```
> model_base <- ergm(n1 ~ edges+degree(1))
```

```
Iteration 1 of at most 20:
Convergence test P-value: 2.3e-27
The log-likelihood improved by 0.5436
Iteration 2 of at most 20:
Convergence test P-value: 3.3e-19
The log-likelihood improved by 0.3567
Iteration 3 of at most 20:
Convergence test P-value: 2.9e-15
The log-likelihood improved by 0.3184
Iteration 4 of at most 20:
Convergence test P-value: 3e-42
The log-likelihood improved by 0.2939
Iteration 5 of at most 20:
Convergence test P-value: 3.4e-21
The log-likelihood improved by 0.1283
Iteration 6 of at most 20:
Convergence test P-value: 4.1e-14
The log-likelihood improved by 0.05055
Iteration 7 of at most 20:
Convergence test P-value: 9.1e-05
The log-likelihood improved by 0.01616
Iteration 8 of at most 20:
Convergence test P-value: 2.2e-01
The log-likelihood improved by 0.003225
Iteration 9 of at most 20:
Convergence test P-value: 4.4e-01
The log-likelihood improved by 0.001786
Iteration 10 of at most 20:
Convergence test P-value: 8.5e-01
```
Convergence detected. Stopping.
The log-likelihood improved by 0.0005741

```
> summary(model_base)
```

```
==========================
Summary of model fit
==========================
```

```
Formula:   n1 ~ edges + degree(1)
```

```
Iterations:   20
```

Monte Carlo MLE Results:

	Estimate	Std. Error	MCMC %	p-value	
edges	−3.21882	0.20173	20	<1e−04	***
degree1	2.63232	0.37375	20	<1e−04	***

```
---
```
Signif. codes: 0 "*" 0.001 "**" 0.01 "*" 0.05 "." 0.1 " " 1**

```
     Null Deviance: 7714.7  on 5565  degrees of freedom
 Residual Deviance:  955.3  on 5562  degrees of freedom
```

```
AIC: 961.3    BIC: 981.2    (Smaller is better.)
```

```
> gof(model_base)

Goodness-of-fit for degree

     obs min   mean max MC p-value
0     0   0   1.49   5        0.40
1    67  49  67.11  81        1.00
2    12   3   7.77  16        0.08
3    17   2   8.39  15        0.00
4     2   2   7.78  19        0.02
5     1   0   5.22  13        0.04
6     2   0   3.65  11        0.70
7     1   0   1.61   6        1.00
8     0   0   0.89   4        0.88
9     0   0   0.49   2        1.00
10    0   0   0.30   2        1.00
11    0   0   0.13   2        1.00
12    0   0   0.08   1        1.00
13    1   0   0.02   1        0.04
14    1   0   0.04   1        0.08
15    1   0   0.01   1        0.02
16    0   0   0.01   1        1.00
17    0   0   0.02   1        1.00
18    0   0   0.03   1        1.00
19    0   0   0.04   1        1.00
20    0   0   0.09   1        1.00
21    0   0   0.03   1        1.00
22    0   0   0.11   1        1.00
23    0   0   0.06   1        1.00
24    1   0   0.11   1        0.22
25    0   0   0.08   1        1.00
26    0   0   0.08   1        1.00
27    0   0   0.05   1        1.00
28    0   0   0.08   1        1.00
29    0   0   0.05   1        1.00
30    0   0   0.04   1        1.00
31    0   0   0.05   1        1.00
32    0   0   0.02   1        1.00
33    0   0   0.02   1        1.00
34    0   0   0.03   1        1.00
35    0   0   0.01   1        1.00
37    0   0   0.01   1        1.00

Goodness-of-fit for edgewise shared partner

       obs min   mean max MC p-value
esp0   120  80  96.95 127        0.02
esp1     0   6  18.19  39        0.00
esp2     0   0   4.40  14        0.16
esp3     0   0   1.00   7        0.90
esp4     0   0   0.25   2        1.00
esp5     0   0   0.03   1        1.00
esp6     0   0   0.01   1        1.00
esp9     0   0   0.01   1        1.00

Goodness-of-fit for minimum geodesic distance

       obs min     mean   max MC p-value
```

```
1      120  91  120.84   156        0.98
2      655 266  549.42   839        0.42
3      809 437 1020.72  1664        0.42
4     1414 469 1013.03  1436        0.04
5      837 214  591.72  1005        0.18
6      741  18  221.17   554        0.00
7      380   0   58.46   237        0.00
8       74   0   11.93   123        0.06
9       30   0    2.78    64        0.06
10       0   0    0.77    26        1.00
11       0   0    0.09     5        1.00
12       0   0    0.01     1        1.00
Inf    505 905 1974.06  3738        0.00

> mcmc.diagnostics(model_base)
Sample statistics summary:

Iterations = 10000:1009900
Thinning interval = 100
Number of chains = 1
Sample size per chain = 10000
```

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

```
                   Mean     SD Naive SE Time-series SE
edges          -0.1439  14.97   0.1497         1.1506
degree1         0.1558   6.67   0.0667         0.4535
```

2. Quantiles for each variable:

```
                2.5% 25% 50% 75% 97.5%
edges            -26 -11  -1  10    31
degree1          -13  -4   0   5    12
```

Are sample statistics significantly different from observed?

	edges	degree1	Overall (Chi^2)
diff.	-0.1439000	0.1558000	NA
test stat.	-0.1250666	0.3435344	0.8063061
P-val.	0.9004709	0.7311965	0.8479581

Sample statistics cross-correlations:

```
                    edges      degree1 nodecov.features
edges           1.0000000 -0.8767134        0.6755583
degree1        -0.8767134  1.0000000       -0.4611390
```

Sample statistics auto-correlation:
Chain 1

```
            edges     degree1
Lag 0    1.0000000 1.0000000
Lag 100  0.9516084 0.9008448
Lag 200  0.9119373 0.8374290
Lag 300  0.8752097 0.7898382
Lag 400  0.8422160 0.7479431
Lag 500  0.8092260 0.7123876
```

Sample statistics burn-in diagnostic (Geweke):
Chain 1

```
Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

           edges          degree1
         -0.8652           0.8777


P-values (lower = worse):
           edges          degree1
       0.3869519        0.3801096
```
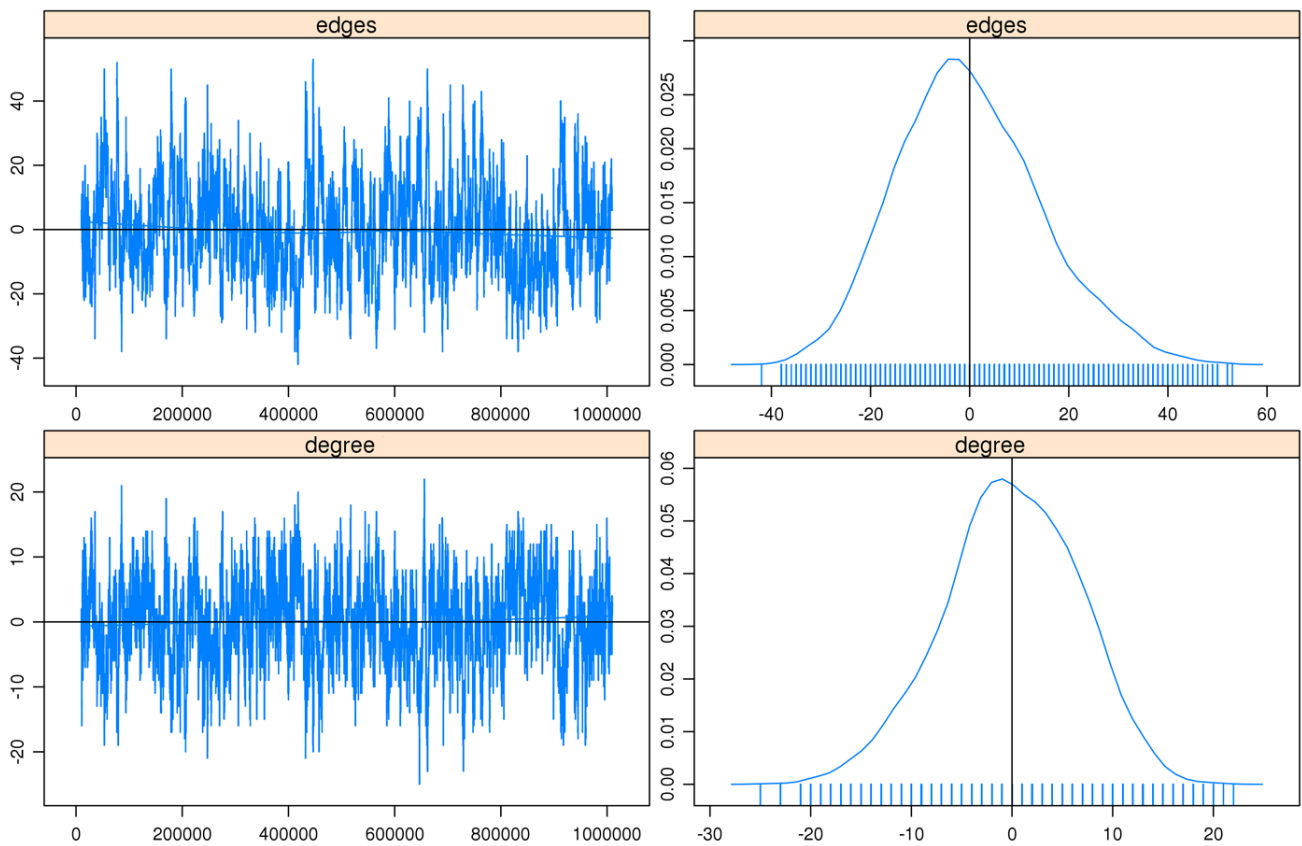

Sample statistics

Supplementary Figure 1. Simulation details (left) and related statistics (right) of the stochastic analysis about the two components estimator for the graph describing the HOXB cluster of genes according to the Lieberman-Aiden et al. Hi-C experiment.

> model_ctcf <- ergm(n1 ~ edges+degree(1)+nodecov("ctcf"))

```
Iteration 1 of at most 20:
Convergence test P-value: 1.1e-46
The log-likelihood improved by 0.7188
Iteration 2 of at most 20:
Convergence test P-value: 3.7e-45
The log-likelihood improved by 0.4368
Iteration 3 of at most 20:
Convergence test P-value: 5.9e-25
The log-likelihood improved by 0.2327
Iteration 4 of at most 20:
Convergence test P-value: 1.3e-29
The log-likelihood improved by 0.1199
Iteration 5 of at most 20:
Convergence test P-value: 1.6e-11
The log-likelihood improved by 0.04484
Iteration 6 of at most 20:
Convergence test P-value: 2.8e-04
The log-likelihood improved by 0.01505
Iteration 7 of at most 20:
Convergence test P-value: 4.3e-04
The log-likelihood improved by 0.01176
Iteration 8 of at most 20:
Convergence test P-value: 2.6e-01
The log-likelihood improved by 0.0027
Iteration 9 of at most 20:
Convergence test P-value: 3e-01
The log-likelihood improved by 0.002686
Iteration 10 of at most 20:
Convergence test P-value: 7.6e-01
```
Convergence detected. Stopping.
The log-likelihood improved by 0.0007933

```
> summary(model_ctcf)
```

```
==========================
Summary of model fit
==========================
```

```
Formula:   n1 ~ edges + degree(1) + nodecov("ctcf")
```

```
Iterations:  20
```

Monte Carlo MLE Results:

	Estimate	Std. Error	MCMC %	p-value	
edges	-3.22486	0.20126	17	<1e-04	***
degree1	2.62902	0.36735	16	<1e-04	***
nodecov.ctcf	0.52386	0.04158	6	<1e-04	***

```
---
Signif. codes:  0 "***" 0.001 "**" 0.01 "*" 0.05 "." 0.1 " " 1
```

```
     Null Deviance: 7714.7  on 5565  degrees of freedom
 Residual Deviance:  954.5  on 5562  degrees of freedom
```

```
AIC: 960.5    BIC: 980.4    (Smaller is better.)
```

```
> gof(model_ctcf)

Goodness-of-fit for degree

     obs min   mean max MC p-value
0     0   0   1.39   5        0.44
1    67  55  68.07  87        0.98
2    12   2   7.85  15        0.18
3    17   2   8.71  16        0.00
4     2   1   7.65  16        0.04
5     1   0   4.91  11        0.10
6     2   0   3.05   9        0.92
7     1   0   1.55   7        1.00
8     0   0   0.84   5        0.80
9     0   0   0.41   3        1.00
10    0   0   0.26   2        1.00
11    0   0   0.12   2        1.00
12    0   0   0.10   1        1.00
13    1   0   0.02   1        0.04
14    1   0   0.06   1        0.12
15    1   0   0.02   1        0.04
16    0   0   0.01   1        1.00
17    0   0   0.07   1        1.00
18    0   0   0.03   1        1.00
19    0   0   0.02   1        1.00
20    0   0   0.03   1        1.00
21    0   0   0.09   1        1.00
22    0   0   0.08   1        1.00
23    0   0   0.07   1        1.00
24    1   0   0.08   1        0.16
25    0   0   0.11   1        1.00
26    0   0   0.09   1        1.00
27    0   0   0.05   1        1.00
28    0   0   0.07   1        1.00
29    0   0   0.09   1        1.00
30    0   0   0.04   1        1.00
31    0   0   0.02   1        1.00
32    0   0   0.02   1        1.00
33    0   0   0.01   1        1.00
38    0   0   0.01   1        1.00

Goodness-of-fit for edgewise shared partner

       obs min   mean max MC p-value
esp0  120  76  97.88 120        0.02
esp1    0   0  15.54  36        0.02
esp2    0   0   3.29  13        0.40
esp3    0   0   0.83   5        1.00
esp4    0   0   0.11   3        1.00
esp5    0   0   0.03   1        1.00




Goodness-of-fit for minimum geodesic distance

      obs min    mean   max MC p-value
1     120  86  117.68  144        0.82
2     655 221  519.89  924        0.20
```

```
3     809 301   954.78 1496        0.60
4    1414 238   970.08 1471        0.02
5     837  78   582.70  994        0.16
6     741  30   231.17  616        0.00
7     380   0    72.54  281        0.00
8      74   0    20.04  256        0.18
9      30   0     6.80  203        0.12
10      0   0     2.63  130        1.00
11      0   0     0.76   52        1.00
12      0   0     0.16   16        1.00
Inf   505 511  2085.77 4194        0.00

> mcmc.diagnostics(model_ctcf)
Sample statistics summary:


Iterations = 10000:1009900
Thinning interval = 100
Number of chains = 1
Sample size per chain = 10000


1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                   Mean      SD Naive SE Time-series SE
edges          -0.8918 13.957  0.13957         0.9713
degree1         0.2751  6.575  0.06575         0.4017
nodecov.ctcf   -2.4106 32.056  0.32056         2.4000


2. Quantiles for each variable:

                2.5% 25% 50% 75% 97.5%
edges            -26 -11  -2   8 29.00
degree1          -13  -4   1   5 12.02
nodecov.ctcf     -66 -24  -2  20 58.00
```

Are sample statistics significantly different from observed?

	edges	**degree1**	**nodecov.ctcf**	**Overall (Chi^2)**
diff.	-0.8918000	0.2751000	-1.4106000	**NA**
test stat.	-0.9181081	0.6848680	-1.0044315	1.1555172
P-val.	0.3585622	0.4934272	0.3151707	0.7636917

```
Sample statistics cross-correlations:
                  edges     degree1 nodecov.ctcf
edges         1.0000000 -0.8753849    0.6168059
degree1      -0.8753849  1.0000000   -0.4054477
nodecov.ctcf  0.6168059 -0.4054477    1.0000000

Sample statistics auto-correlation:
Chain 1
            edges    degree1 nodecov.ctcf
Lag 0   1.0000000 1.0000000    1.0000000
Lag 100 0.9449862 0.8970551    0.9613638
Lag 200 0.8985582 0.8262543    0.9260649
Lag 300 0.8582403 0.7722118    0.8939116
Lag 400 0.8207605 0.7273405    0.8629792
Lag 500 0.7861635 0.6889831    0.8338639

Sample statistics burn-in diagnostic (Geweke):
Chain 1
```
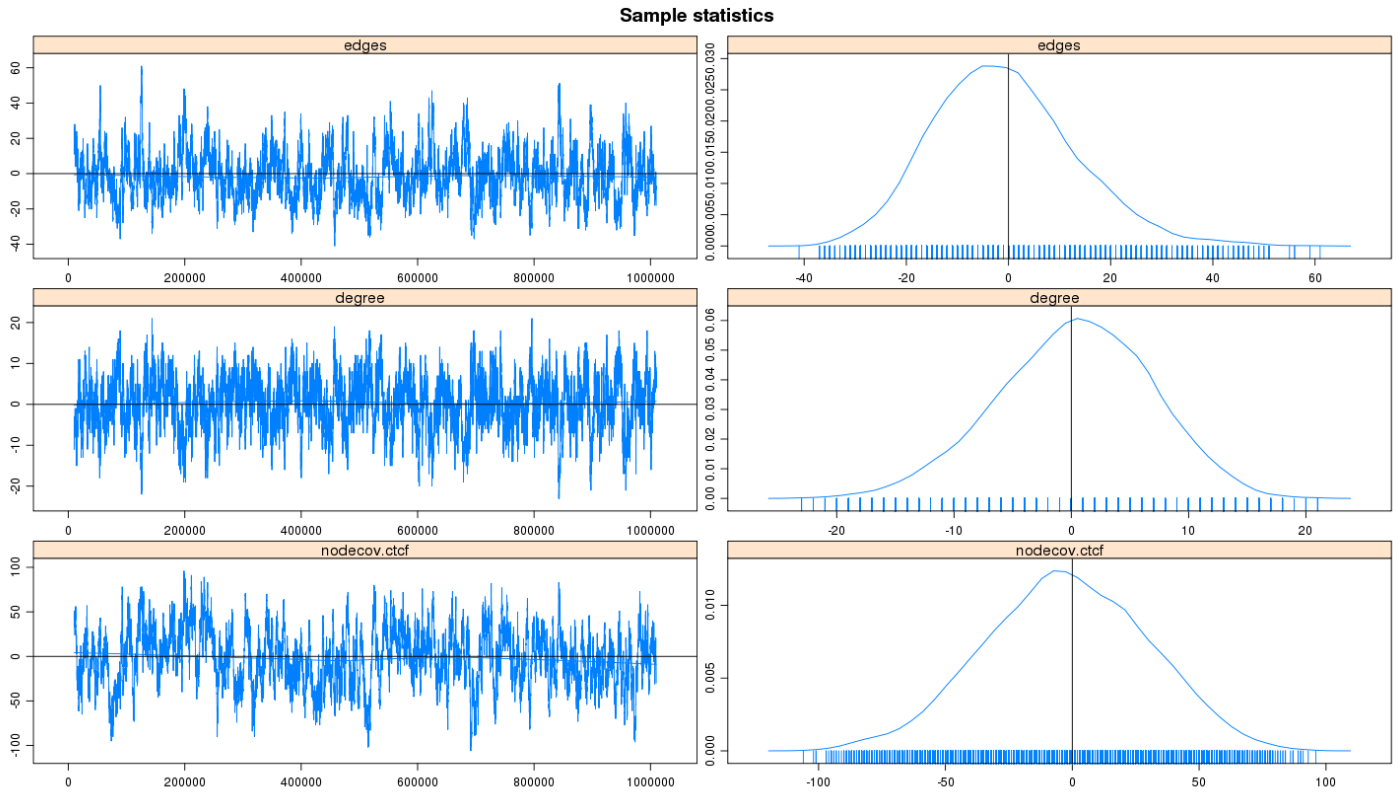
```
Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

        edges       degree1 nodecov.ctcf
      -0.3159       -0.1597      -1.0137


P-values (lower = worse):
        edges       degree1 nodecov.ctcf
    0.7520804     0.8731382     0.3107134
```


Supplementary Figure 2. Simulation details (left) and related statistics (right) of the stochastic analysis about the three components estimator (edges, degree, and nodecov.ctcf) for the graph describing the HOXB cluster of genes according to the Lieberman-Aiden et al. Hi-C experiment.

> model_rss <- ergm(n1 ~ edges+degree(1)+nodecov("rss"))

```
Iteration 1 of at most 20:
Convergence test P-value: 4.2e-213
The log-likelihood improved by 1.639
Iteration 2 of at most 20:
Convergence test P-value: 2.7e-27
The log-likelihood improved by 0.5103
Iteration 3 of at most 20:
Convergence test P-value: 1.1e-34
The log-likelihood improved by 0.5345
Iteration 4 of at most 20:
Convergence test P-value: 4.8e-33
The log-likelihood improved by 0.3403
Iteration 5 of at most 20:
Convergence test P-value: 1.1e-40
The log-likelihood improved by 0.2575
Iteration 6 of at most 20:
Convergence test P-value: 7.9e-28
The log-likelihood improved by 0.1187
Iteration 7 of at most 20:
Convergence test P-value: 8.4e-14
The log-likelihood improved by 0.04614
Iteration 8 of at most 20:
Convergence test P-value: 7.3e-02
The log-likelihood improved by 0.004191
Iteration 9 of at most 20:
Convergence test P-value: 4.4e-01
The log-likelihood improved by 0.001731
Iteration 10 of at most 20:
Convergence test P-value: 3.4e-01
The log-likelihood improved by 0.00267
Iteration 11 of at most 20:
Convergence test P-value: 3.7e-01
The log-likelihood improved by 0.001355
Iteration 12 of at most 20:
Convergence test P-value: 8.3e-03
The log-likelihood improved by 0.004198
Iteration 13 of at most 20:
Convergence test P-value: 2.9e-01
The log-likelihood improved by 0.0019
Iteration 14 of at most 20:
Convergence test P-value: 3.4e-01
The log-likelihood improved by 0.001825
Iteration 15 of at most 20:
Convergence test P-value: 9.9e-02
The log-likelihood improved by 0.004545
Iteration 16 of at most 20:
Convergence test P-value: 9.7e-01
```
Convergence detected. Stopping.
The log-likelihood improved by 0.0001182

```
> summary(model_rss)

==========================
Summary of model fit
==========================
```

```
Formula:   n1 ~ edges + degree(1) + nodecov("rss")

Iterations:  20

Monte Carlo MLE Results:
            Estimate Std. Error MCMC %  p-value
edges        -3.36306    0.22717      28  <1e-04 ***
degree1       2.60012    0.38793      25  <1e-04 ***
nodecov.rss   0.39780    0.03176      12  <1e-04 ***
---
Signif. codes:  0 "***" 0.001 "**" 0.01 "*" 0.05 "." 0.1 " " 1

      Null Deviance: 7714.7  on 5565  degrees of freedom
 Residual Deviance:  954.1  on 5562  degrees of freedom

AIC: 960.1     BIC: 980     (Smaller is better.)

> gof(model_rss)

Goodness-of-fit for degree

     obs min  mean max MC p-value
0     0   0   1.43   5        0.52
1    67  49  67.01  78        0.92
2    12   3   8.37  14        0.38
3    17   3   8.94  19        0.06
4     2   2   7.77  15        0.04
5     1   1   4.83  12        0.08
6     2   0   2.78   7        0.92
7     1   0   1.80   6        0.96
8     0   0   0.93   4        0.82
9     0   0   0.50   2        1.00
10    0   0   0.25   2        1.00
11    0   0   0.20   2        1.00
12    0   0   0.07   1        1.00
13    1   0   0.06   1        0.12
14    1   0   0.03   1        0.06
15    1   0   0.01   1        0.02
16    0   0   0.06   1        1.00
17    0   0   0.02   1        1.00
18    0   0   0.06   1        1.00
19    0   0   0.05   1        1.00
20    0   0   0.07   1        1.00
21    0   0   0.04   1        1.00
22    0   0   0.10   1        1.00
23    0   0   0.14   1        1.00
24    1   0   0.10   1        0.20
25    0   0   0.07   1        1.00
26    0   0   0.09   1        1.00
27    0   0   0.05   1        1.00
28    0   0   0.03   1        1.00
29    0   0   0.04   1        1.00
30    0   0   0.03   1        1.00
31    0   0   0.03   1        1.00
32    0   0   0.01   1        1.00
34    0   0   0.01   1        1.00
38    0   0   0.01   1        1.00
39    0   0   0.01   1        1.00
```

Goodness-of-fit for edgewise shared partner

	obs	min	mean	max	MC p-value
esp0	120	81	97.59	130	0.06
esp1	0	0	16.67	40	0.02
esp2	0	0	3.74	12	0.22
esp3	0	0	0.78	4	1.00
esp4	0	0	0.18	3	1.00
esp5	0	0	0.03	1	1.00
esp6	0	0	0.01	1	1.00

Goodness-of-fit for minimum geodesic distance

	obs	min	mean	max	MC p-value
1	120	97	119.00	160	0.90
2	655	305	512.67	941	0.28
3	809	484	951.40	1558	0.66
4	1414	439	972.45	1603	0.10
5	837	234	594.14	948	0.18
6	741	49	237.53	532	0.00
7	380	2	70.43	270	0.00
8	74	0	16.48	114	0.08
9	30	0	3.41	65	0.04
10	0	0	0.65	32	1.00
11	0	0	0.21	15	1.00
Inf	505	412	2086.63	3609	0.02

```
> mcmc.diagnostics(model_rss)
Sample statistics summary:


Iterations = 10000:1009900
Thinning interval = 100
Number of chains = 1
Sample size per chain = 10000
```

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
edges	0.0505	14.077	0.14077	0.9633
degree1	-0.1124	6.372	0.06372	0.3876
nodecov.rss	0.0745	47.443	0.47443	3.5640

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
edges	-25	-10	-1	9	31
degree1	-13	-4	0	4	12
nodecov.rss	-90	-32	-1	33	93

Are sample statistics significantly different from observed?

	edges	degree1	nodecov.rss	Overall (Chi^2)
diff.	0.0505000	-0.1124000	0.07450000	NA
test stat.	0.0524262	-0.2899927	0.02090356	0.2673271
P-val.	0.9581891	0.7718218	0.98332259	0.9660515

Sample statistics cross-correlations:

	edges	degree1	nodecov.rss
edges	1.0000000	-0.8706452	0.7568610

```
degree1      -0.8706452  1.0000000  -0.5582727
nodecov.rss   0.7568610 -0.5582727   1.0000000


Sample statistics auto-correlation:
Chain 1
             edges     degree1 nodecov.rss
Lag 0    1.0000000 1.0000000   1.0000000
Lag 100  0.9459533 0.8933994   0.9634909
Lag 200  0.8991287 0.8238714   0.9300327
Lag 300  0.8585887 0.7727913   0.8985329
Lag 400  0.8181824 0.7267730   0.8671116
Lag 500  0.7807026 0.6866192   0.8378673


Sample statistics burn-in diagnostic (Geweke):
Chain 1


Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5


      edges      degree1 nodecov.rss
     -1.309        1.319      -1.213


P-values (lower = worse):
      edges      degree1 nodecov.rss
  0.1905293    0.1870648   0.2249617
```
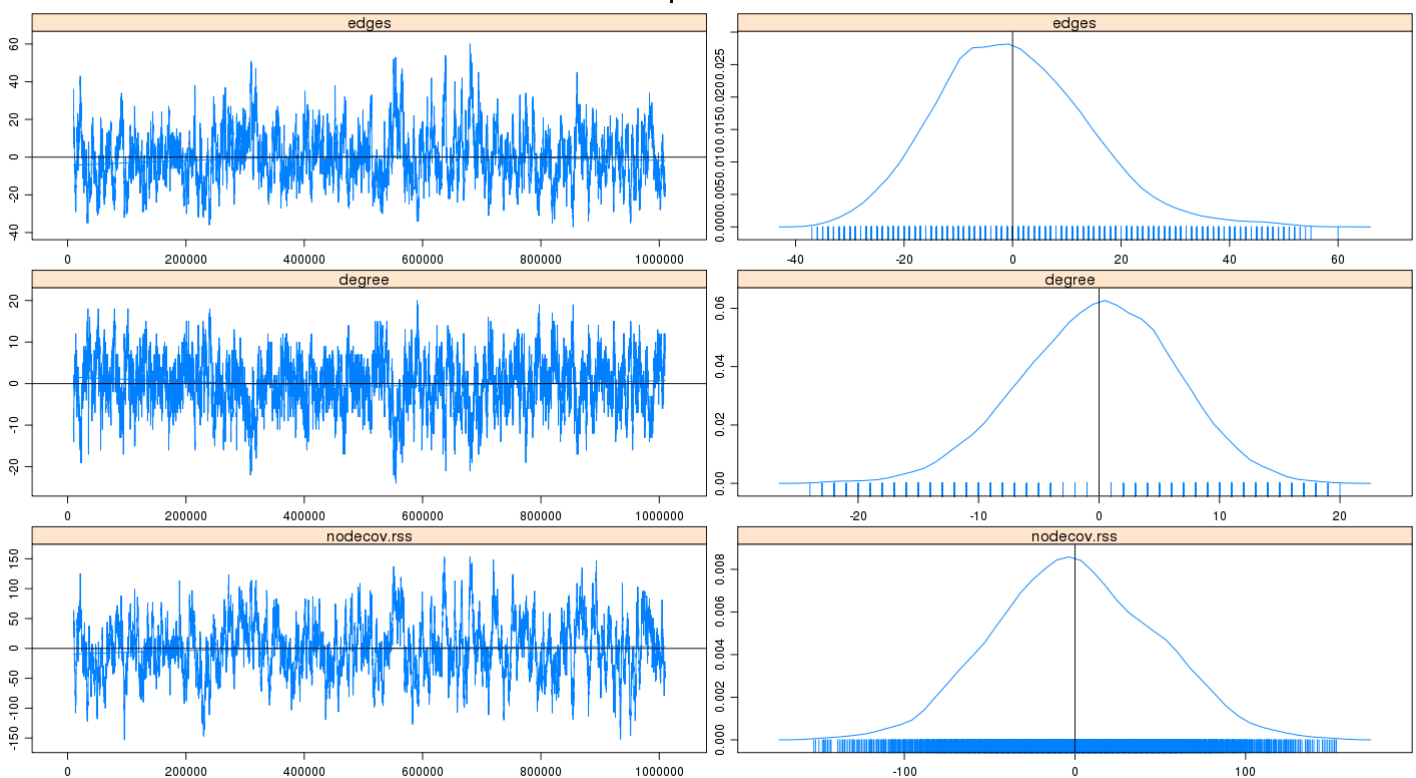

Supplementary Figure 3. Simulation details (left) and related statistics (right) of the stochastic analysis about the three components estimator (edges, degree, and nodecov.rss) for the graph describing the HOXB cluster of genes according to the Lieberman-Aiden et al. Hi-C experiment.

```
> model_iso <- ergm(n1 ~ edges+degree(1)+nodecov("iso"))

Iteration 1 of at most 20:
Convergence test P-value: 0e+00
The log-likelihood improved by 1.494
Iteration 2 of at most 20:
Convergence test P-value: 4.2e-97
The log-likelihood improved by 0.2085
Iteration 3 of at most 20:
Convergence test P-value: 2.4e-16
The log-likelihood improved by 0.04267
Iteration 4 of at most 20:
Convergence test P-value: 1.6e-04
The log-likelihood improved by 0.01003
Iteration 5 of at most 20:
Convergence test P-value: 9.6e-04
The log-likelihood improved by 0.007459
Iteration 6 of at most 20:
Convergence test P-value: 8e-02
The log-likelihood improved by 0.004762
Iteration 7 of at most 20:
Convergence test P-value: 5.2e-01
Convergence detected. Stopping.
The log-likelihood improved by 0.002215


> summary(model_iso)

==========================
Summary of model fit
==========================

Formula:   n1 ~ edges + degree(1) + nodecov("iso")

Iterations:  20

Monte Carlo MLE Results:
            Estimate Std. Error MCMC %  p-value
edges       -3.307232   0.438861     83  < 1e-04 ***
degree1      2.474114   0.693693     79 0.000365 ***
nodecov.iso -0.840357   0.092697     62  < 1e-04 ***
---
Signif. codes:  0 "***" 0.001 "**" 0.01 "*" 0.05 "." 0.1 " " 1

     Null Deviance: 7714.7  on 5565  degrees of freedom
 Residual Deviance:  918.2  on 5562  degrees of freedom

AIC: 924.2    BIC: 944     (Smaller is better.)


> gof(model_iso)

Goodness-of-fit for degree

    obs min  mean max MC p-value
0    0   0  1.75   6        0.34
1   67  54 68.76  83        0.82
2   12   1  8.54  15        0.30
3   17   2  9.00  18        0.04
4    2   2  6.96  16        0.04
```

```
5    1   0   4.54   12         0.16
6    2   0   2.51    7         1.00
7    1   0   1.15    5         1.00
8    0   0   0.65    3         0.98
9    0   0   0.51    3         1.00
10   0   0   0.32    2         1.00
11   0   0   0.15    2         1.00
12   0   0   0.07    1         1.00
13   1   0   0.05    2         0.08
14   1   0   0.02    1         0.04
15   1   0   0.02    1         0.04
20   0   0   0.01    1         1.00
22   0   0   0.01    1         1.00
24   1   0   0.01    1         0.02
25   0   0   0.02    1         1.00
26   0   0   0.05    1         1.00
27   0   0   0.08    1         1.00
28   0   0   0.03    1         1.00
29   0   0   0.10    1         1.00
30   0   0   0.06    1         1.00
31   0   0   0.06    1         1.00
32   0   0   0.08    1         1.00
33   0   0   0.05    1         1.00
34   0   0   0.12    1         1.00
35   0   0   0.10    1         1.00
36   0   0   0.05    1         1.00
37   0   0   0.03    1         1.00
38   0   0   0.04    1         1.00
39   0   0   0.03    1         1.00
40   0   0   0.03    1         1.00
41   0   0   0.01    1         1.00
42   0   0   0.01    1         1.00
43   0   0   0.01    1         1.00
49   0   0   0.01    1         1.00
```

Goodness-of-fit for edgewise shared partner

```
      obs min   mean max MC p-value
esp0 120   73 92.59 116        0.00
esp1   0    6 18.19  35        0.00
esp2   0    0  5.19  14        0.08
esp3   0    0  1.36   8        0.68
esp4   0    0  0.31   3        1.00
esp5   0    0  0.08   2        1.00
esp6   0    0  0.06   1        1.00
```

Goodness-of-fit for minimum geodesic distance

```
      obs min    mean   max MC p-value
1    120   91  117.78  149        0.78
2    655  404  709.56 1267        0.80
3    809  608 1151.63 1740        0.12
4   1414  431  959.08 1411        0.00
5    837  166  463.41  997        0.04
6    741    9  149.05  417        0.00
7    380    0   34.75  207        0.00
8     74    0    5.29   57        0.00
9     30    0    0.49    9        0.00
10     0    0    0.04    3        1.00
Inf  505  808 1973.92 3714        0.00
```

```
> mcmc.diagnostics(model_iso)
Sample statistics summary:

Iterations = 10000:1009900
Thinning interval = 100
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                 Mean      SD Naive SE Time-series SE
edges        -0.5141  13.547  0.13547         0.8256
degree1       0.0550   6.715  0.06715         0.3728
nodecov.iso  -8.2234  24.476  2.24476         9.5127

2. Quantiles for each variable:

                2.5%   25% 50% 75% 97.5%
edges        -24.00   -10  -2   8    28
degree1      -13.02    -4   0   5    13
nodecov.iso  -45.02   -18 -38  12    19
```

Are sample statistics significantly different from observed?

	edges	degree1	nodecov.iso	Overall (Chi^2)
diff.	**-0.5141000**	**0.0550000**	**-2.2234000**	**NA**
test stat.	**-0.6227272**	**0.1475413**	**-0.4464095**	**1.2645635**
P-val.	**0.5334638**	**0.8827047**	**0.1480624**	**0.5193436**

```
Sample statistics cross-correlations:
                  edges     degree1 nodecov.iso
edges         1.0000000 -0.8637495   0.5834390
degree1      -0.8637495  1.0000000  -0.3559374
nodecov.iso   0.5834390 -0.3559374   1.0000000

Sample statistics auto-correlation:
Chain 1
             edges    degree1 nodecov.iso
Lag 0    1.0000000 1.0000000   1.0000000
Lag 100  0.9418846 0.8945609   0.9724958
Lag 200  0.8910281 0.8251952   0.9471588
Lag 300  0.8448309 0.7672479   0.9230766
Lag 400  0.8019794 0.7181222   0.9000278
Lag 500  0.7615925 0.6739926   0.8768215

Sample statistics burn-in diagnostic (Geweke):
Chain 1

Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

     edges    degree1 nodecov.iso
   0.61736    0.06172     2.15205

P-values (lower = worse):
     edges    degree1 nodecov.iso
 0.53699653 0.95078271  0.31393487
```
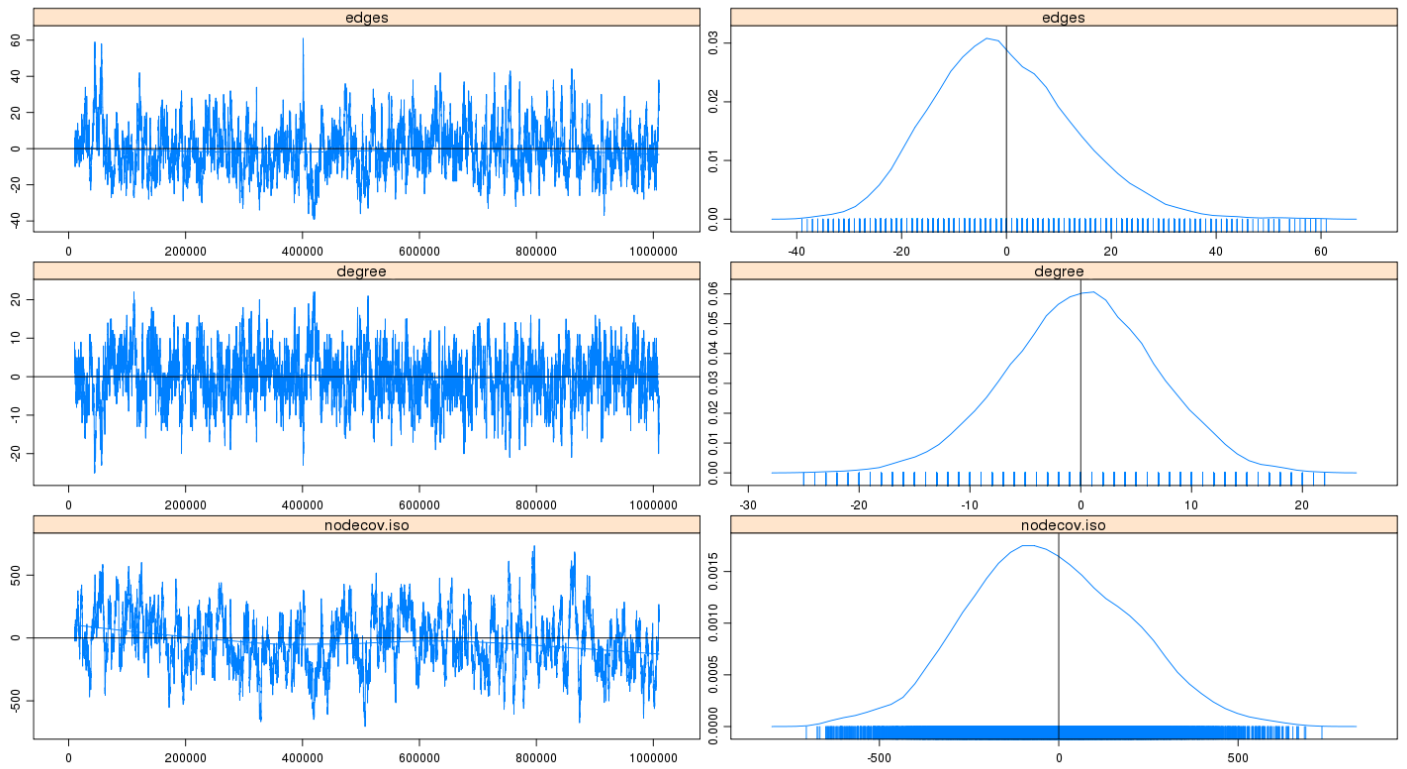
Supplementary Figure 4. Simulation details (left) and related statistics (right) of the stochastic analysis about the three components estimator (edges, degree, and nodecov.iso) for the graph describing the HOXB cluster of genes according to the Lieberman-Aiden et al. Hi-C experiment.

> model_dnase <- ergm(n1 ~ edges+degree(1)+nodecov("dnase"))

```
Iteration 1 of at most 20:
Convergence test P-value: 0e+00
The log-likelihood improved by 5.794
Iteration 2 of at most 20:
Convergence test P-value: 1.1e-60
The log-likelihood improved by 1.245
Iteration 3 of at most 20:
Convergence test P-value: 6.6e-90
The log-likelihood improved by 0.6984
Iteration 4 of at most 20:
Convergence test P-value: 3.5e-89
The log-likelihood improved by 0.4642
Iteration 5 of at most 20:
Convergence test P-value: 7.7e-37
The log-likelihood improved by 0.1958
Iteration 6 of at most 20:
Convergence test P-value: 1.3e-22
The log-likelihood improved by 0.08744
Iteration 7 of at most 20:
Convergence test P-value: 1.3e-05
The log-likelihood improved by 0.01626
Iteration 8 of at most 20:
Convergence test P-value: 3.9e-03
The log-likelihood improved by 0.005713
Iteration 9 of at most 20:
Convergence test P-value: 2.4e-01
The log-likelihood improved by 0.001532
Iteration 10 of at most 20:
Convergence test P-value: 5.1e-01
```
Convergence detected. Stopping.
The log-likelihood improved by 0.0009326

```
> summary(model_dnase)

==========================
Summary of model fit
==========================

Formula:   n1 ~ edges + degree(1) + nodecov("dnase")

Iterations:  20
```

Monte Carlo MLE Results:

	Estimate	Std. Error	MCMC %	p-value	
edges	-3.38574	0.22362	12	<1e-04	***
degree1	2.59670	0.35767	12	<1e-04	***
nodecov.dnase	0.86291	0.07961	6	<1e-04	***

```
---
Signif. codes:  0 "***" 0.001 "**" 0.01 "*" 0.05 "." 0.1 " " 1

     Null Deviance: 7714.7  on 5565  degrees of freedom
 Residual Deviance:  974.6  on 5562  degrees of freedom

AIC: 980.6    BIC: 1000    (Smaller is better.)

> gof(model_dnase)
```

```
Goodness-of-fit for degree

     obs min   mean max MC p-value
0     0   0   1.52    4        0.32
1    67  46  66.46   80        1.00
2    12   1   7.14   17        0.08
3    17   2   8.51   17        0.04
4     2   0   6.69   14        0.16
5     1   1   5.46   13        0.04
6     2   0   3.45   10        0.74
7     1   0   2.14    6        0.78
8     0   0   1.43    5        0.38
9     0   0   0.91    4        0.78
10    0   0   0.65    3        1.00
11    0   0   0.51    2        1.00
12    0   0   0.27    2        1.00
13    1   0   0.19    2        0.36
14    1   0   0.16    1        0.32
15    1   0   0.13    1        0.26
16    0   0   0.10    1        1.00
17    0   0   0.08    2        1.00
18    0   0   0.05    1        1.00
19    0   0   0.06    1        1.00
20    0   0   0.06    1        1.00
22    0   0   0.01    1        1.00
23    0   0   0.01    1        1.00
24    1   0   0.01    1        0.02


Goodness-of-fit for edgewise shared partner

       obs min    mean max MC p-value
esp0  120  84  101.00 125        0.12
esp1    0   3   16.82  34        0.00
esp2    0   0    3.64  15        0.26
esp3    0   0    0.66   5        1.00
esp4    0   0    0.13   2        1.00
esp5    0   0    0.02   1        1.00


Goodness-of-fit for minimum geodesic distance

       obs min     mean    max MC p-value
1      120  96   122.27    173        0.98
2      655 245   417.37    736        0.02
3      809 449   875.90   1541        0.84
4     1414 537  1036.78   1626        0.12
5      837 307   710.92   1043        0.44
6      741  55   304.11    704        0.00
7      380   0    94.74    510        0.04
8       74   0    26.29    225        0.20
9       30   0     7.49    133        0.20
10       0   0     2.09     82        1.00
11       0   0     0.35     22        1.00
12       0   0     0.06      6        1.00
Inf    505 513  1966.63   3582        0.00


> mcmc.diagnostics(model_dnase)
Sample statistics summary:

Iterations = 10000:1009900
Thinning interval = 100
```

```
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                  Mean    SD Naive SE Time-series SE
edges           1.0849 13.23   0.1323         0.7842
degree1        -0.4358  5.92   0.0592         0.3313
nodecov.dnase   1.0124 21.30   0.2130         1.4731

2. Quantiles for each variable:

              2.5% 25% 50% 75% 97.5%
edges          -23  -8   1   9    29
degree1        -13  -4   0   4    10
nodecov.dnase  -43 -13   1  16    42
```

Are sample statistics significantly different from observed?

	edges	**degree1**	**nodecov.dnase**	**Overall (Chi^2)**
diff.	1.0849000	-0.4358000	1.0124000	NA
test stat.	1.3833705	-1.3154983	0.6872654	1.3255196
P-val.	0.1665513	0.1883425	0.4919155	0.5076497

```
Sample statistics cross-correlations:
                   edges    degree1 nodecov.dnase
edges          1.0000000 -0.8322978     0.7842621
degree1       -0.8322978  1.0000000    -0.5092799
nodecov.dnase  0.7842621 -0.5092799     1.0000000

Sample statistics auto-correlation:
Chain 1
            edges    degree1 nodecov.dnase
Lag 0   1.0000000 1.0000000     1.0000000
Lag 100 0.9391258 0.8775555     0.9543859
Lag 200 0.8877318 0.7973573     0.9135582
Lag 300 0.8400531 0.7350269     0.8765605
Lag 400 0.7958272 0.6856351     0.8415857
Lag 500 0.7545763 0.6428520     0.8070126

Sample statistics burn-in diagnostic (Geweke):
Chain 1

Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

        edges     degree1 nodecov.dnase
       0.7512     -0.7546        0.4739

P-values (lower = worse):
       edges     degree1 nodecov.dnase
   0.4525065   0.4504791     0.6355580
```
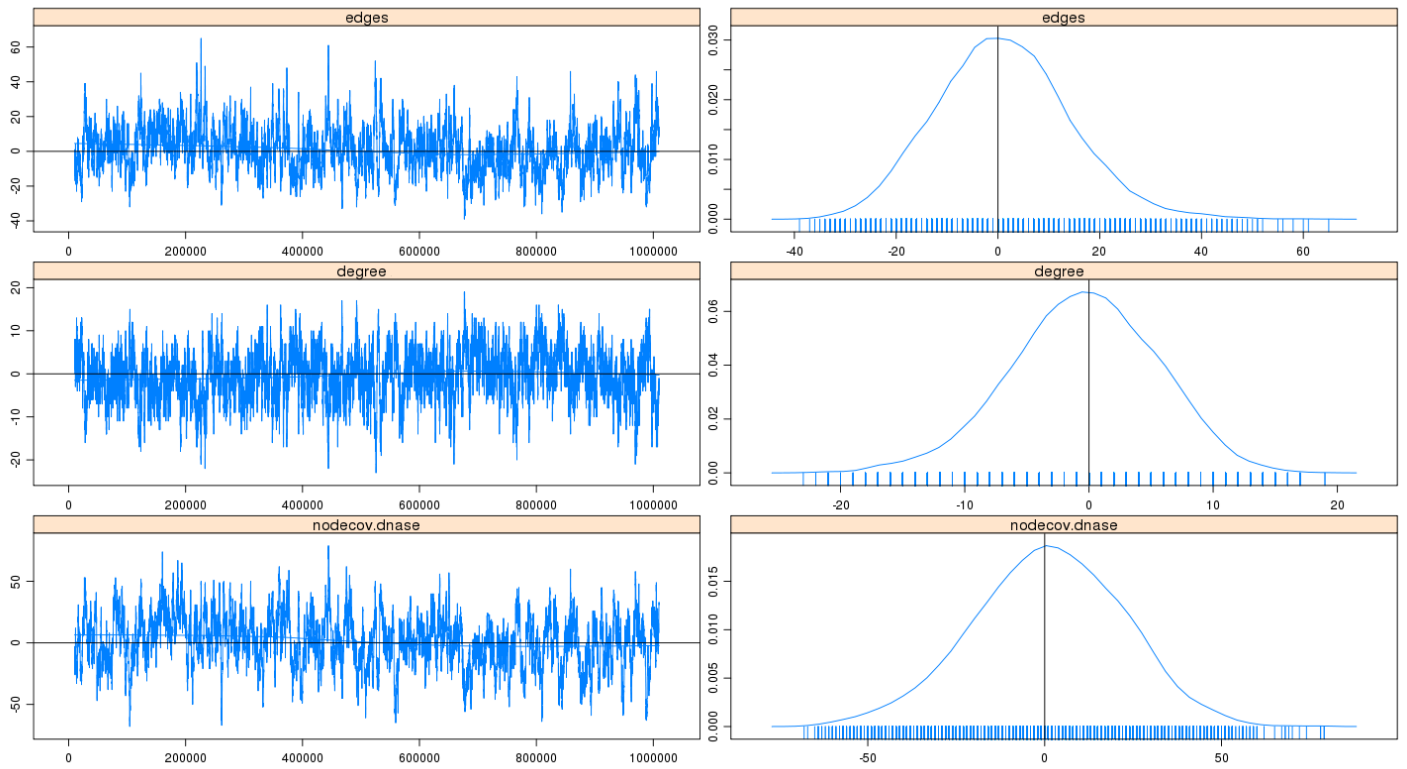
Supplementary Figure 5. Simulation details (left) and related statistics (right) of the stochastic analysis about the three components estimator (edges, degree, and nodecov.dnase) for the graph describing the HOXB cluster of genes according to the Lieberman-Aiden et al. Hi-C experiment.