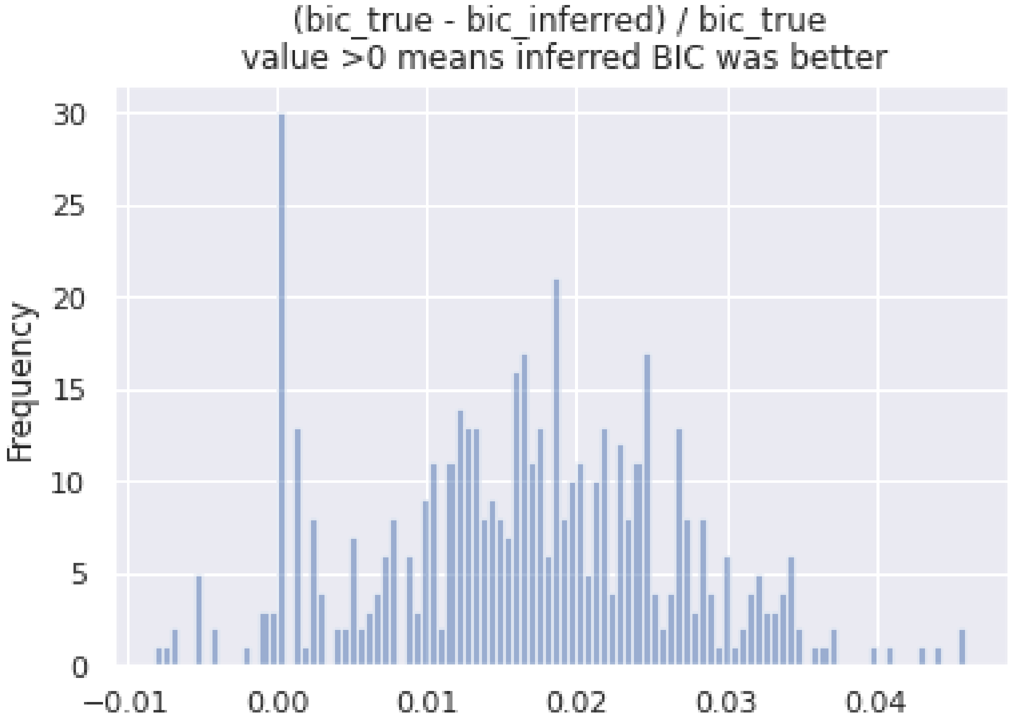
```
<Figure size 432x288 with 0 Axes>
```

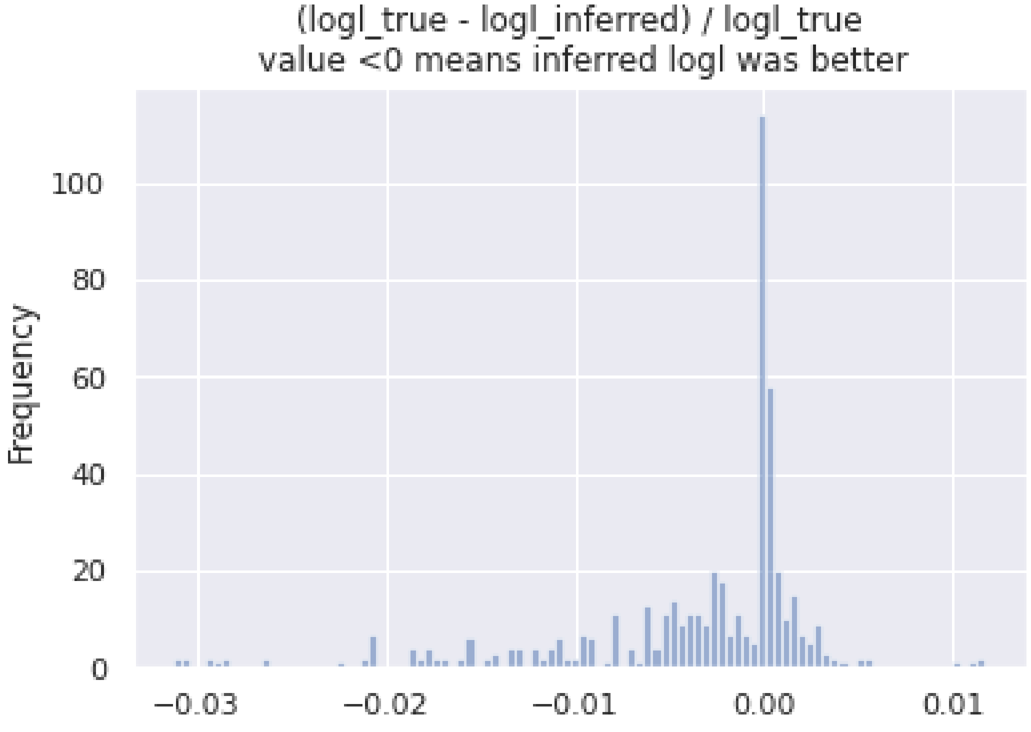


1 Plots for starting with raxml-ng best tree only

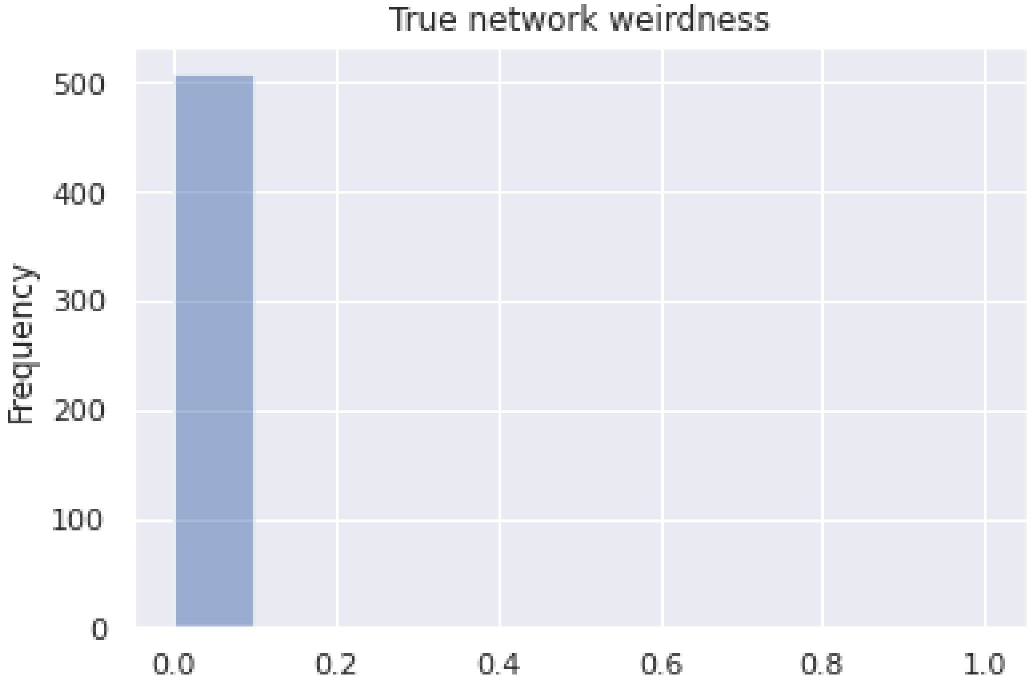
[7]:
```
df_raxml_only = df.query('start_type == "FROM_RAXML"')
build_stats(df_raxml_only)
```

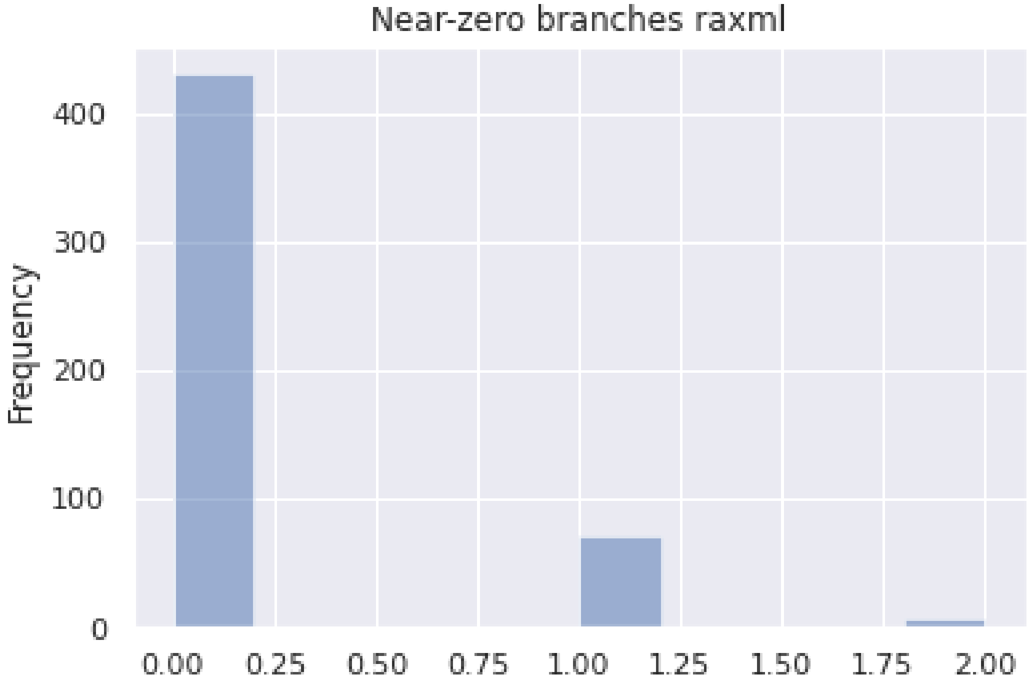
```
Inferred BIC better or equal: 474
Inferred BIC worse: 34

Inferred loglh better or equal: 212
Inferred loglh worse: 296

Inferred n_reticulations less: 462
Inferred n_reticulations equal: 46
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
5
10
15
20
25
30
−0.01
0.00
0.01
0.02
0.03
0.04

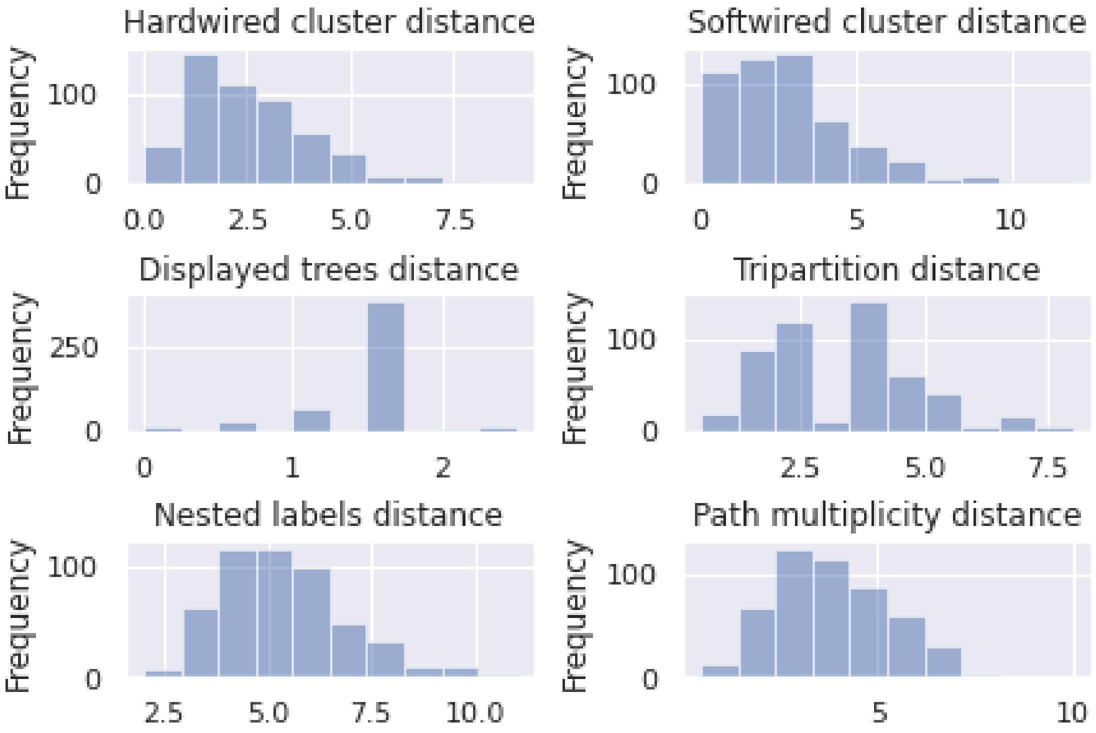

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
20
40
60
80
100
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
100
200
300
400
500
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
100
200
300
400
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

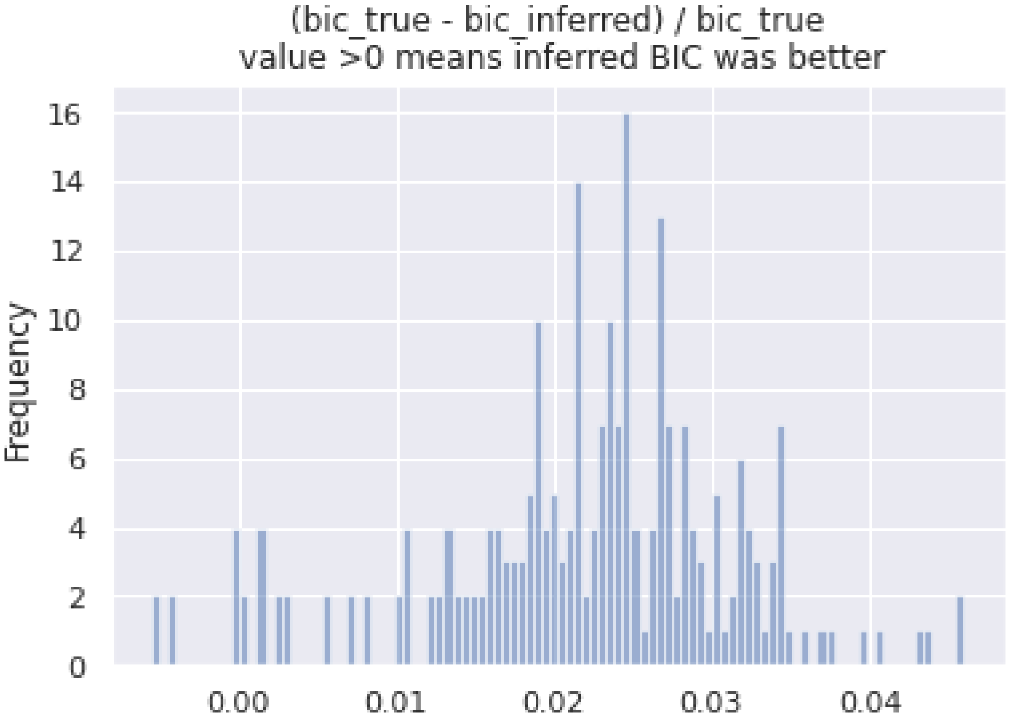
```
<Figure size 432x288 with 0 Axes>
```

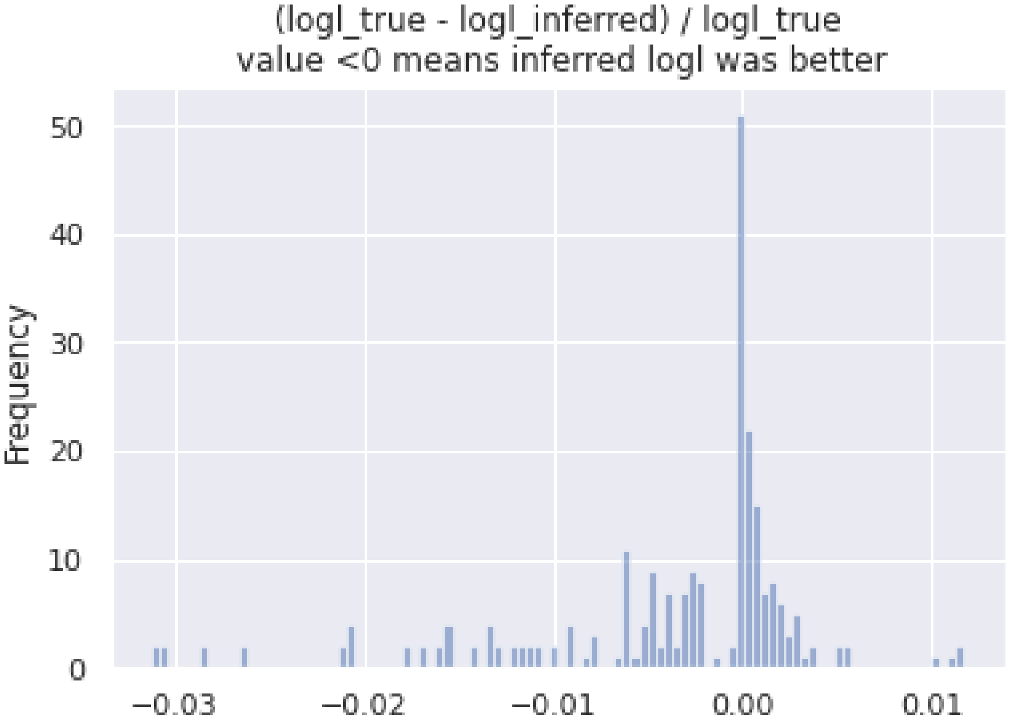


1.1 Plots for MSA_size ~ 100*n_trees

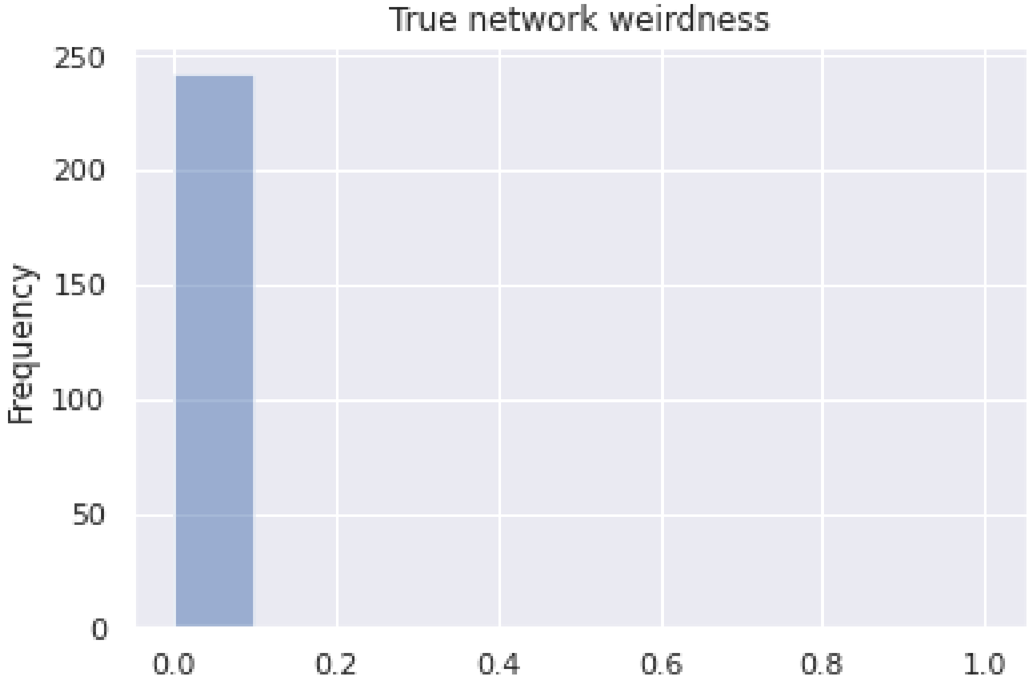
[8]:
```
df_raxml_only_msasize_100 = df_raxml_only.query('msa_size == 101')
build_stats(df_raxml_only_msasize_100)
```

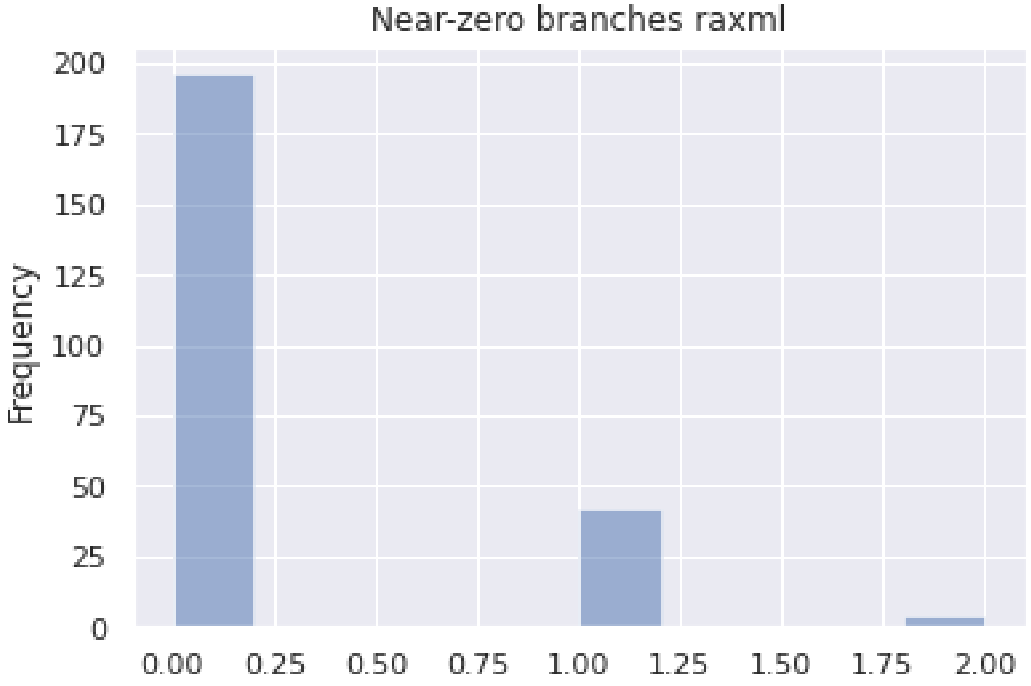
```
Inferred BIC better or equal: 234
Inferred BIC worse: 8

Inferred loglh better or equal: 114
Inferred loglh worse: 128

Inferred n_reticulations less: 230
Inferred n_reticulations equal: 12
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
2
4
6
8
10
12
14
16
0.00
0.01
0.02
0.03
0.04

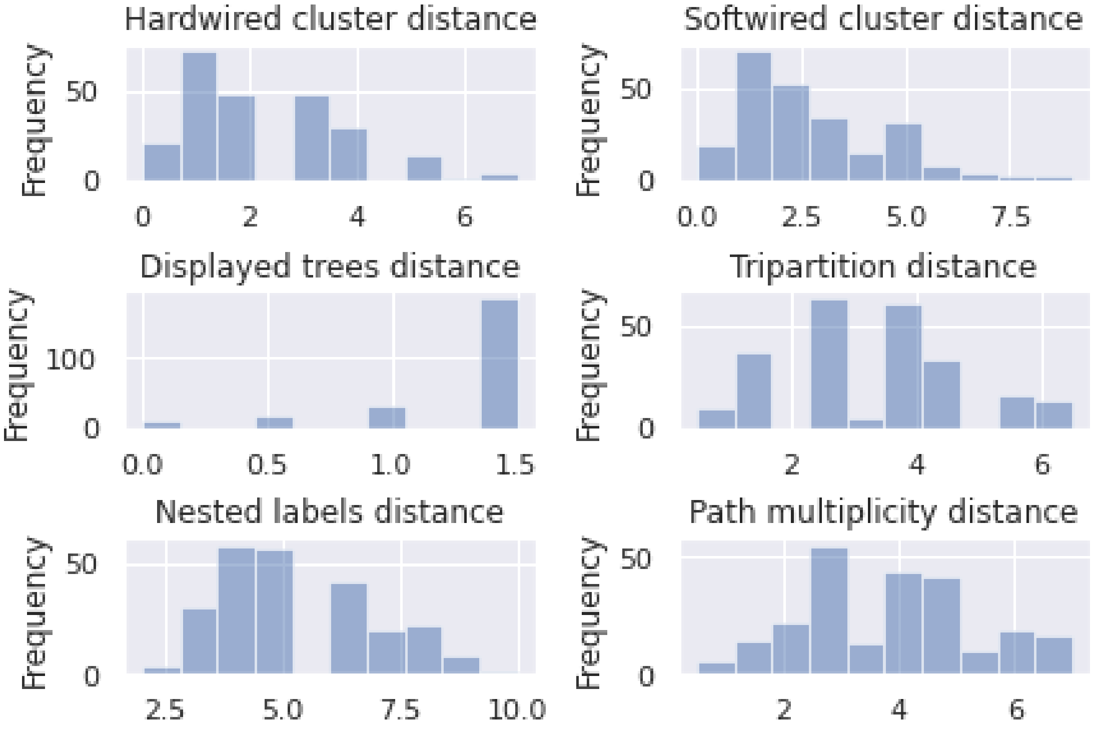

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
10
20
30
40
50
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
250
200
150
100
50
0
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
200
175
150
125
100
75
50
25
0
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

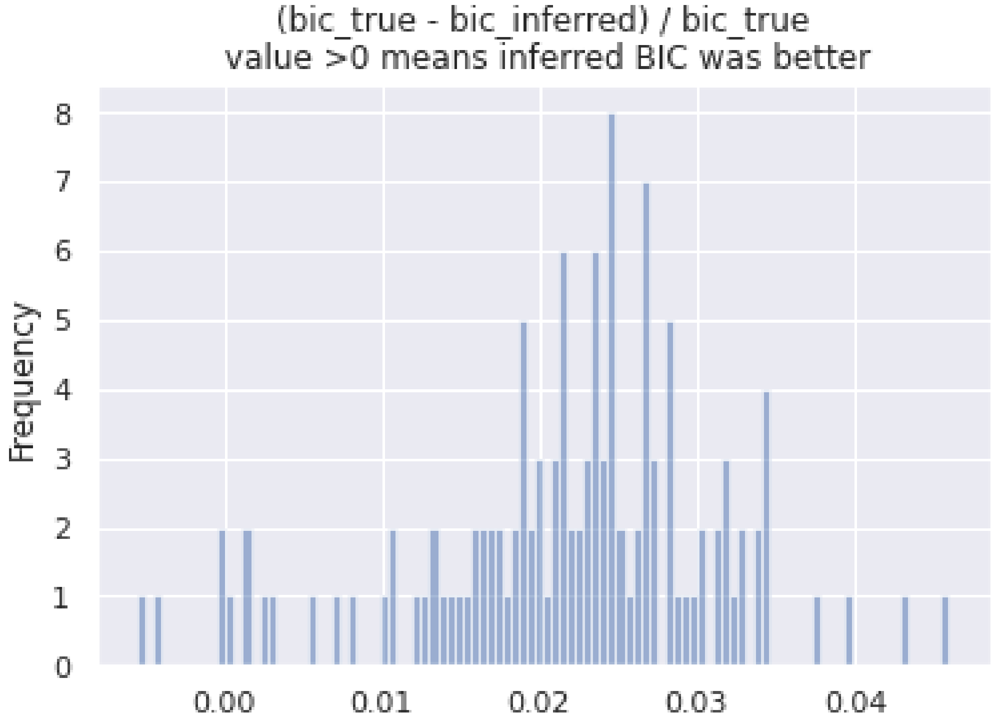
```
<Figure size 432x288 with 0 Axes>
```

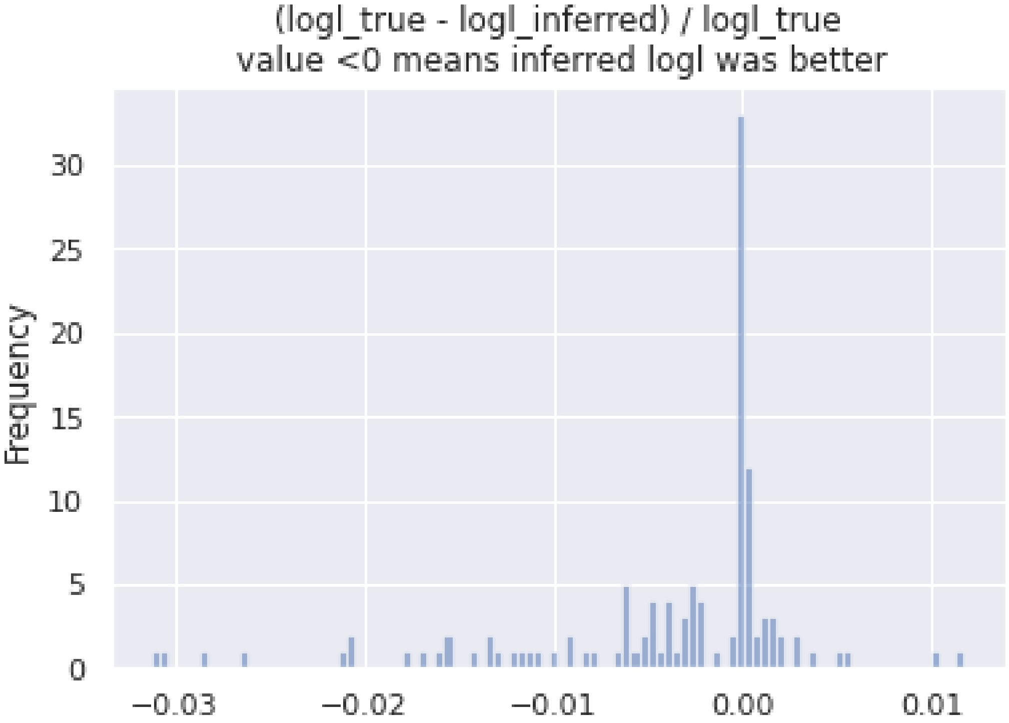


1.1.1 Plots for LikelihodType.AVERAGE

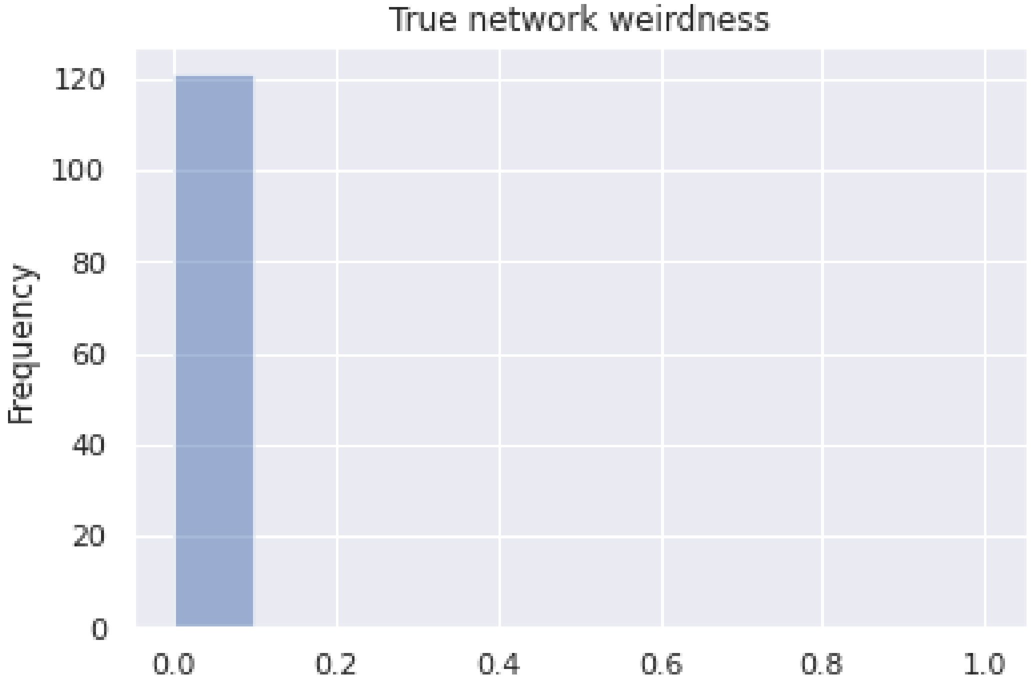
[9]:
```
df_raxml_only_msasize_100_average = df_raxml_only_msasize_100.
 ↪query('likelihood_type == "AVERAGE"')
build_stats(df_raxml_only_msasize_100_average)
```

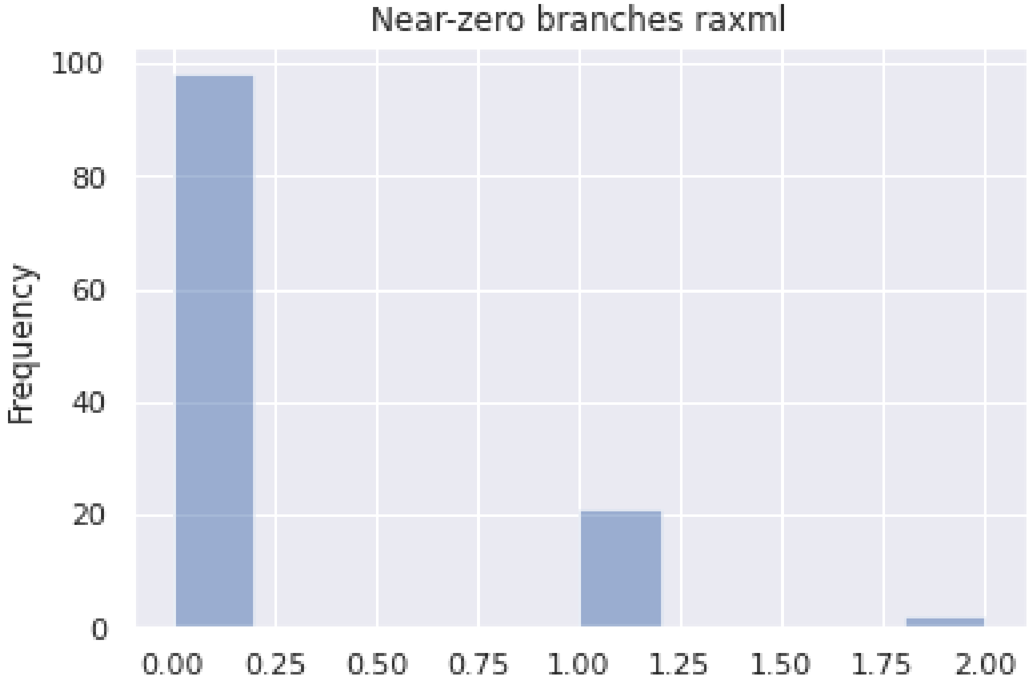
```
Inferred BIC better or equal: 117
Inferred BIC worse: 4

Inferred loglh better or equal: 53
Inferred loglh worse: 68

Inferred n_reticulations less: 115
Inferred n_reticulations equal: 6
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
1
2
3
4
5
6
7
8
0.00
0.01
0.02
0.03
0.04

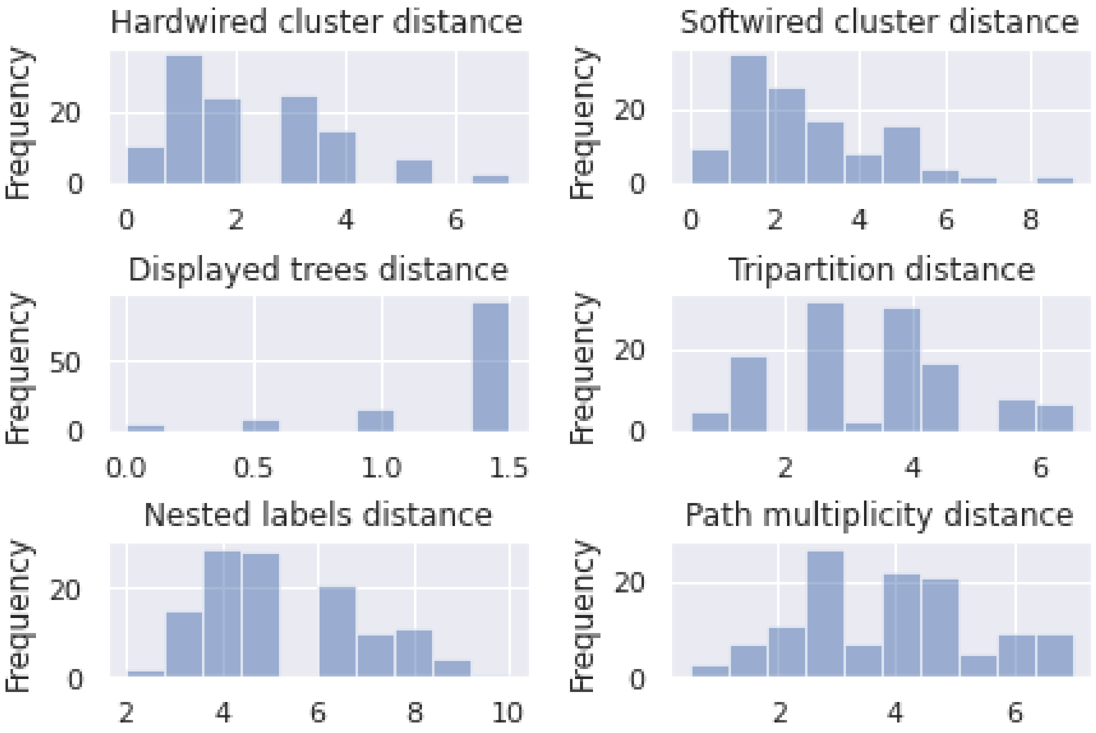

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
5
10
15
20
25
30
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

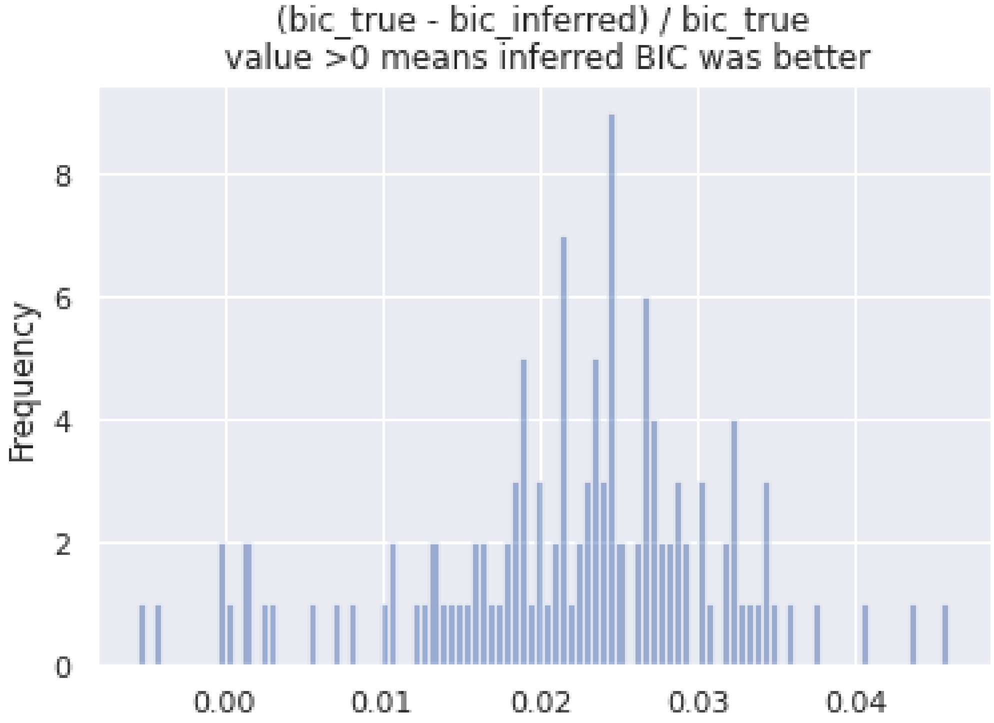
<Figure size 432x288 with 0 Axes>

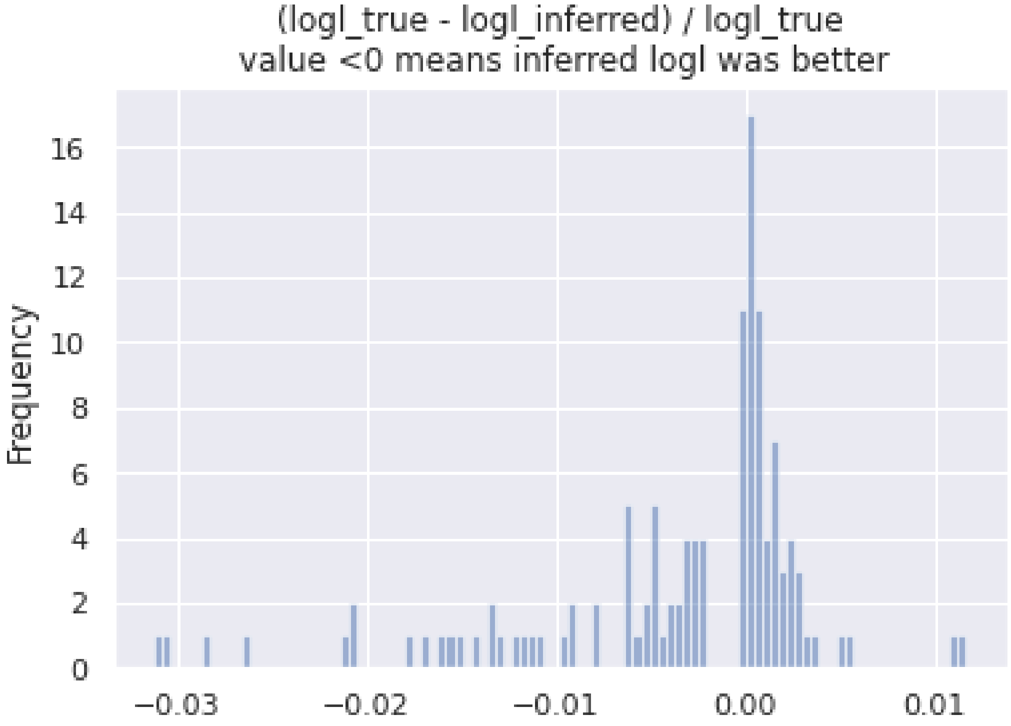


1.1.2 Plots for LikelihoodType.BEST

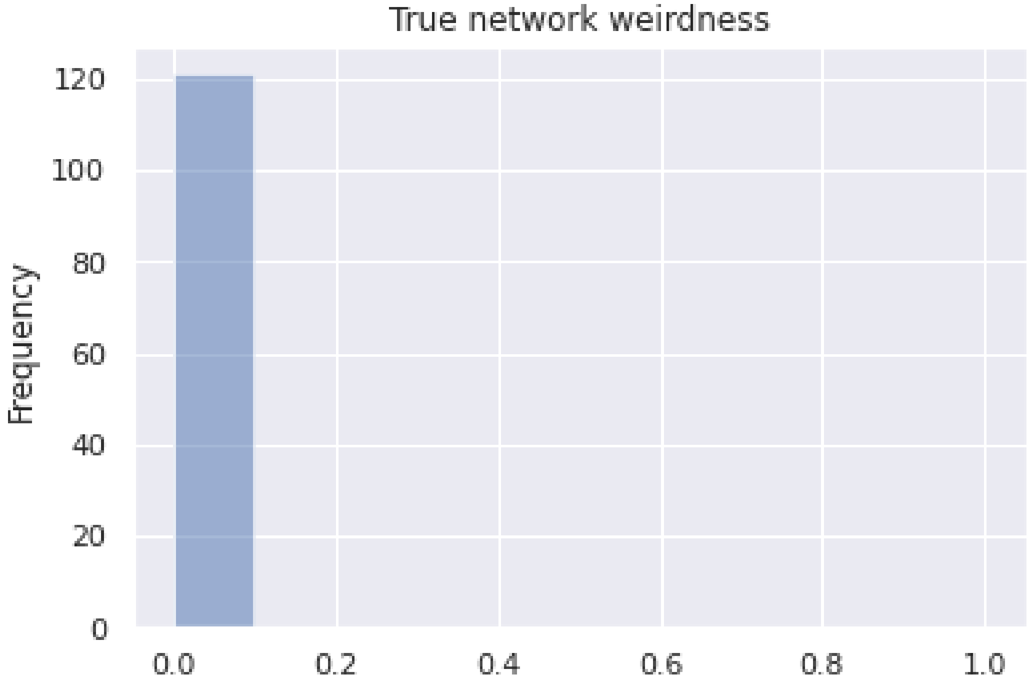
[10]:
```
df_raxml_only_msasize_100_best = df_raxml_only_msasize_100.
 ↪query('likelihood_type == "BEST"')
build_stats(df_raxml_only_msasize_100_best)
```

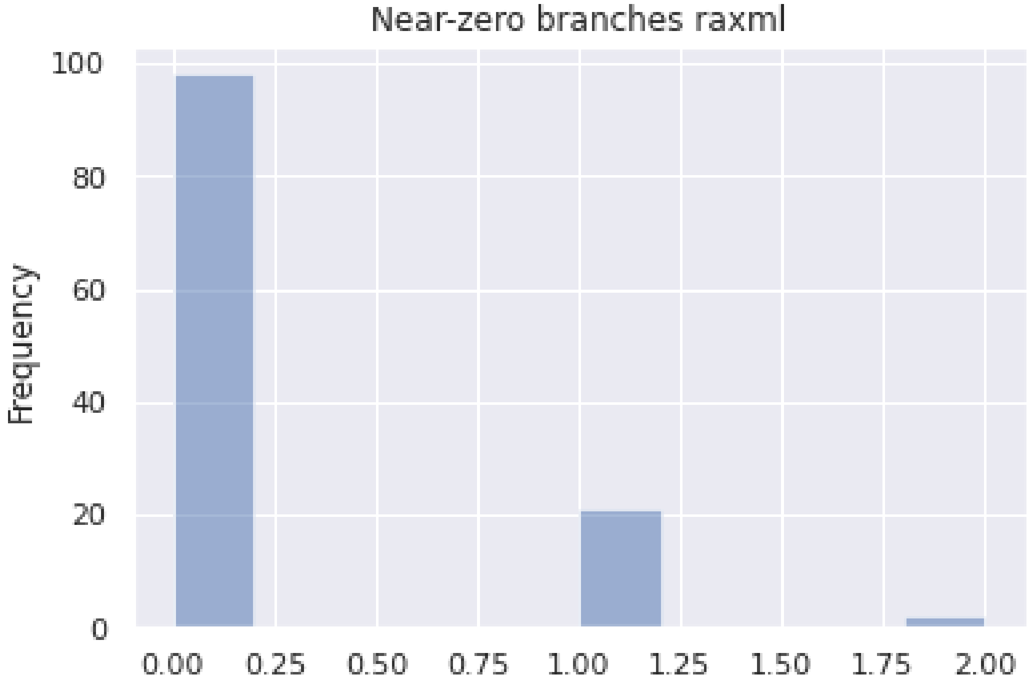
```
Inferred BIC better or equal: 117
Inferred BIC worse: 4

Inferred loglh better or equal: 61
Inferred loglh worse: 60

Inferred n_reticulations less: 115
Inferred n_reticulations equal: 6
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
2
4
6
8
0.00
0.01
0.02
0.03
0.04

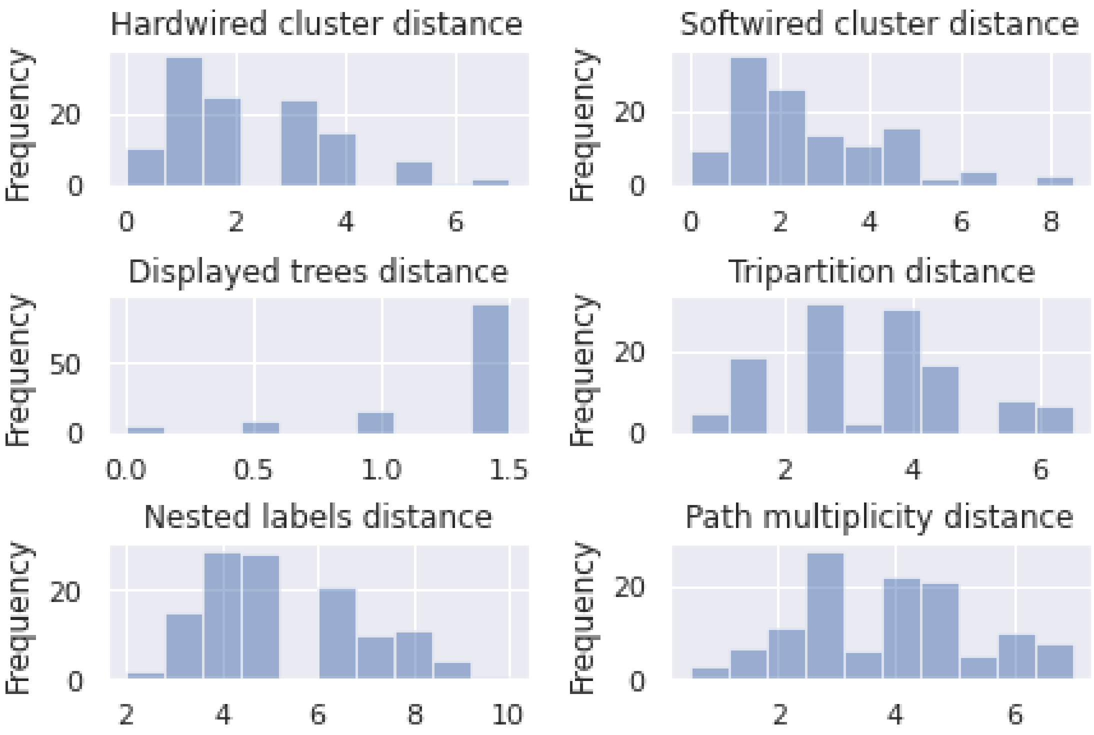

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
2
4
6
8
10
12
14
16
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

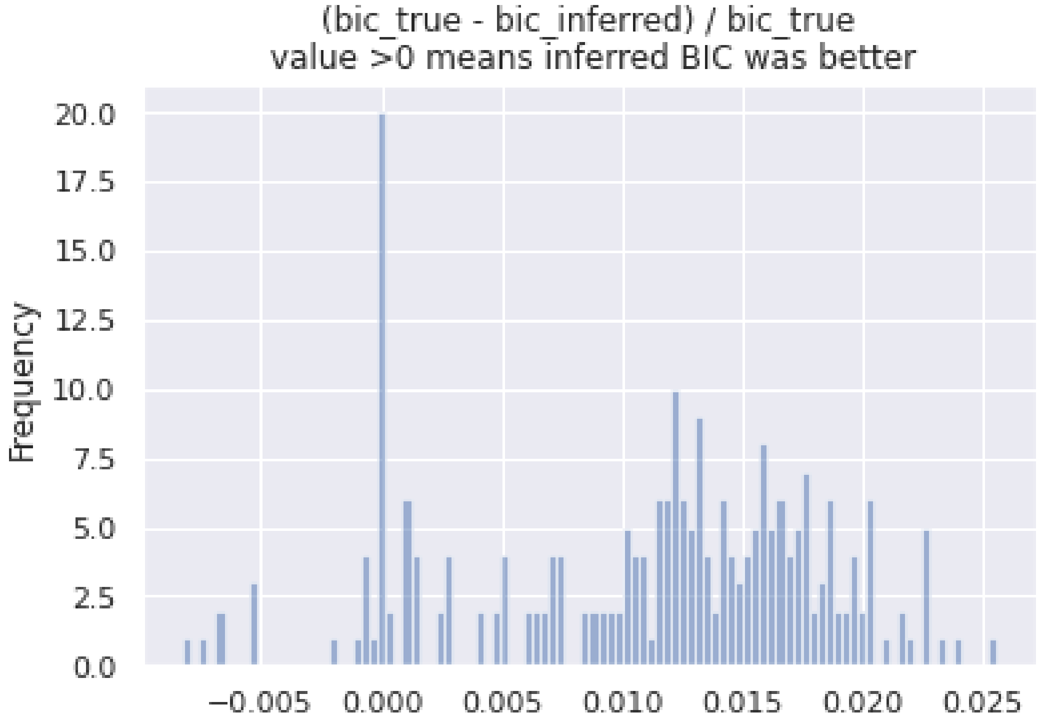
```
<Figure size 432x288 with 0 Axes>
```

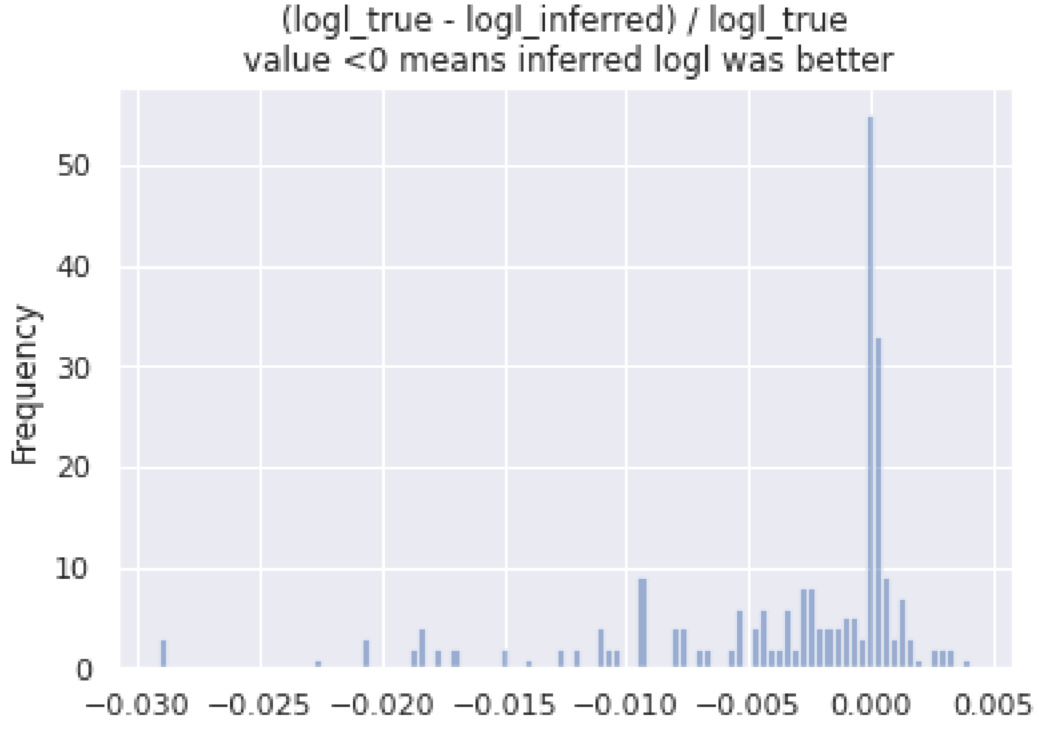


1.2 Plots for MSA_size ~ 200*n_trees

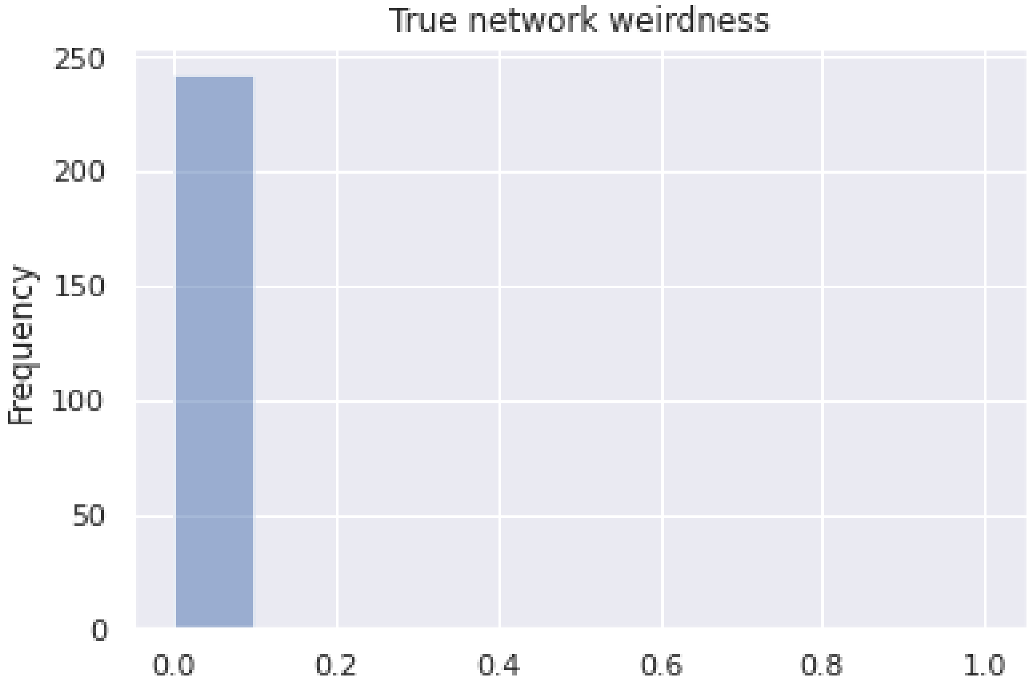
[11]:
```
df_raxml_only_msasize_200 = df_raxml_only.query('msa_size == 201')
build_stats(df_raxml_only_msasize_200)
```

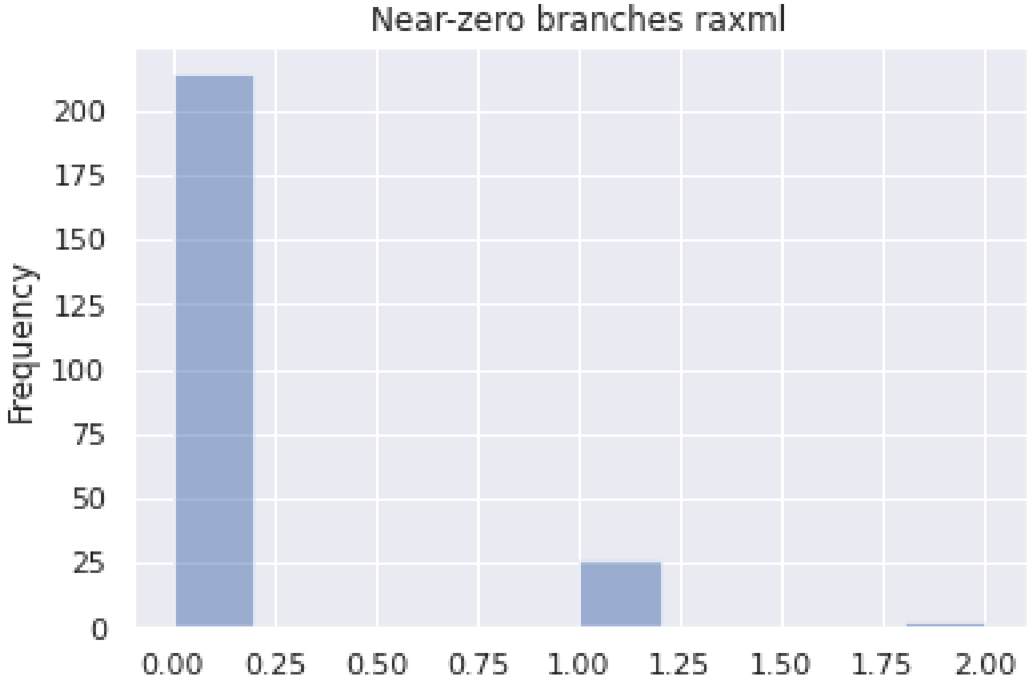
```
Inferred BIC better or equal: 216
Inferred BIC worse: 26

Inferred loglh better or equal: 96
Inferred loglh worse: 146

Inferred n_reticulations less: 208
Inferred n_reticulations equal: 34
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
−0.005
0.000
0.005
0.010
0.015
0.020
0.025

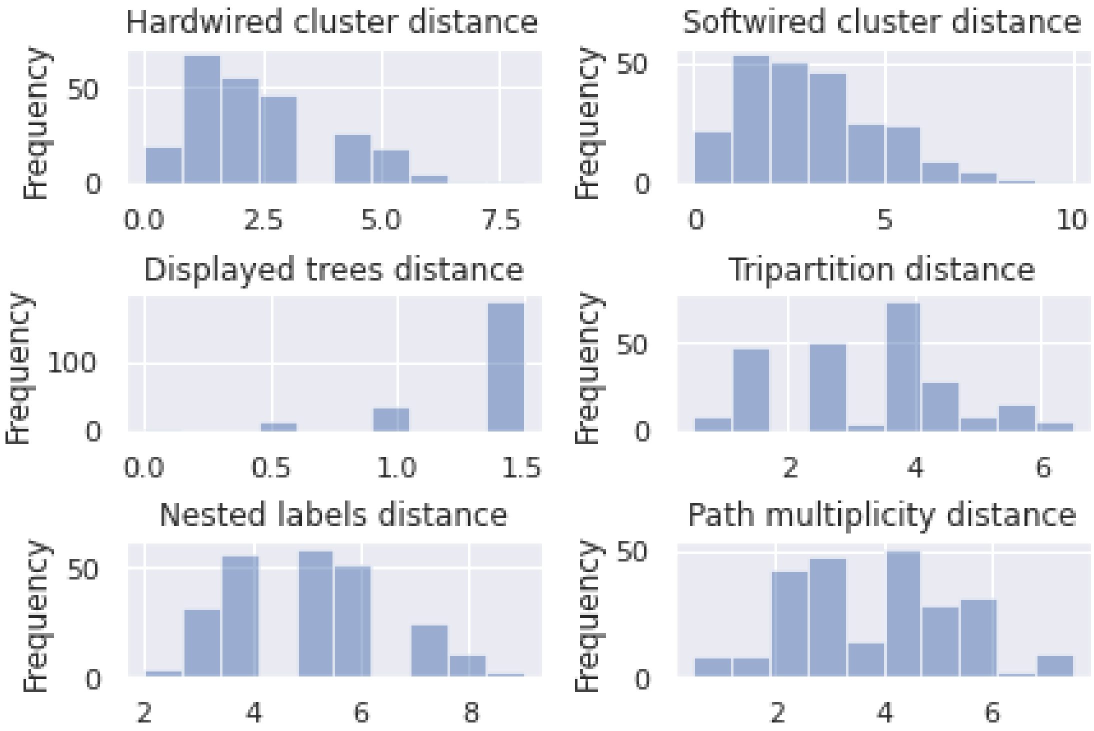

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
50
40
30
20
10
0
−0.030
−0.025
−0.020
−0.015
−0.010
−0.005
0.000
0.005

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
250
200
150
100
50
0
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
200
175
150
125
100
75
50
25
0
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

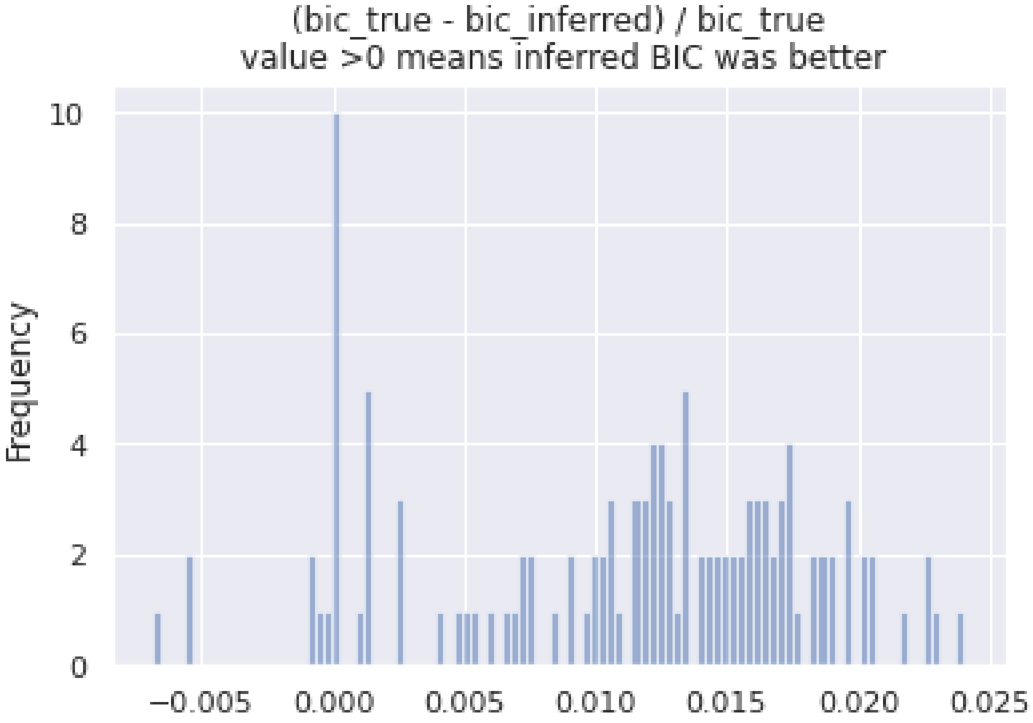
```
<Figure size 432x288 with 0 Axes>
```

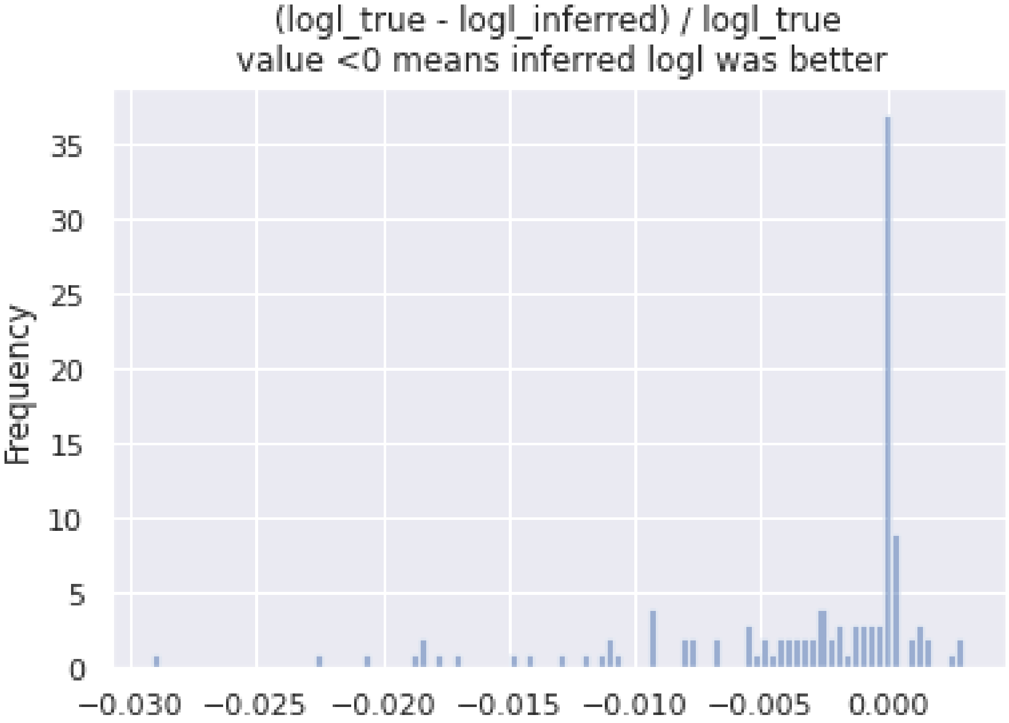


1.2.1 Plots for LikelihodType.AVERAGE

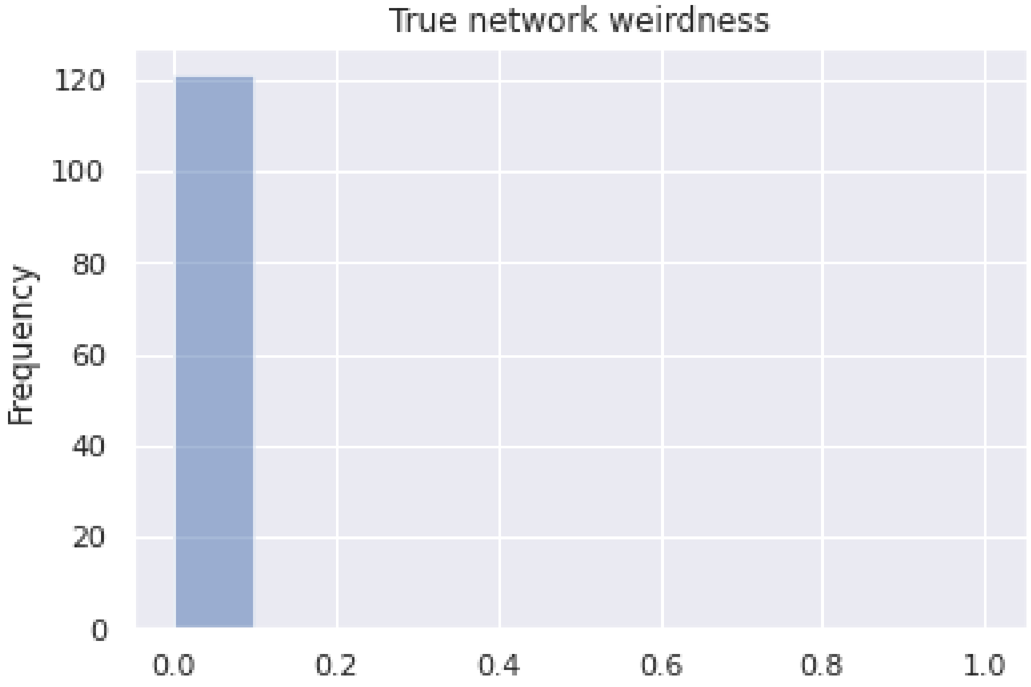
[12]:
```
df_raxml_only_msasize_200_average = df_raxml_only_msasize_200.
 ↪query('likelihood_type == "AVERAGE"')
build_stats(df_raxml_only_msasize_200_average)
```

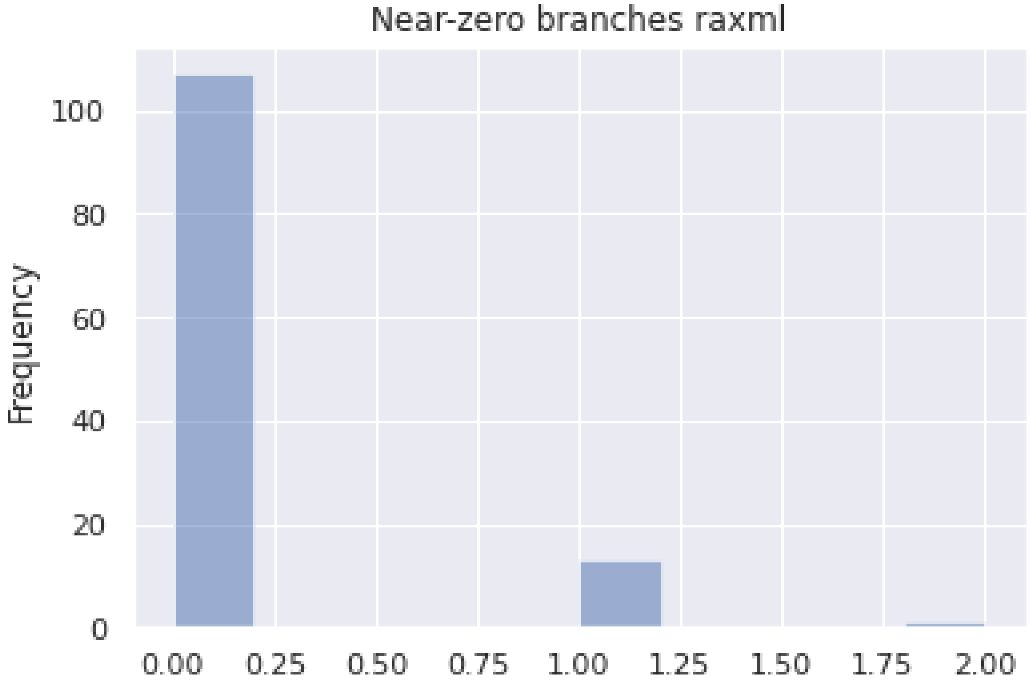
```
Inferred BIC better or equal: 109
Inferred BIC worse: 12

Inferred loglh better or equal: 45
Inferred loglh worse: 76

Inferred n_reticulations less: 104
Inferred n_reticulations equal: 17
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
2
4
6
8
10
−0.005
0.000
0.005
0.010
0.015
0.020
0.025

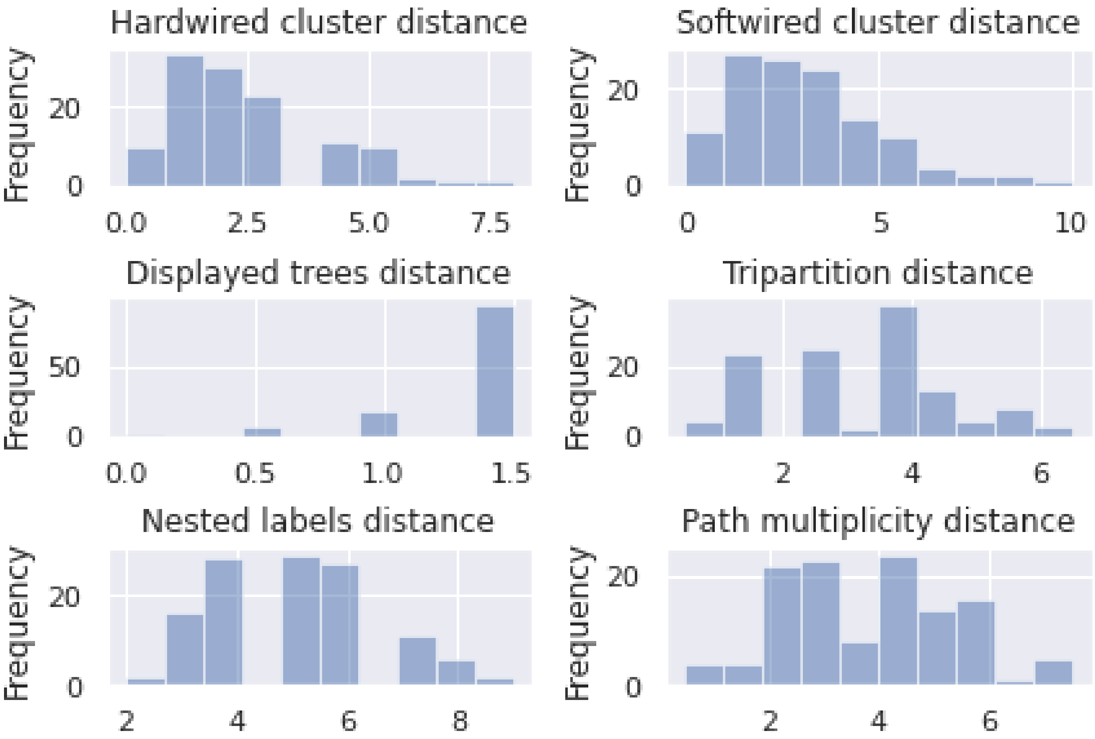

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
5
10
15
20
25
30
35
−0.030
−0.025
−0.020
−0.015
−0.010
−0.005
0.000

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

```
<Figure size 432x288 with 0 Axes>
```



Hardwired cluster distance

Softwired cluster distance

Displayed trees distance

Tripartition distance

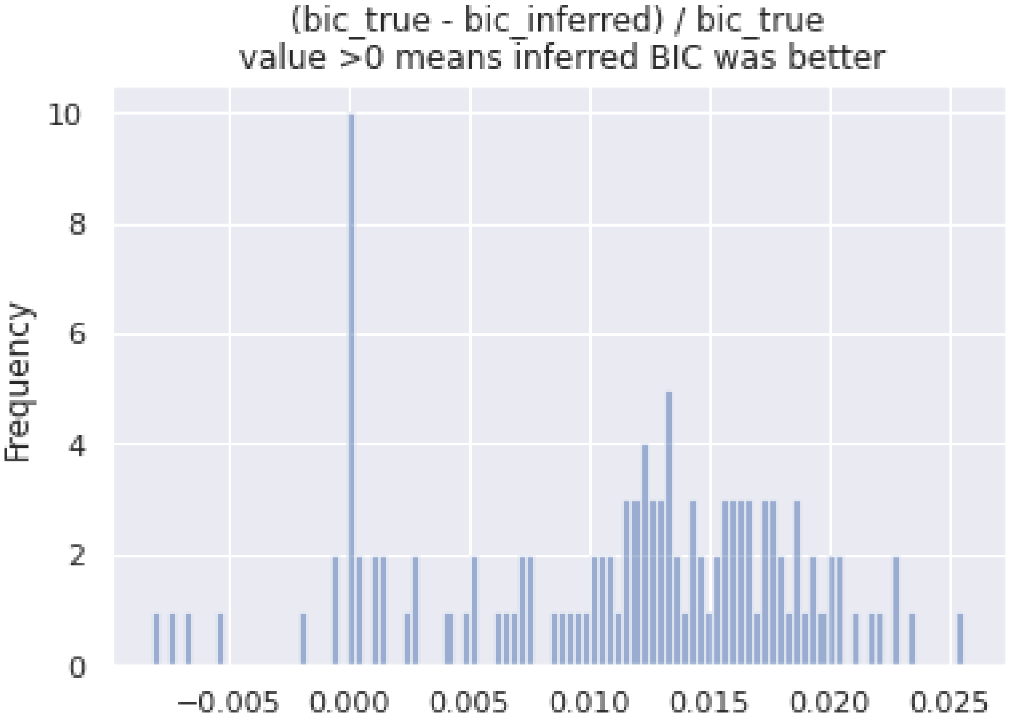
Nested labels distance

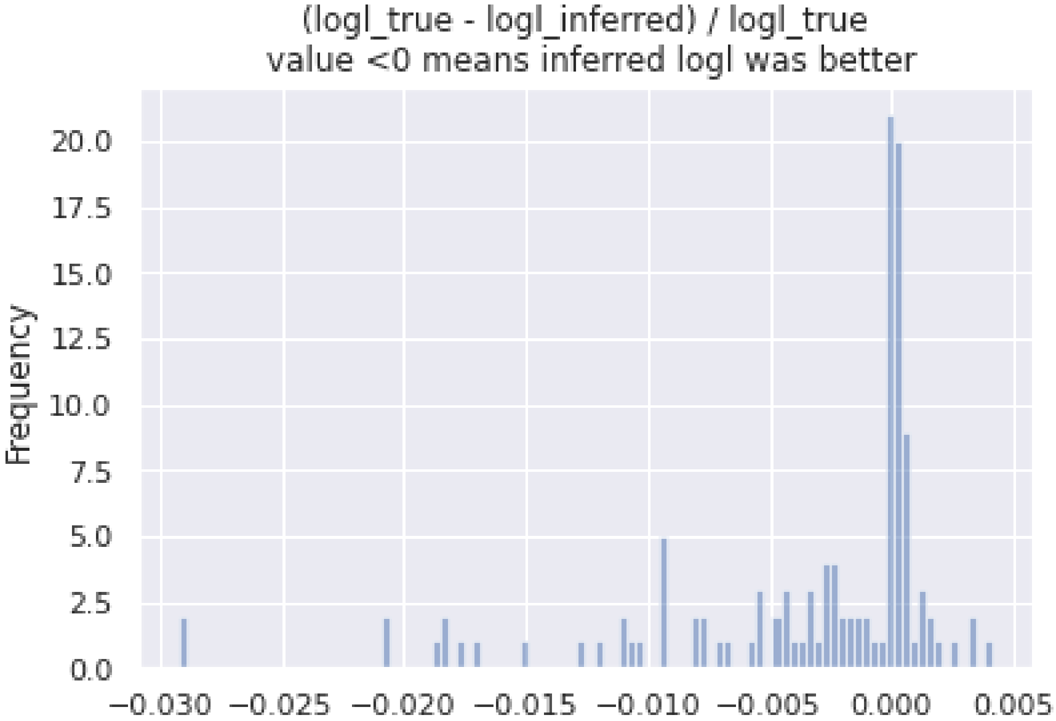
Path multiplicity distance

1.2.2 Plots for LikelihoodType.BEST

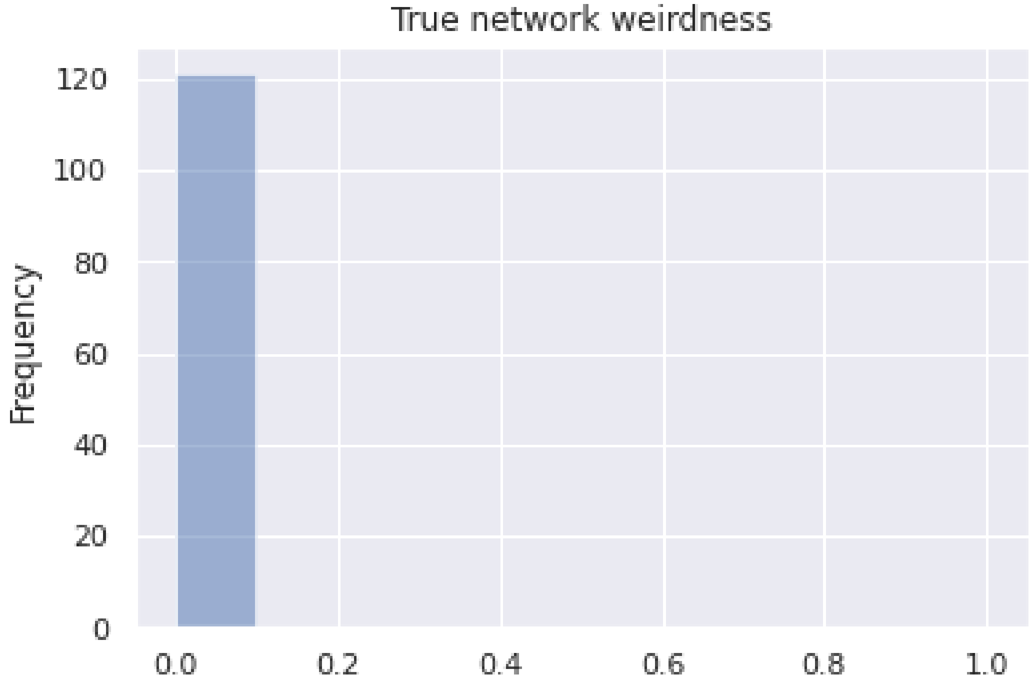
[13]:
```
df_raxml_only_msasize_200_best = df_raxml_only_msasize_200.
 ↪query('likelihood_type == "BEST"')
build_stats(df_raxml_only_msasize_200_best)
```

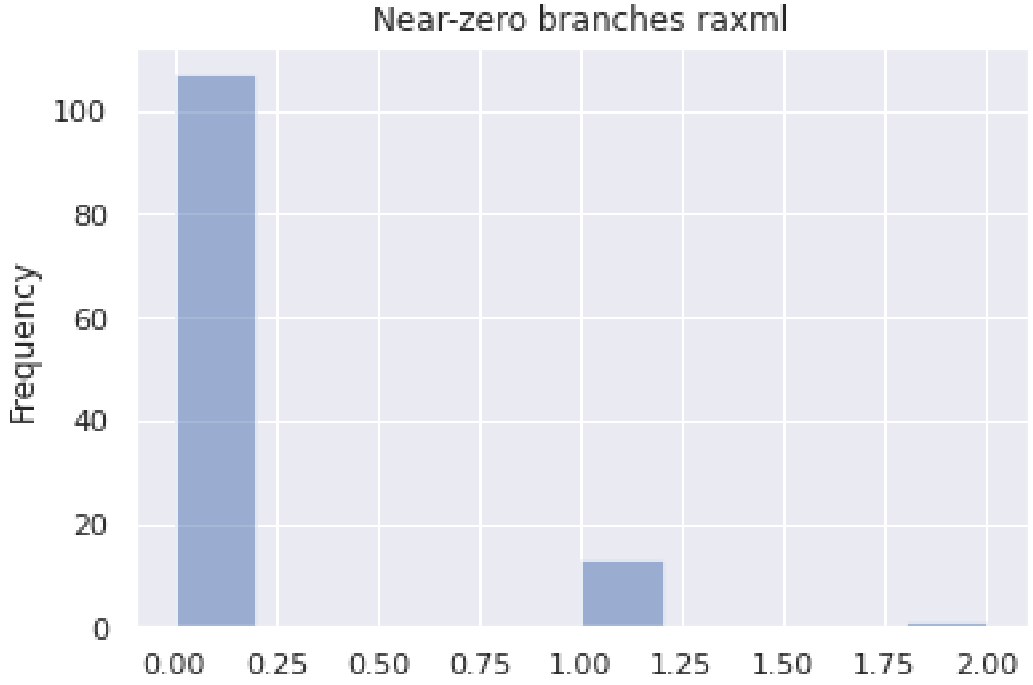
```
Inferred BIC better or equal: 107
Inferred BIC worse: 14

Inferred loglh better or equal: 51
Inferred loglh worse: 70

Inferred n_reticulations less: 104
Inferred n_reticulations equal: 17
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
10
8
6
4
2
0
−0.005
0.000
0.005
0.010
0.015
0.020
0.025

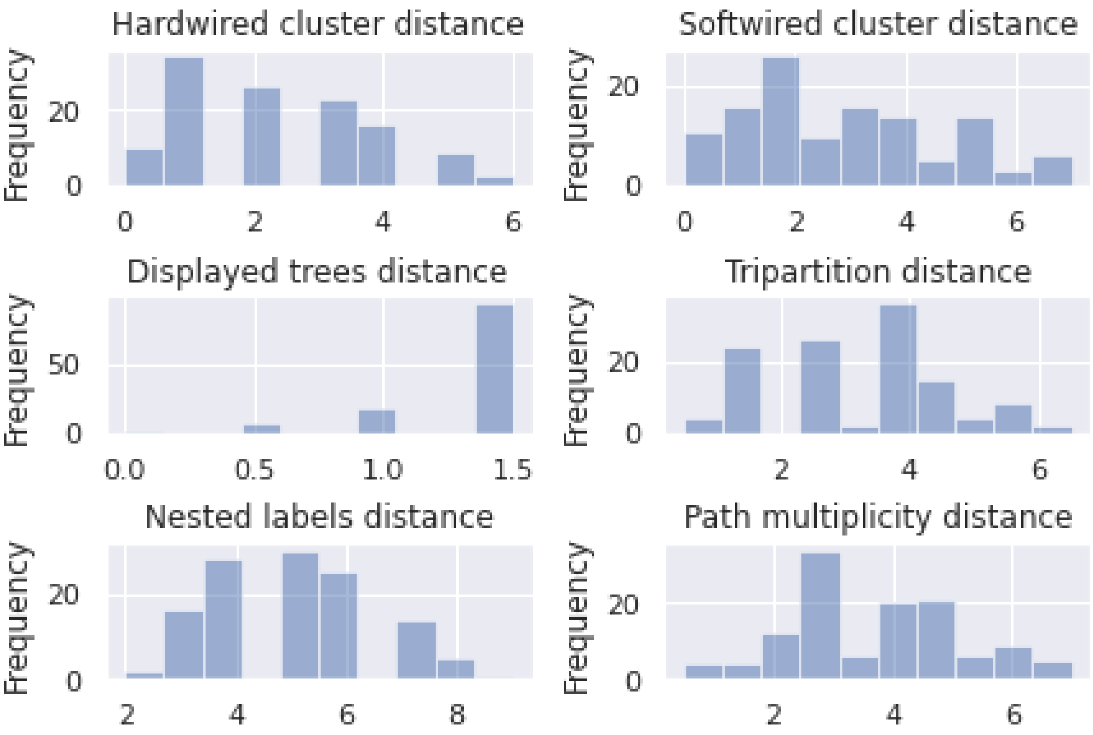

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
−0.030
−0.025
−0.020
−0.015
−0.010
−0.005
0.000
0.005

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

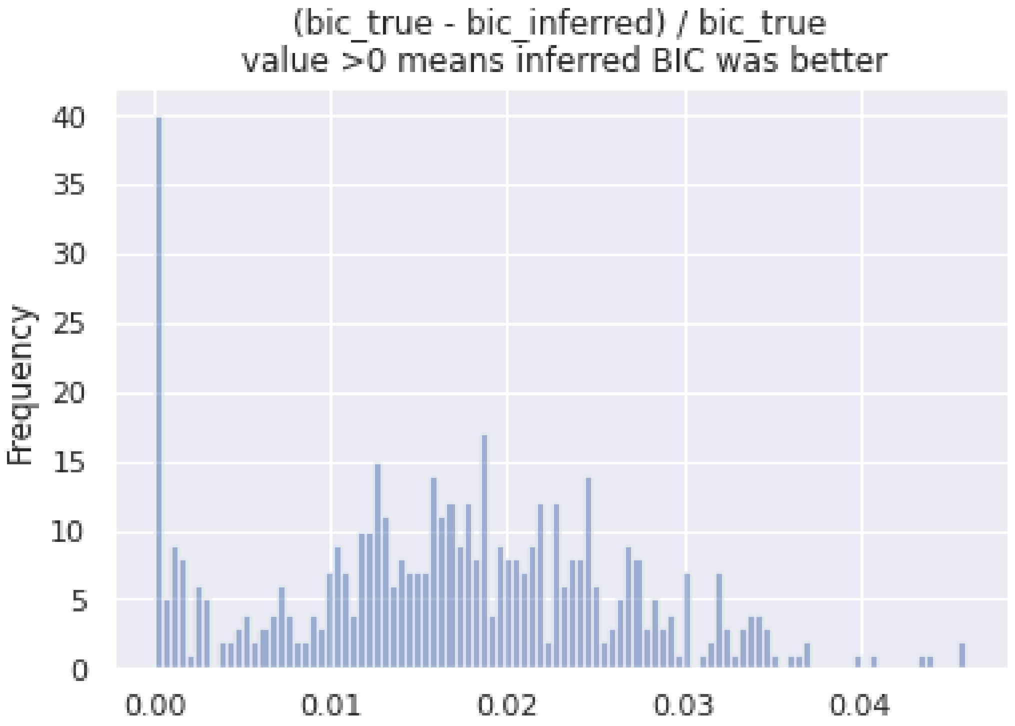
```
<Figure size 432x288 with 0 Axes>
```

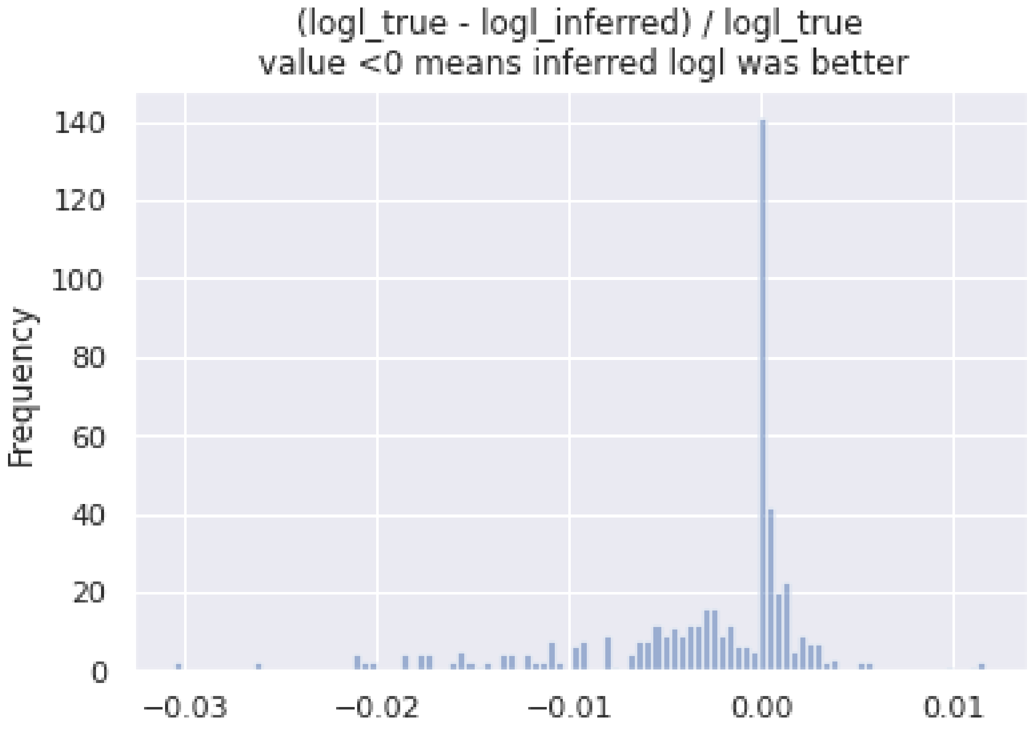


2 Plots for starting with 5 random, 5 parsimony trees

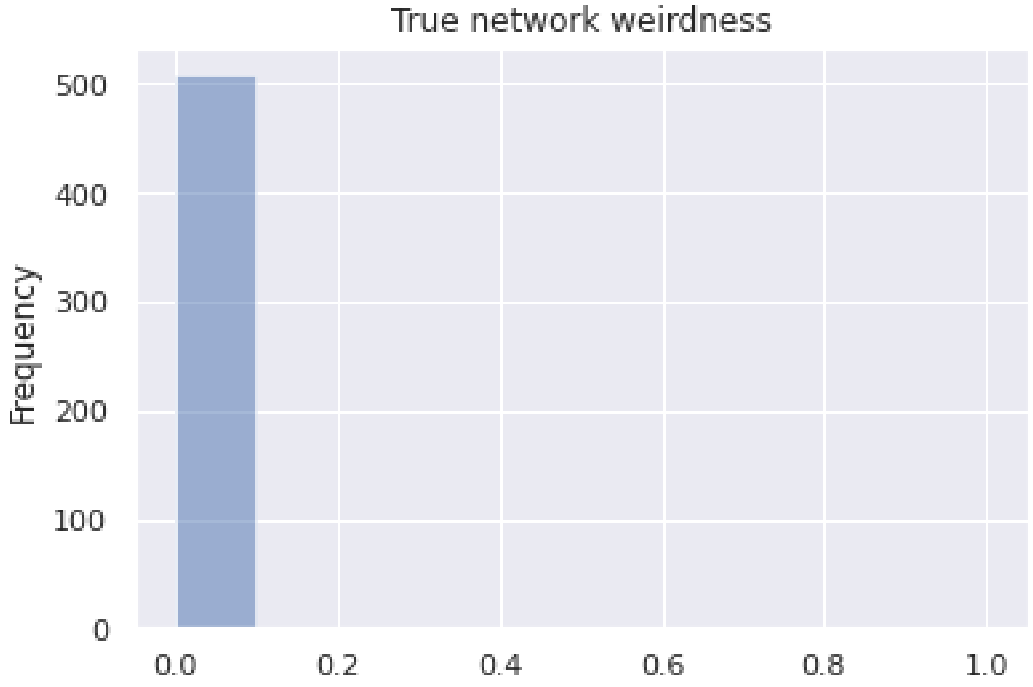
```
[14]: df_random = df.query('start_type == "RANDOM"')
      build_stats(df_random)
```

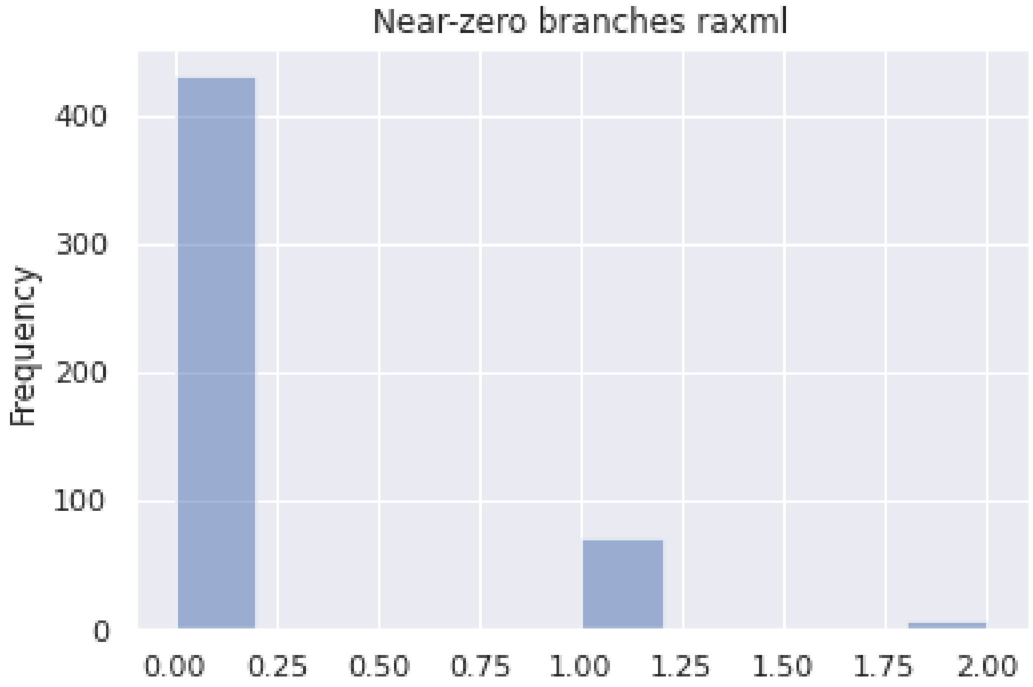
```
Inferred BIC better or equal: 503
Inferred BIC worse: 5

Inferred loglh better or equal: 240
Inferred loglh worse: 268

Inferred n_reticulations less: 450
Inferred n_reticulations equal: 58
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
5
10
15
20
25
30
35
40
0.00
0.01
0.02
0.03
0.04

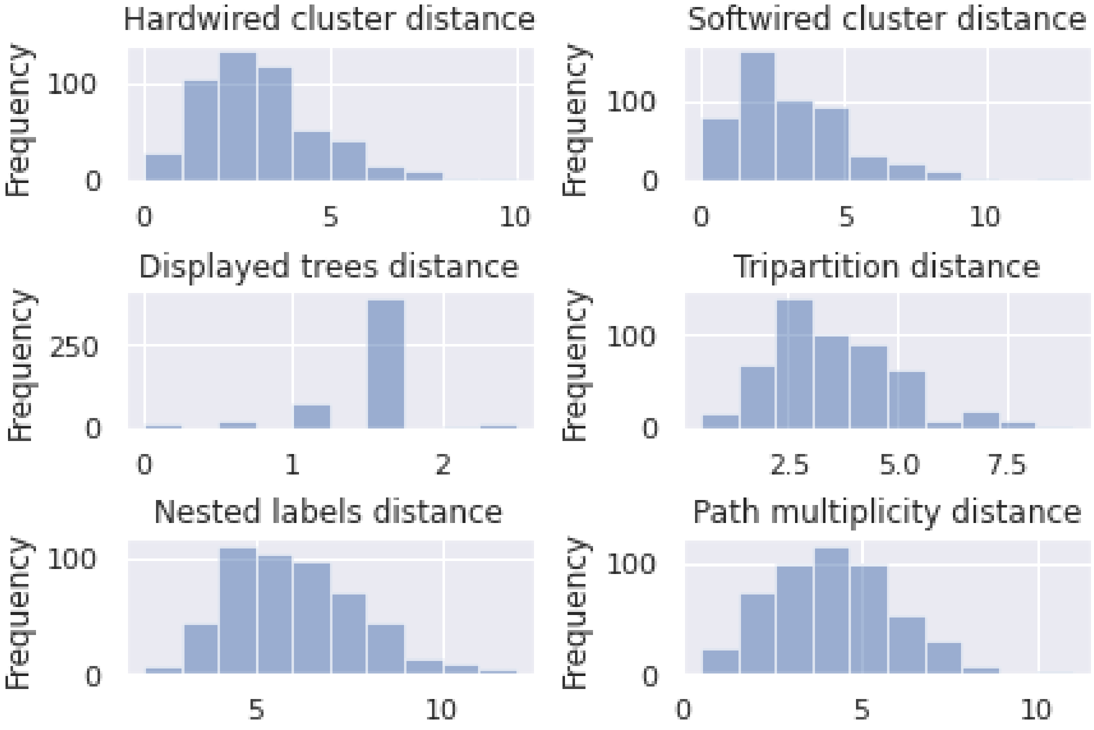

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
20
40
60
80
100
120
140
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
500
400
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
400
300
200
100
0
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

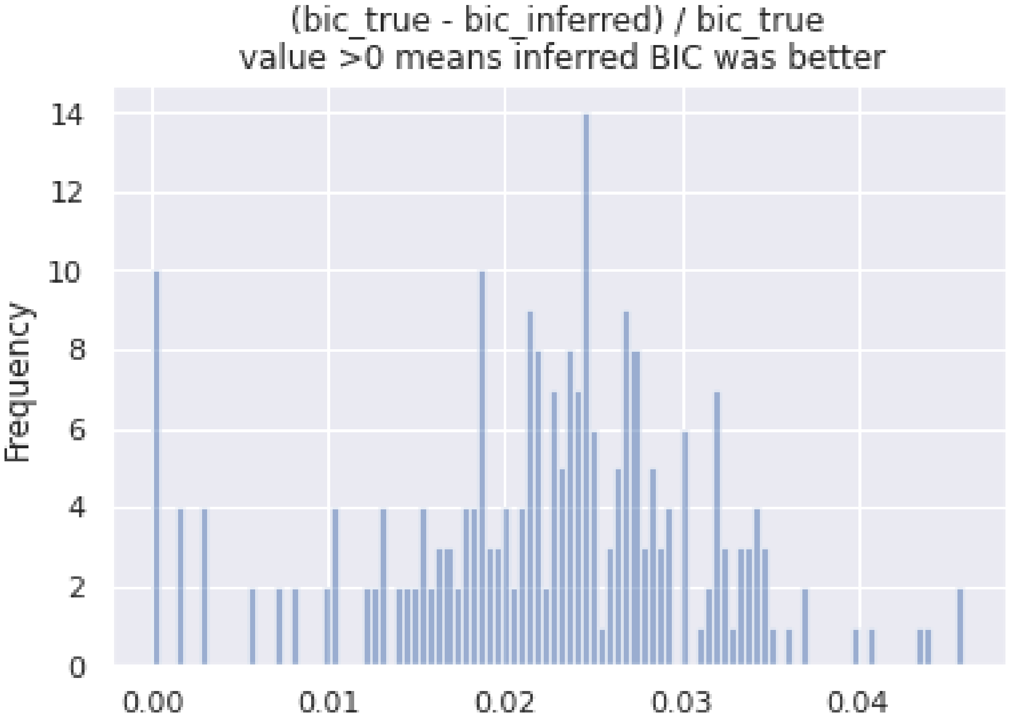
```
<Figure size 432x288 with 0 Axes>
```

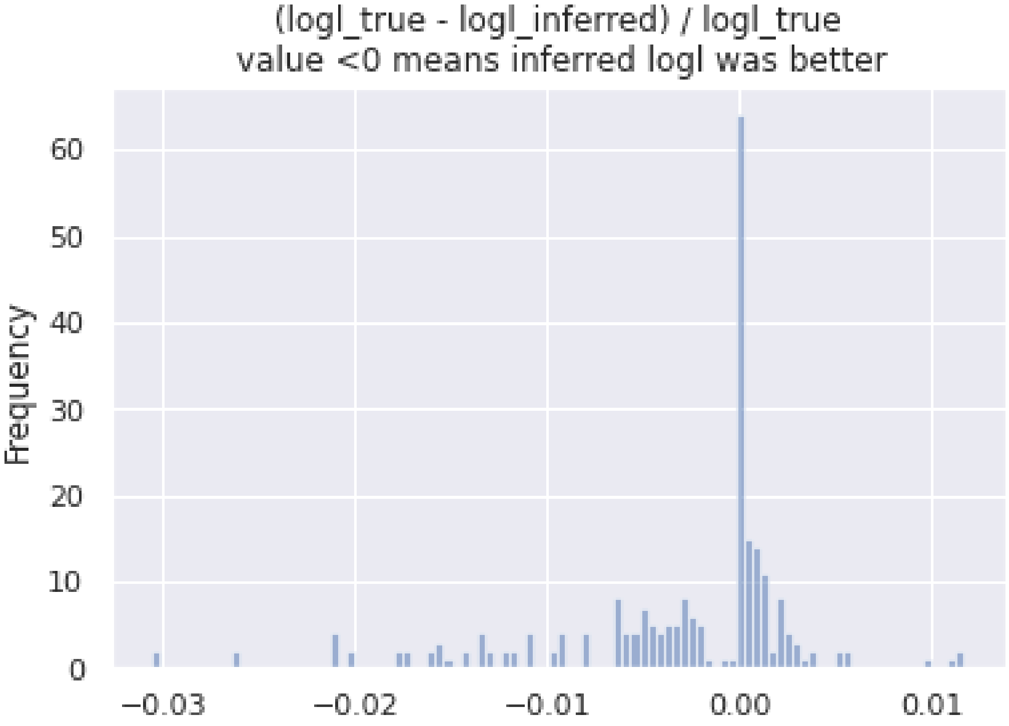


2.1 Plots for MSA_size ~ 100*n_trees

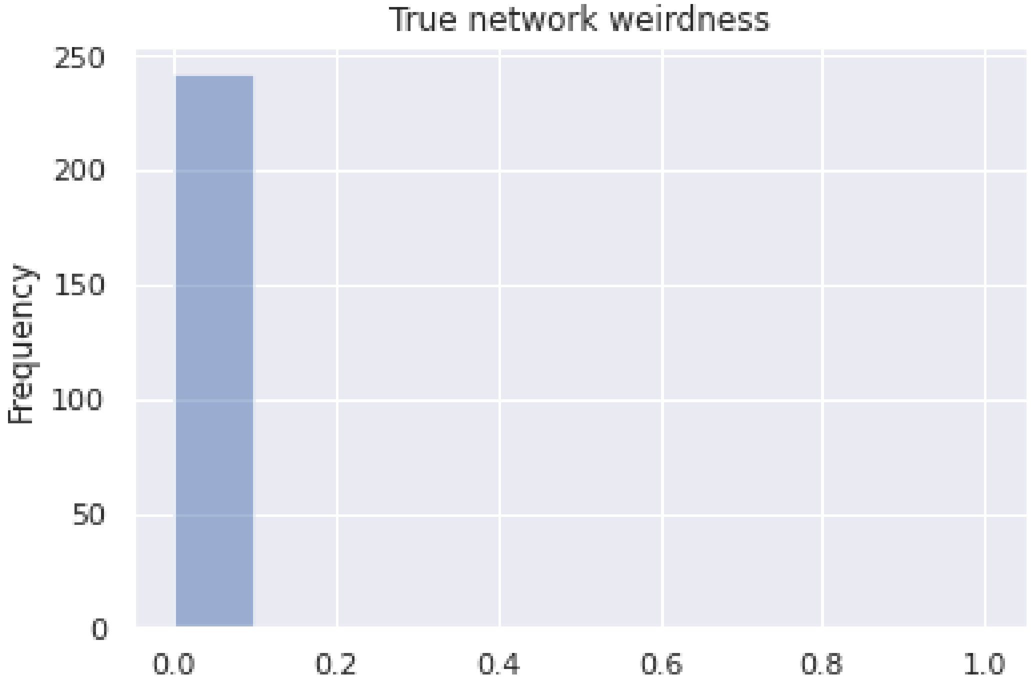
[15]:
```
df_random_msasize_100 = df_random.query('msa_size == 101')
build_stats(df_random_msasize_100)
```

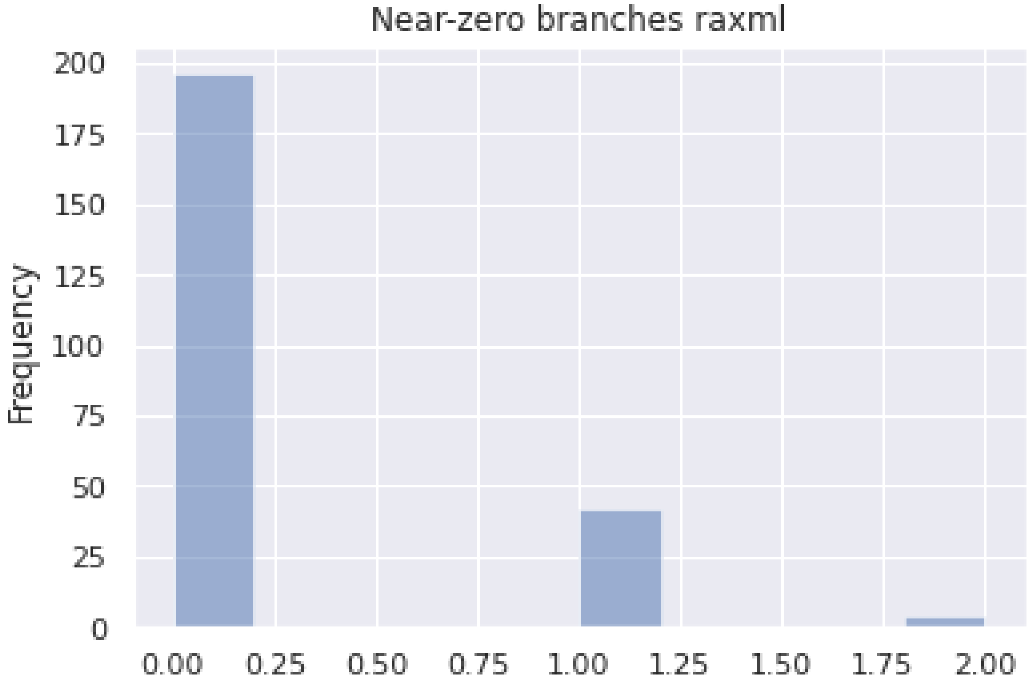
```
Inferred BIC better or equal: 240
Inferred BIC worse: 2

Inferred loglh better or equal: 115
Inferred loglh worse: 127

Inferred n_reticulations less: 226
Inferred n_reticulations equal: 16
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
2
4
6
8
10
12
14
0.00
0.01
0.02
0.03
0.04

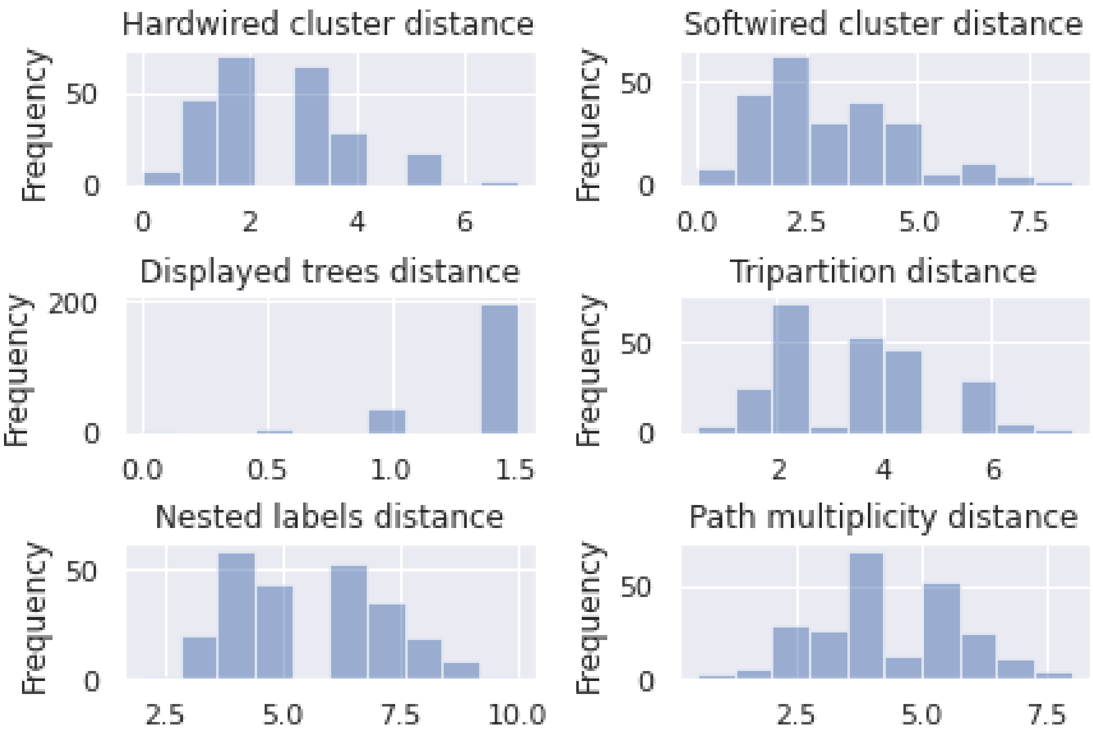

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
10
20
30
40
50
60
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
50
100
150
200
250
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
25
50
75
100
125
150
175
200
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

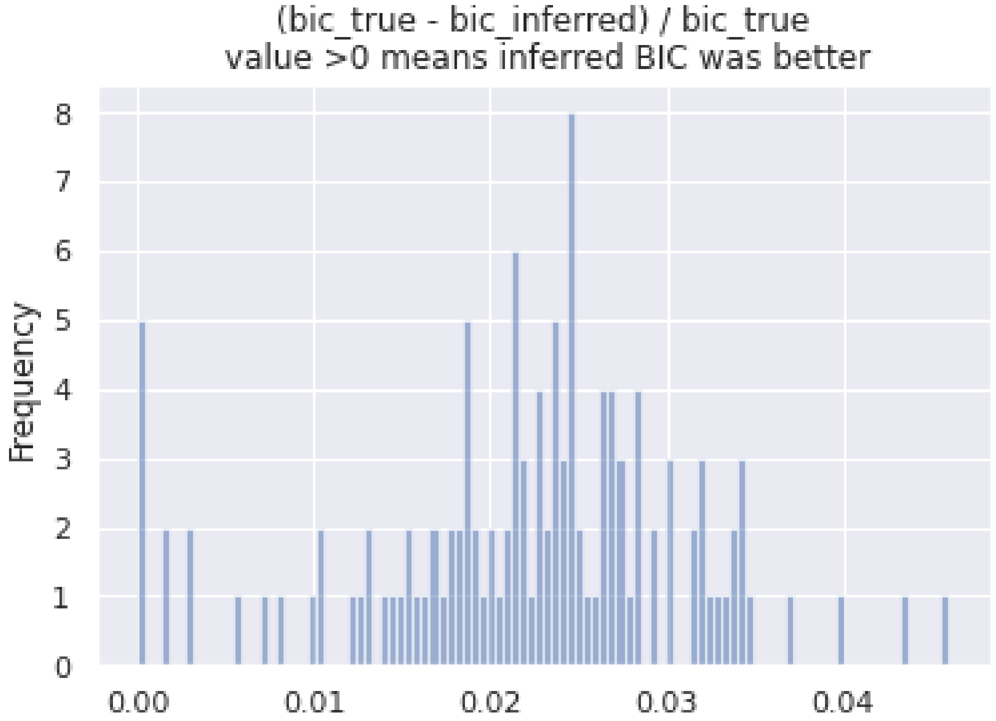
```
<Figure size 432x288 with 0 Axes>
```

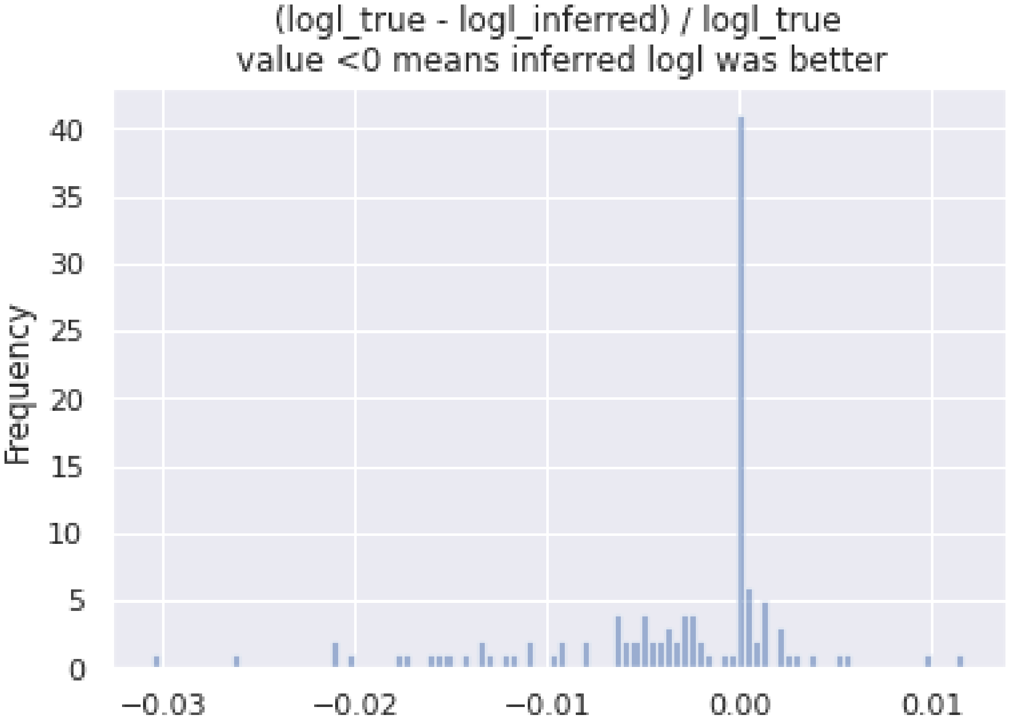


2.1.1 Plots for LikelihodType.AVERAGE

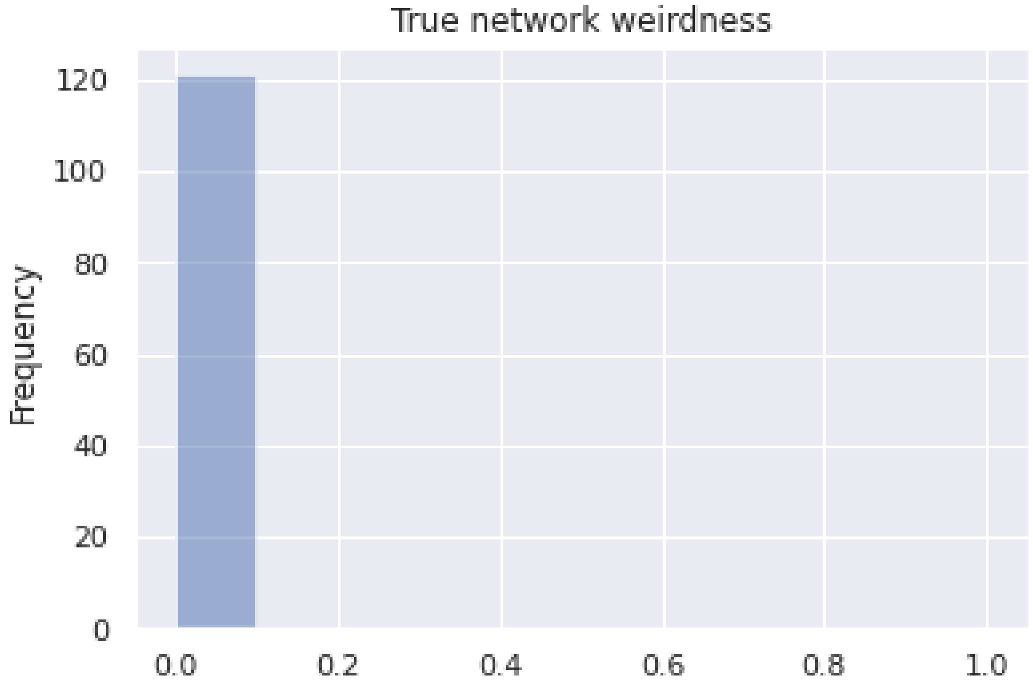
```
[16]: df_random_msasize_100_average = df_random_msasize_100.query('likelihood_type ==␣
      ↪"AVERAGE"')
      build_stats(df_random_msasize_100_average)
```

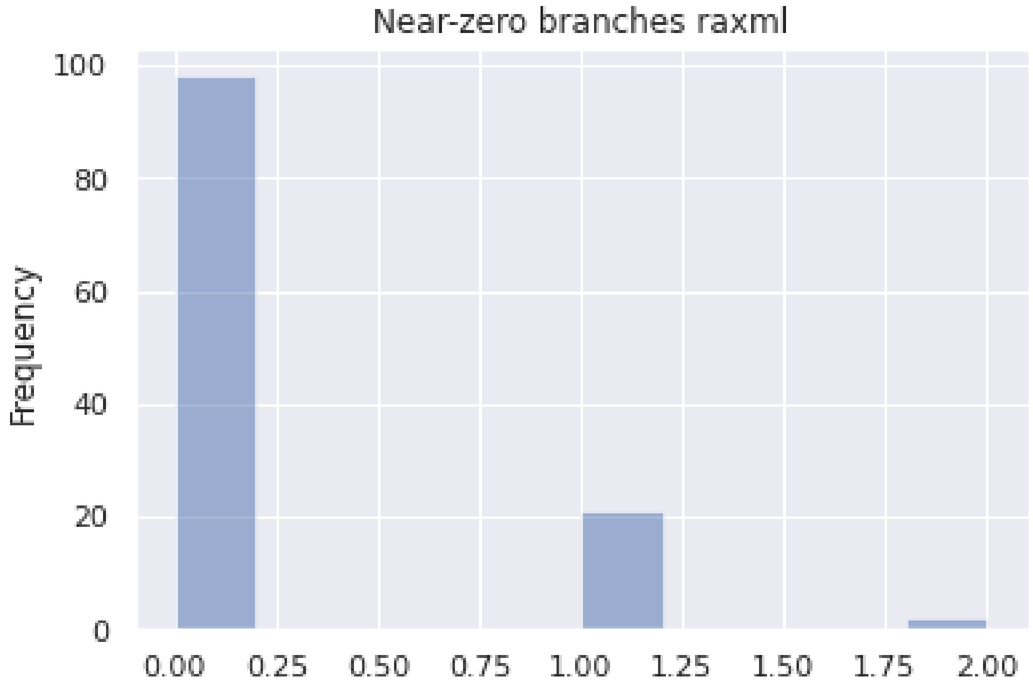
```
Inferred BIC better or equal: 120
Inferred BIC worse: 1

Inferred loglh better or equal: 51
Inferred loglh worse: 70

Inferred n_reticulations less: 113
Inferred n_reticulations equal: 8
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
1
2
3
4
5
6
7
8
0.00
0.01
0.02
0.03
0.04

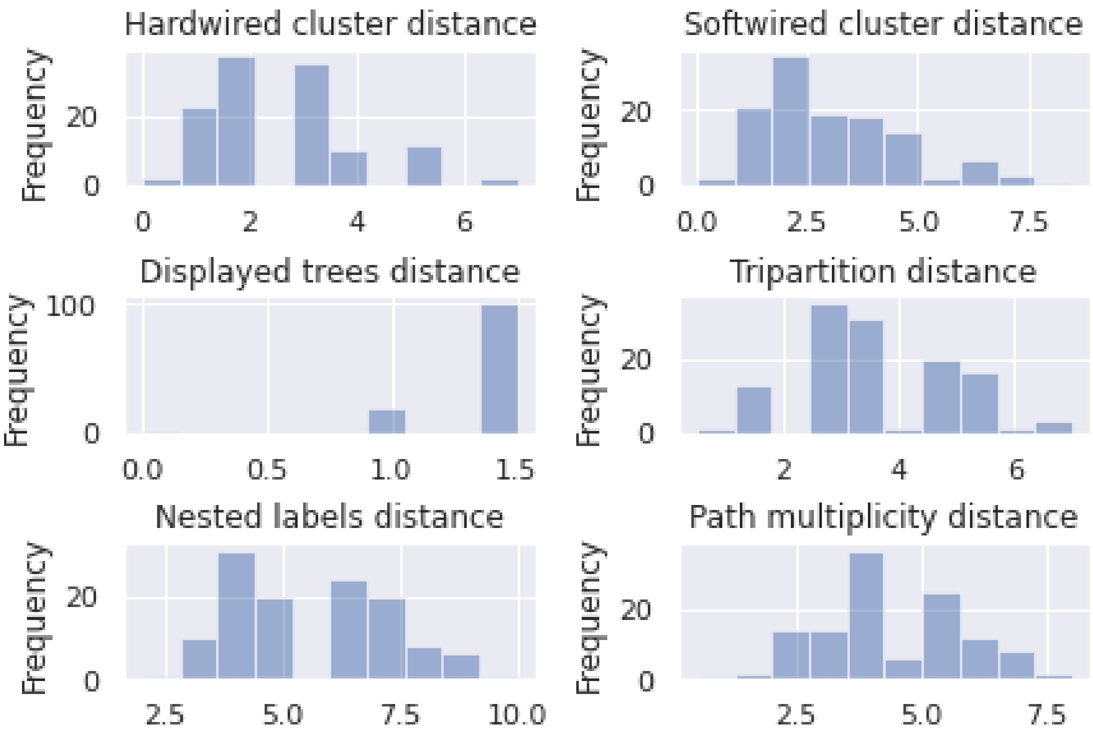

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
5
10
15
20
25
30
35
40
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

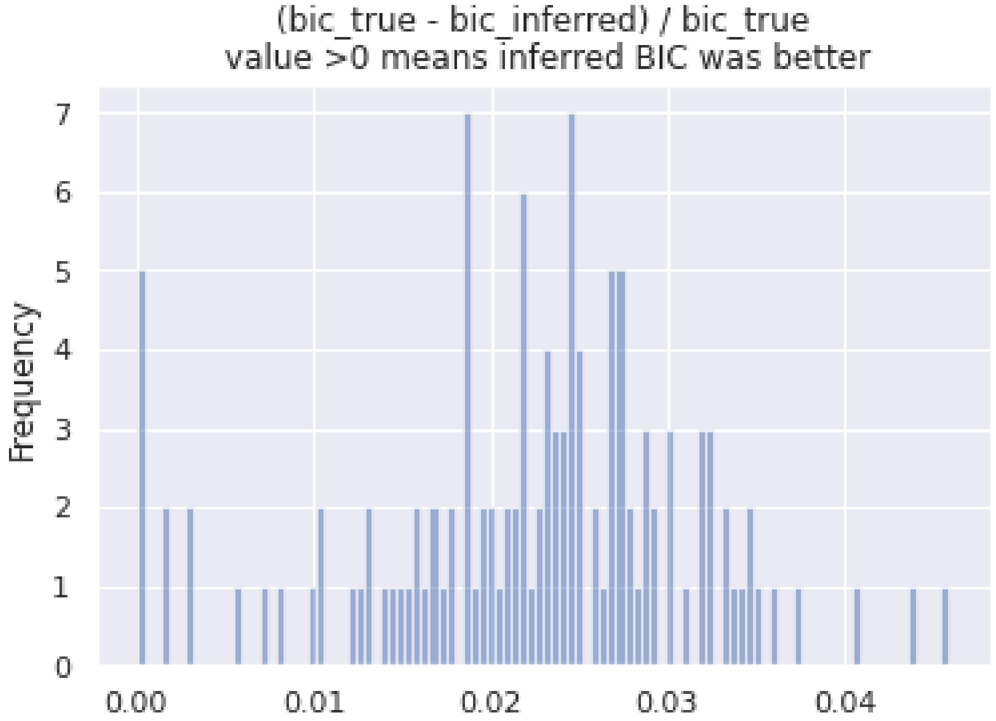
```
<Figure size 432x288 with 0 Axes>
```

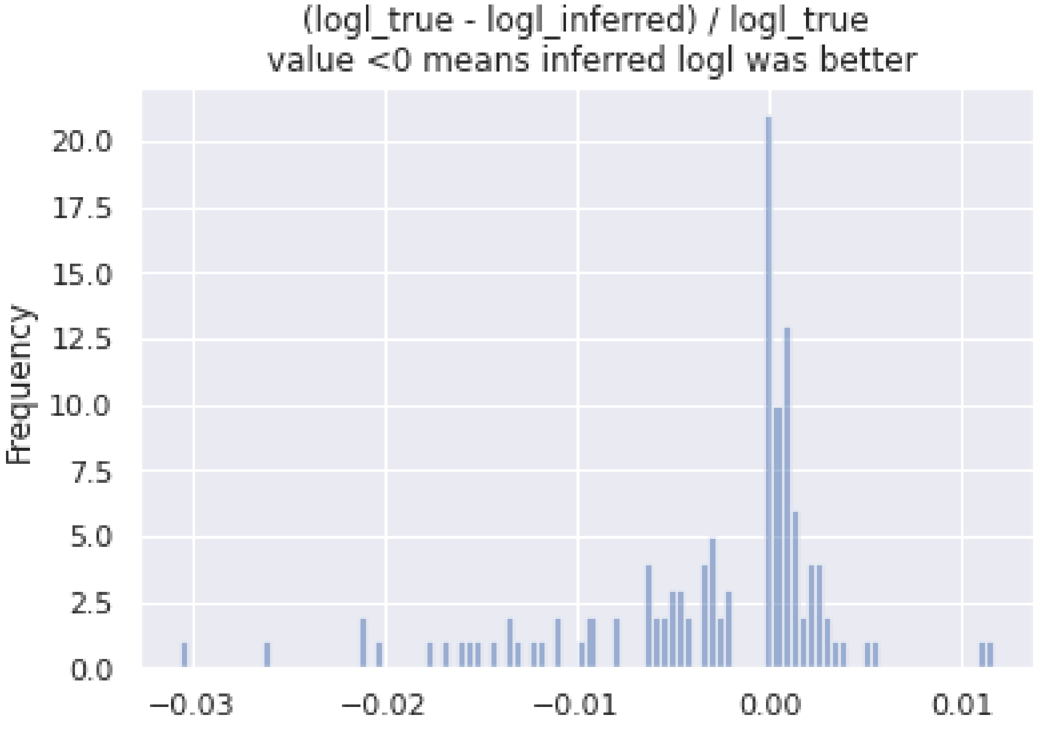


2.1.2 Plots for LikelihoodType.BEST

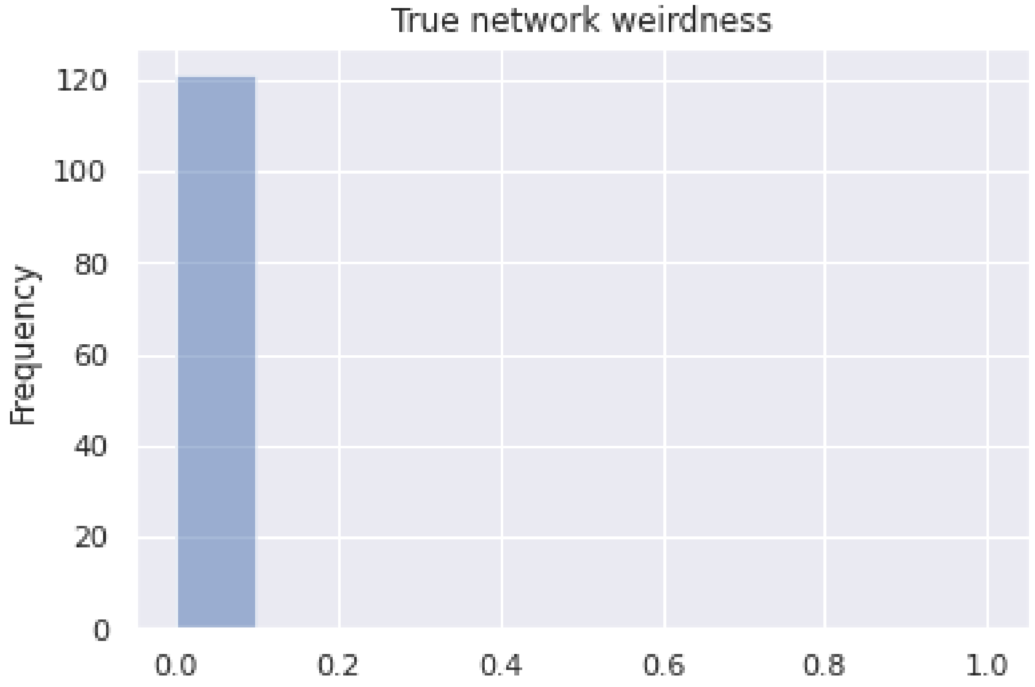
[17]:
```
df_random_msasize_100_best = df_random_msasize_100.query('likelihood_type ==␣
↪"BEST"')
build_stats(df_random_msasize_100_best)
```

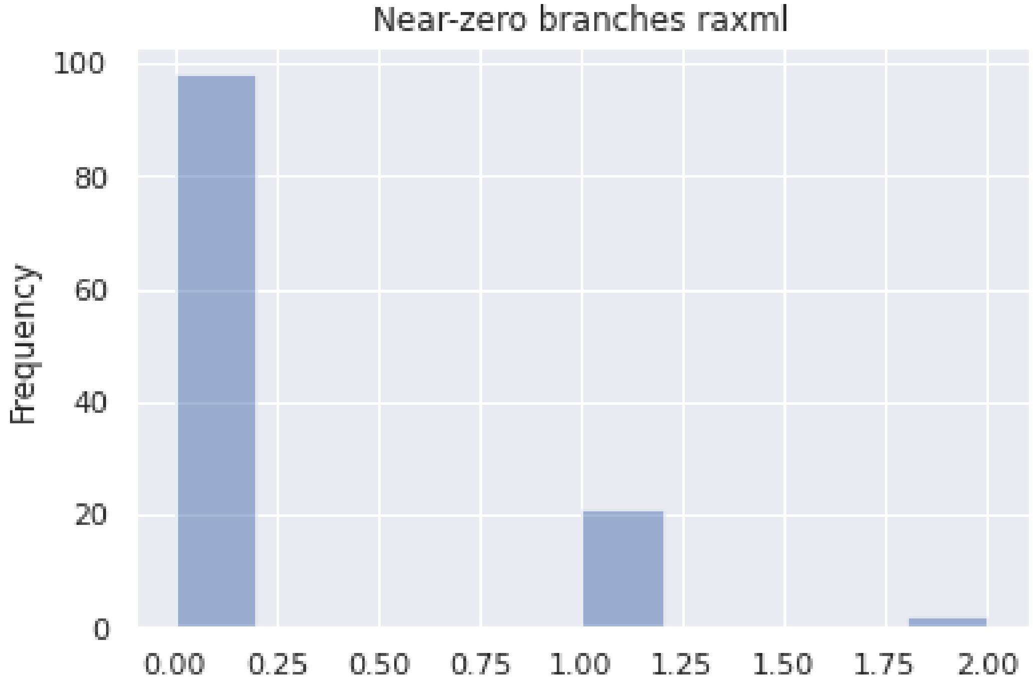
```
Inferred BIC better or equal: 120
Inferred BIC worse: 1

Inferred loglh better or equal: 64
Inferred loglh worse: 57

Inferred n_reticulations less: 113
Inferred n_reticulations equal: 8
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
1
2
3
4
5
6
7
0.00
0.01
0.02
0.03
0.04

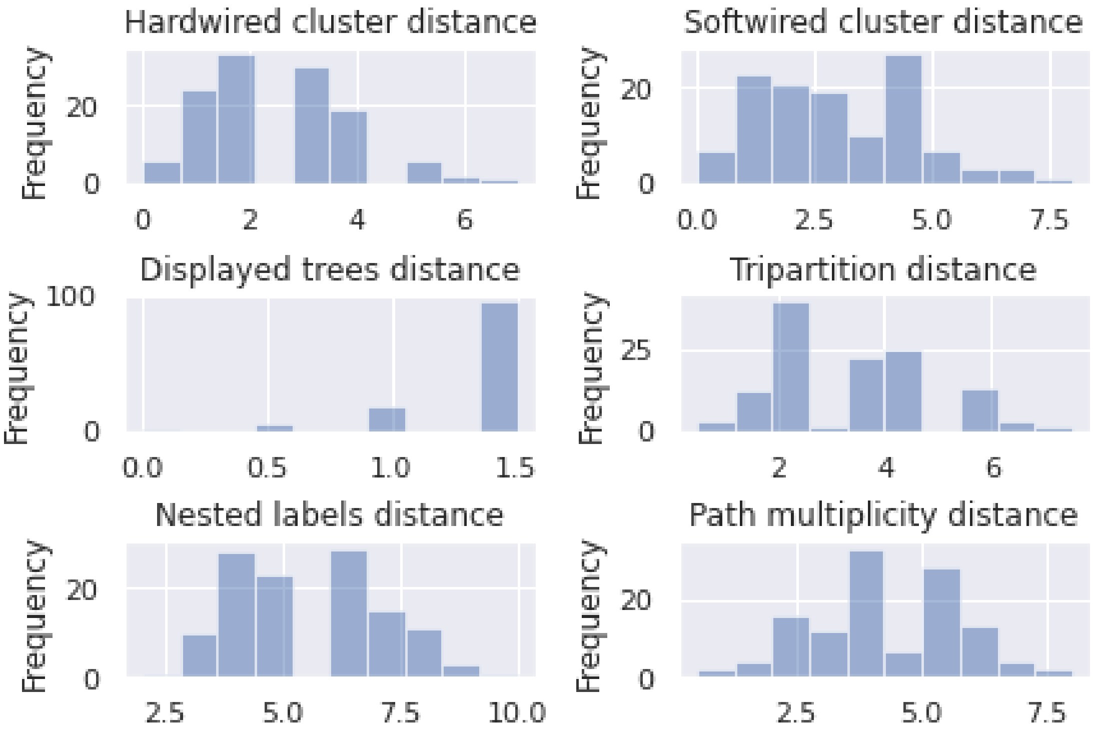

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
−0.03
−0.02
−0.01
0.00
0.01

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

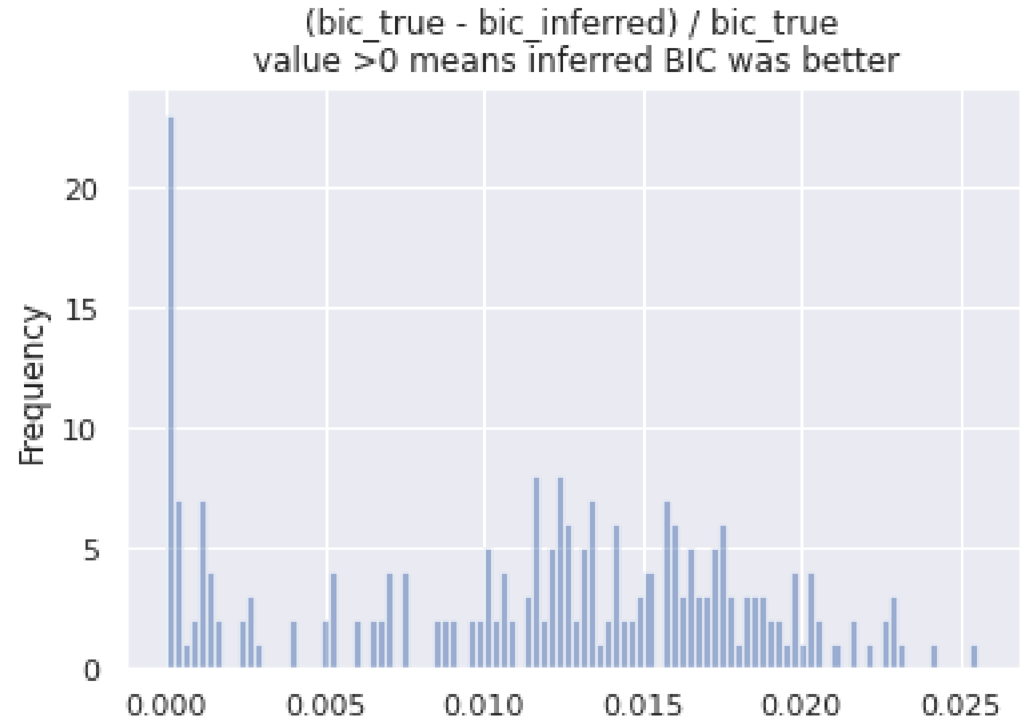
```
<Figure size 432x288 with 0 Axes>
```

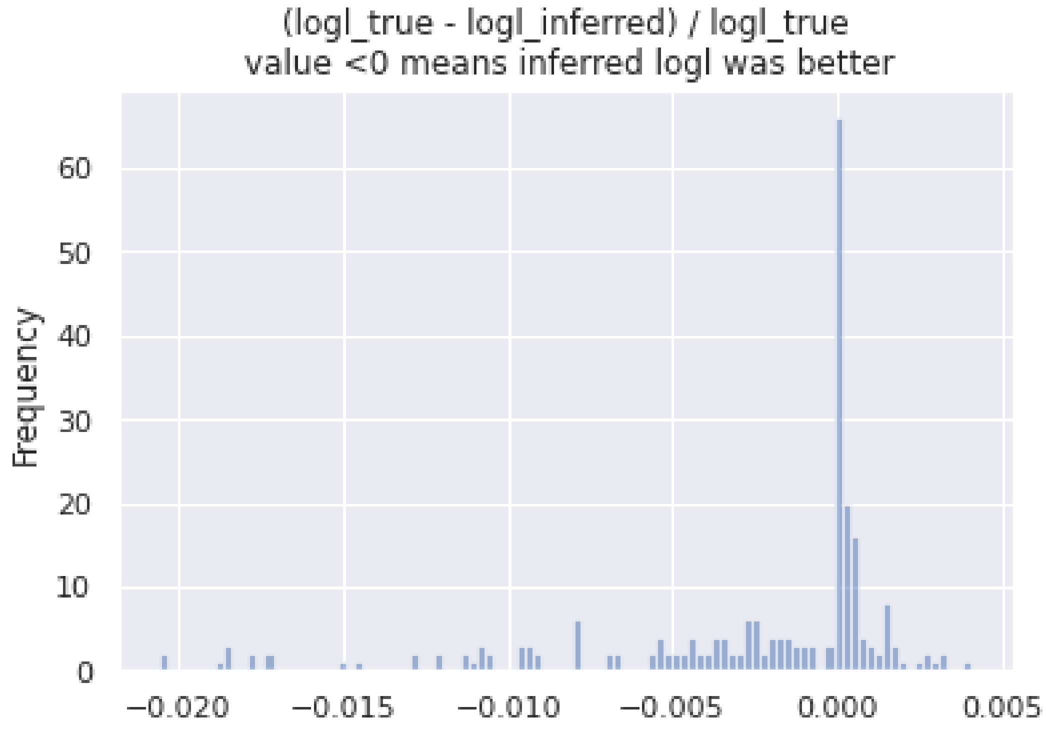


2.2 Plots for MSA_size ~ 200*n_trees

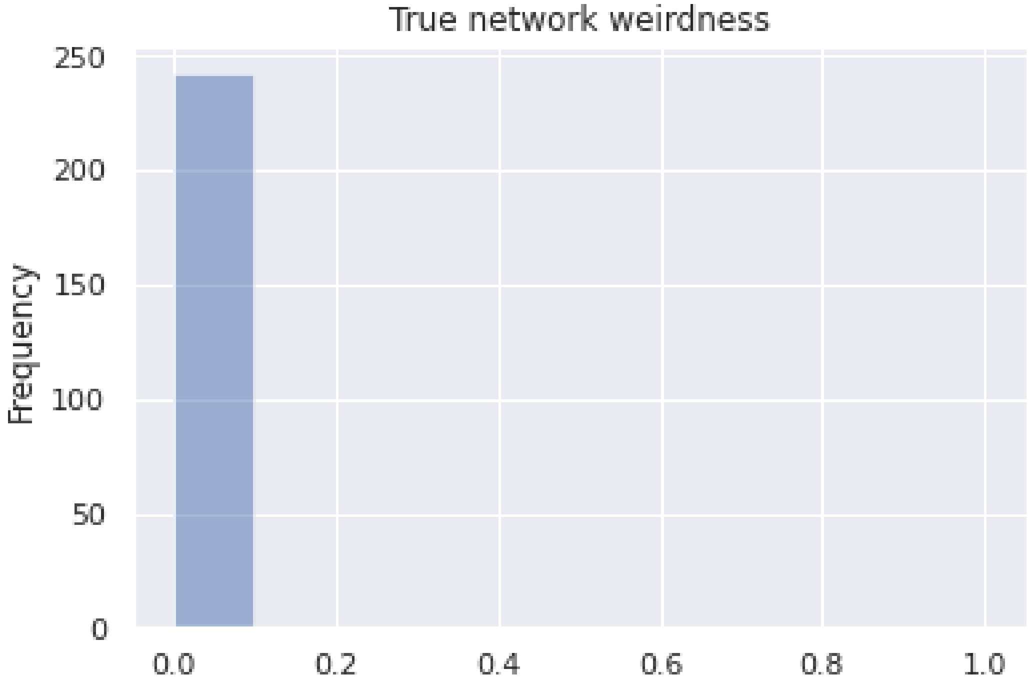
[18]:
```
df_random_msasize_200 = df_random.query('msa_size == 201')
build_stats(df_random_msasize_200)
```

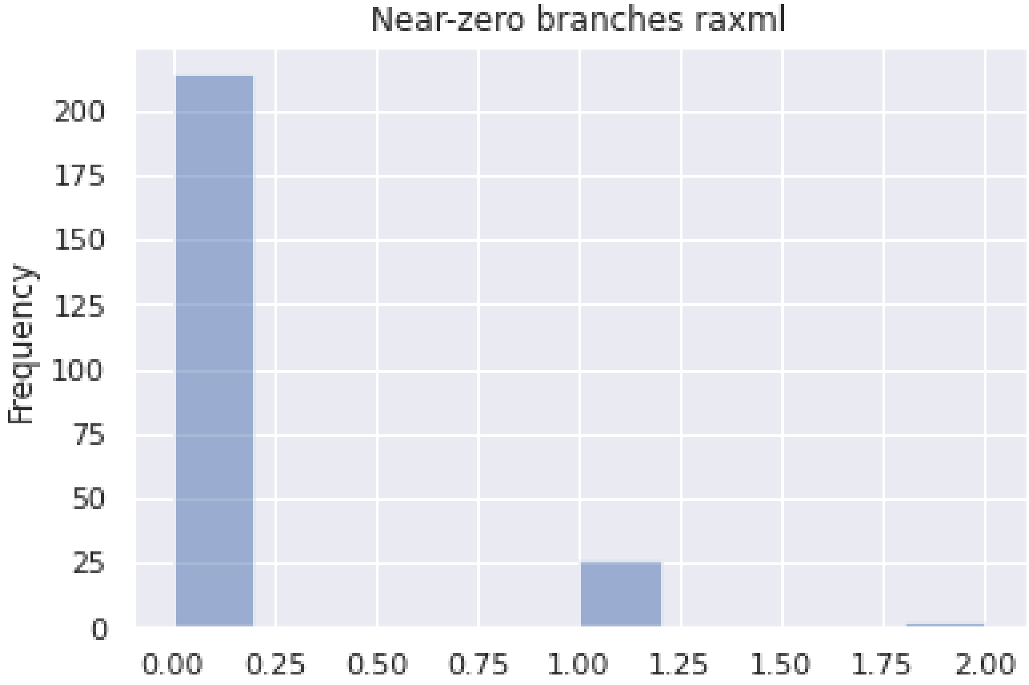
```
Inferred BIC better or equal: 239
Inferred BIC worse: 3

Inferred loglh better or equal: 120
Inferred loglh worse: 122

Inferred n_reticulations less: 200
Inferred n_reticulations equal: 42
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
5
10
15
20
0.000
0.005
0.010
0.015
0.020
0.025

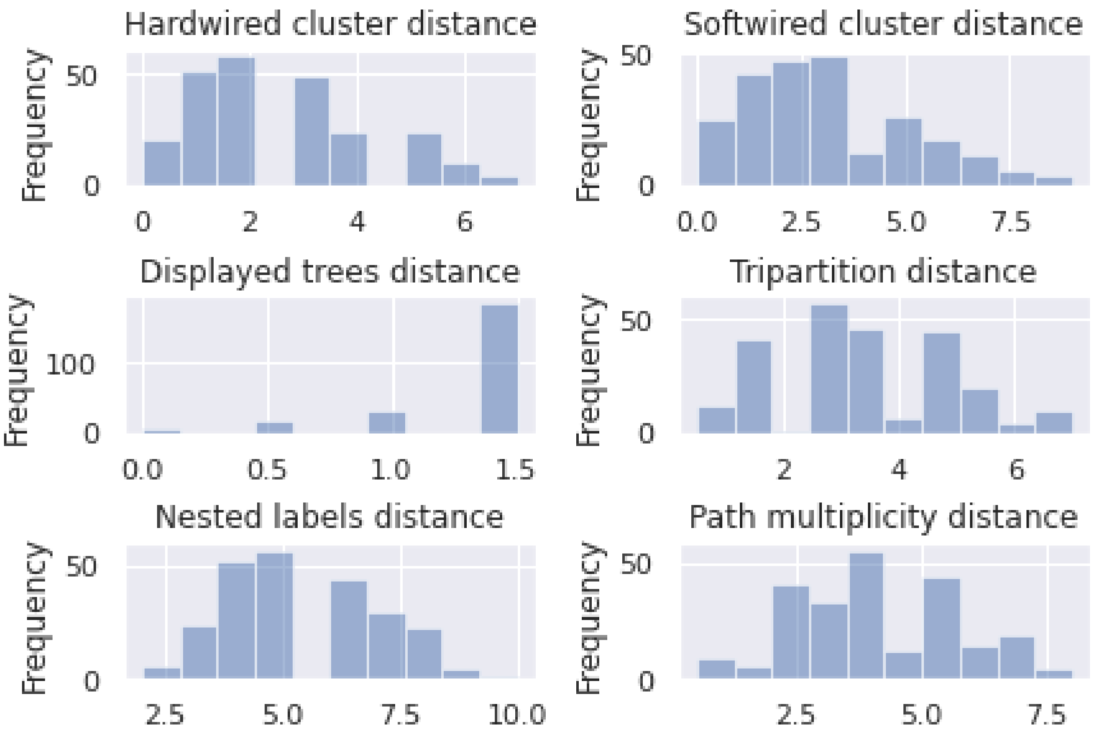

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
10
20
30
40
50
60
−0.020
−0.015
−0.010
−0.005
0.000
0.005

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
250
200
150
100
50
0
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
200
175
150
125
100
75
50
25
0
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

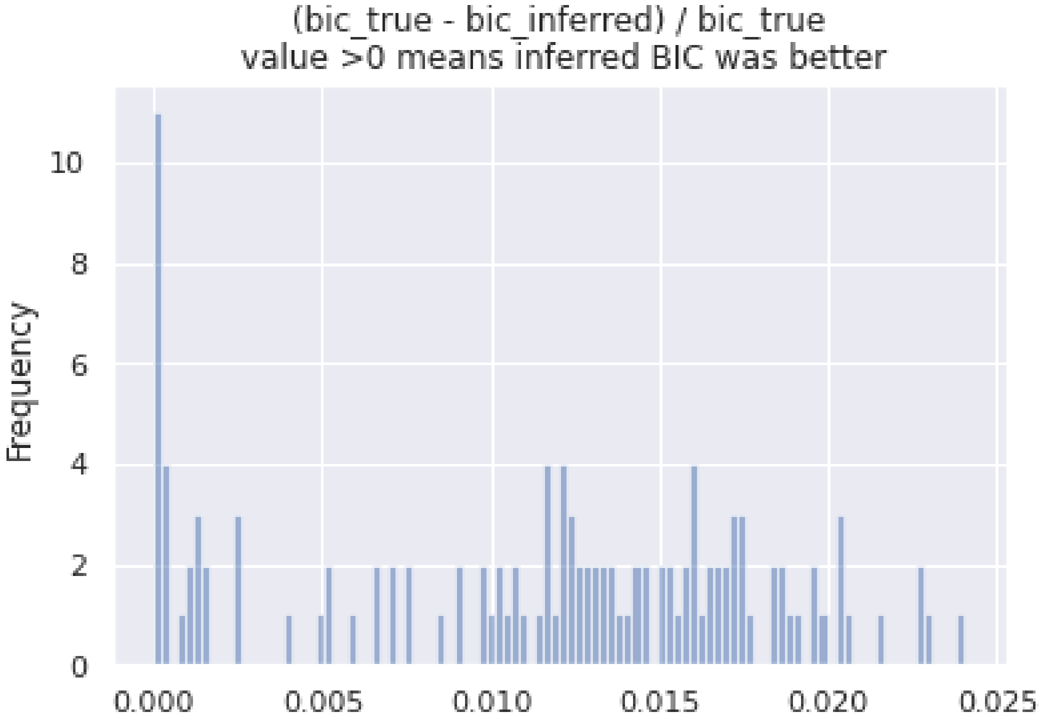
```
<Figure size 432x288 with 0 Axes>
```

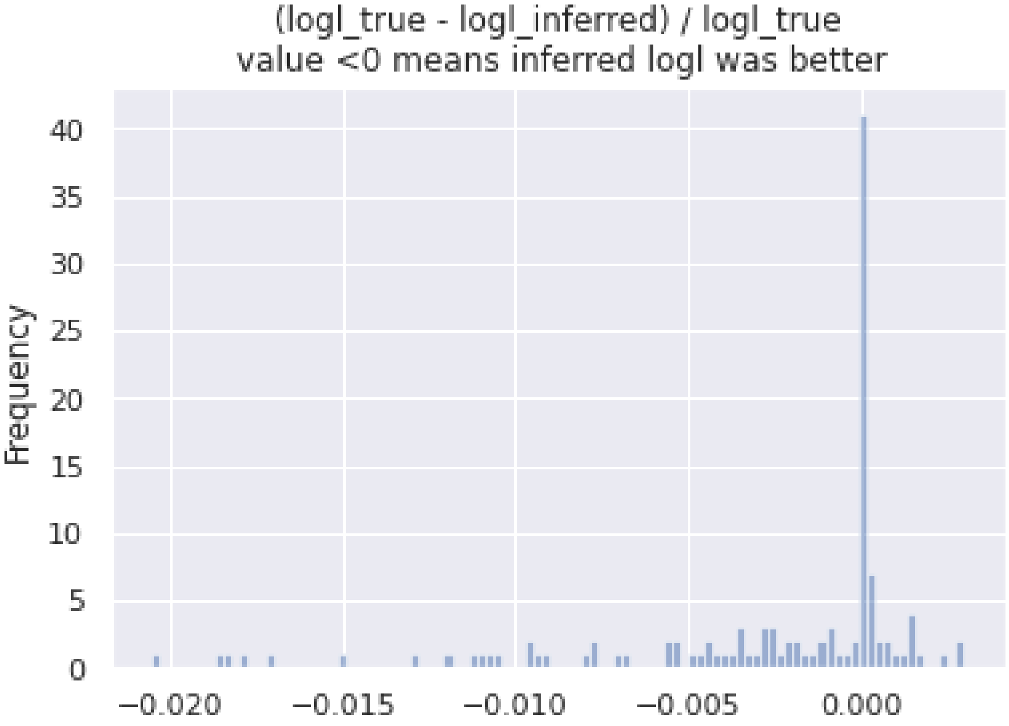


2.2.1 Plots for LikelihodType.AVERAGE

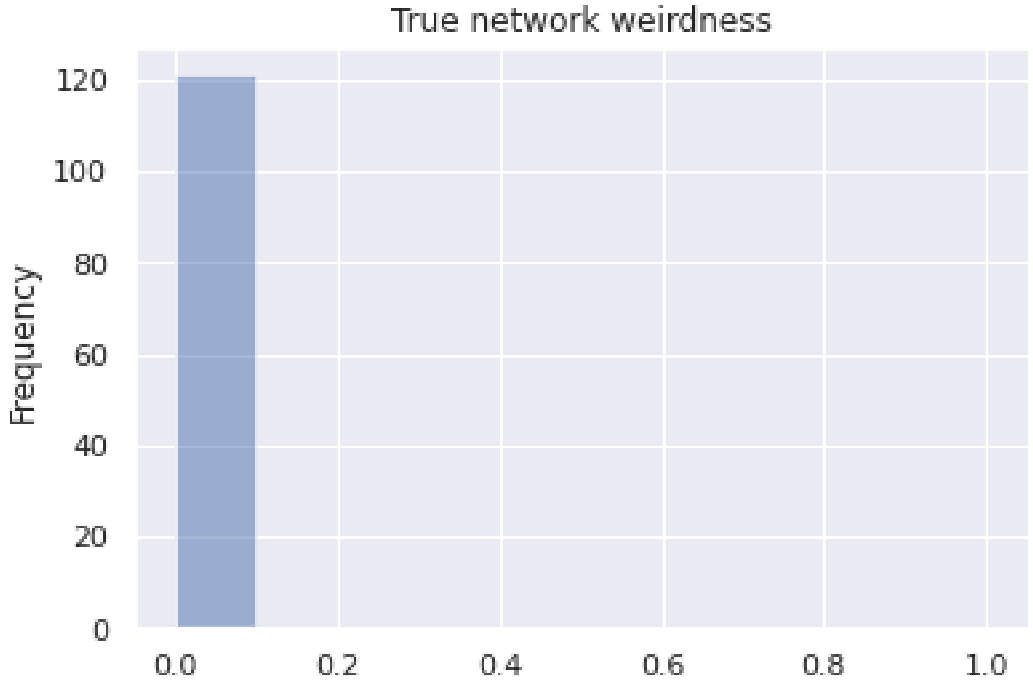
```
[19]: df_random_msasize_200_average = df_random_msasize_200.query('likelihood_type ==␣
       ↪"AVERAGE"')
      build_stats(df_random_msasize_200_average)
```

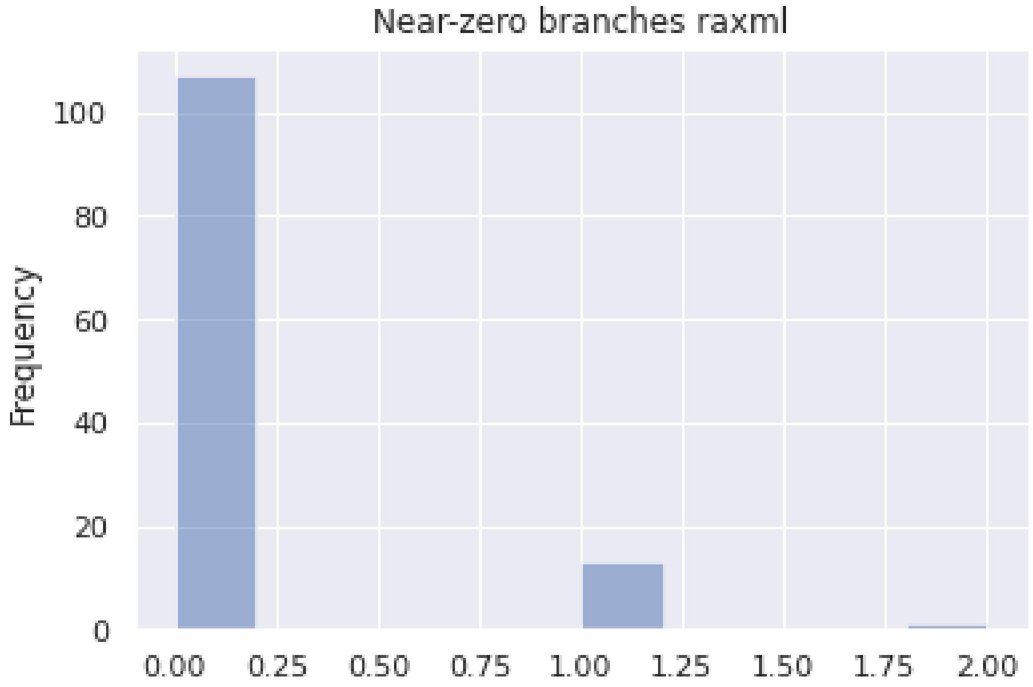
```
Inferred BIC better or equal: 120
Inferred BIC worse: 1

Inferred loglh better or equal: 56
Inferred loglh worse: 65

Inferred n_reticulations less: 100
Inferred n_reticulations equal: 21
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
2
4
6
8
10
0.000
0.005
0.010
0.015
0.020
0.025

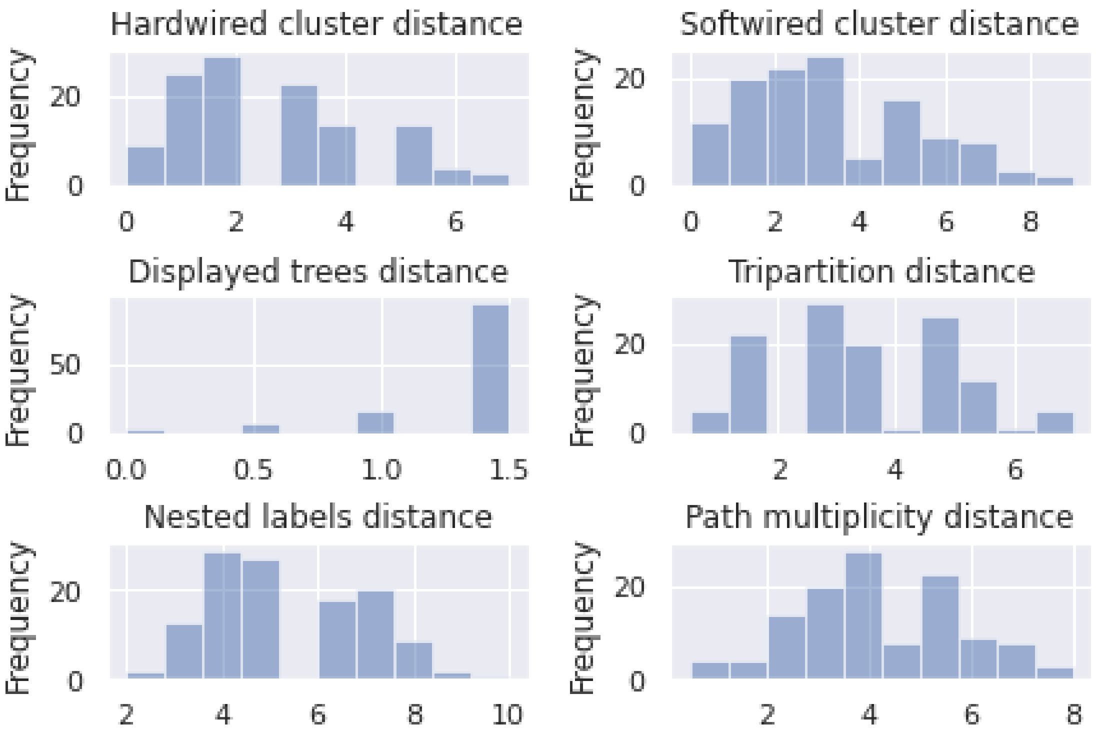

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
5
10
15
20
25
30
35
40
−0.020
−0.015
−0.010
−0.005
0.000

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

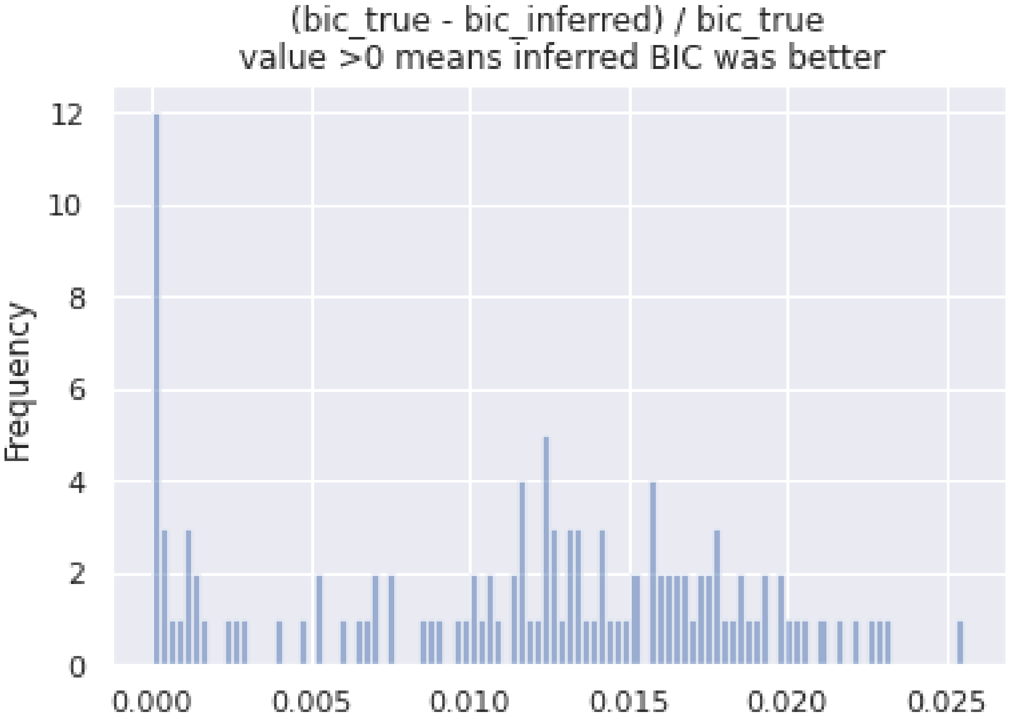
```
<Figure size 432x288 with 0 Axes>
```

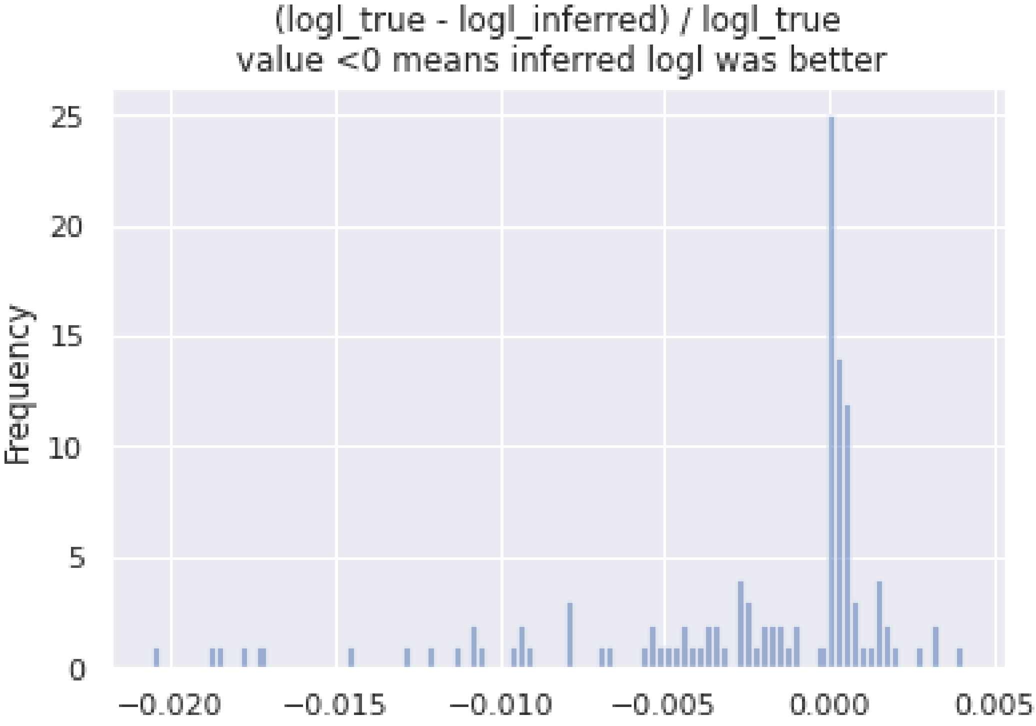


2.2.2 Plots for LikelihoodType.BEST

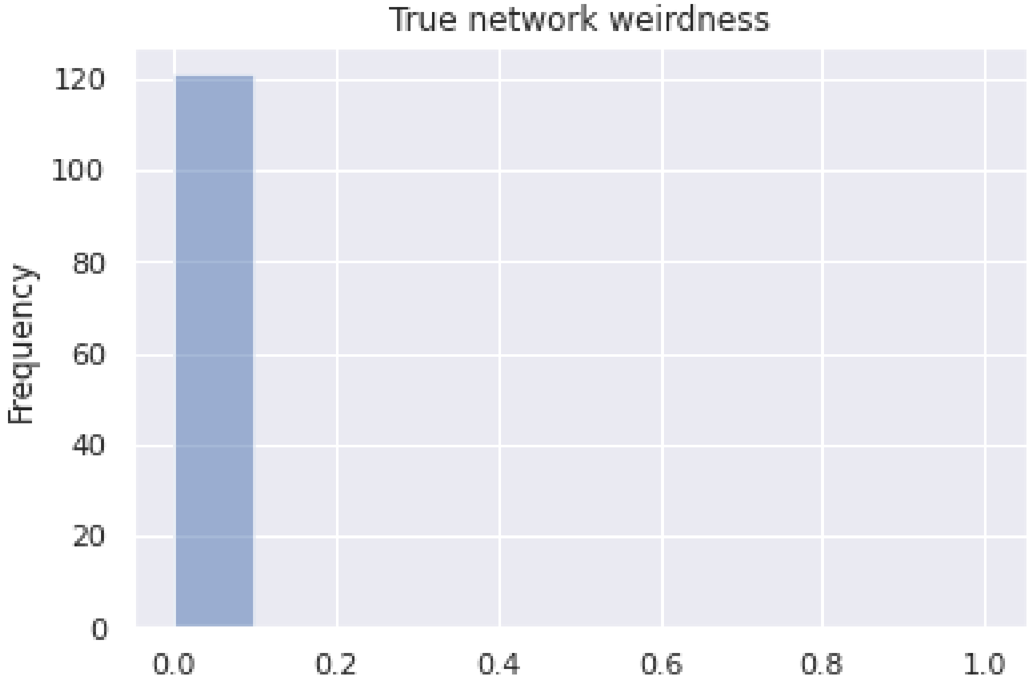
[20]:
```
df_random_msasize_200_best = df_random_msasize_200.query('likelihood_type ==␣
↪"BEST"')
build_stats(df_random_msasize_200_best)
```

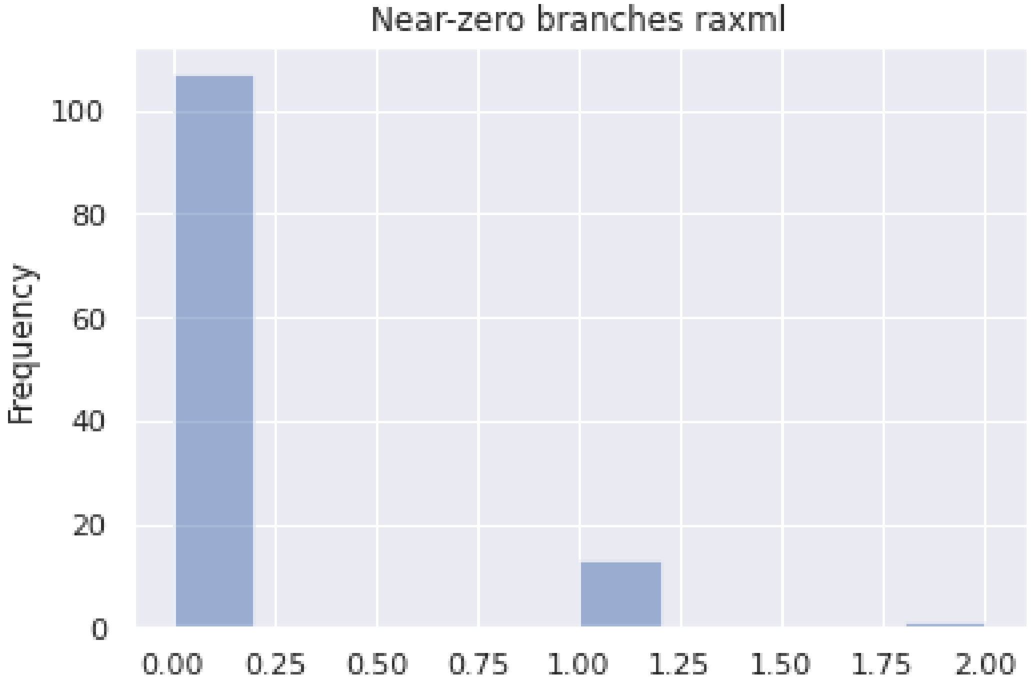
```
Inferred BIC better or equal: 119
Inferred BIC worse: 2

Inferred loglh better or equal: 64
Inferred loglh worse: 57

Inferred n_reticulations less: 100
Inferred n_reticulations equal: 21
Inferred n_reticulations more: 0
```


(bic_true - bic_inferred) / bic_true
value >0 means inferred BIC was better
Frequency
0
2
4
6
8
10
12
0.000
0.005
0.010
0.015
0.020
0.025

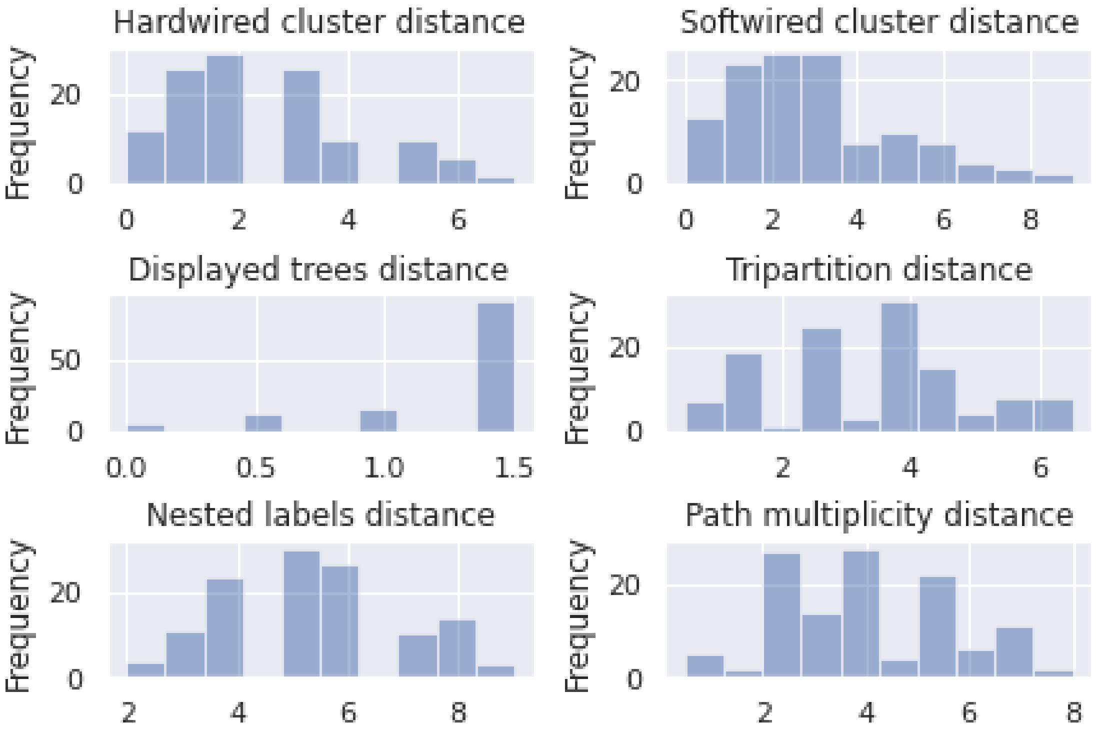

(logl_true - logl_inferred) / logl_true
value <0 means inferred logl was better
Frequency
0
5
10
15
20
25
−0.020
−0.015
−0.010
−0.005
0.000
0.005

```
<Figure size 432x288 with 0 Axes>
```


True network weirdness
Frequency
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0


Near-zero branches raxml
Frequency
0
20
40
60
80
100
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

```
<Figure size 432x288 with 0 Axes>
```


Hardwired cluster distance
Frequency
20
0
0
2
4
6
Softwired cluster distance
Frequency
20
0
0
2
4
6
8
Displayed trees distance
Frequency
50
0
0.0
0.5
1.0
1.5
Tripartition distance
Frequency
20
0
2
4
6
Nested labels distance
Frequency
20
0
2
4
6
8
Path multiplicity distance
Frequency
20
0
2
4
6
8

```
[ ]:
```