

Social Network Position and Strain Network Position

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Simple model

Average strain-sharing rate to the rest of the villages, betweenness centrality

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ between_c_all + age_at_survey + household_wealth_index_w3 +
##   gender + DNA_conc + BMI + sampling_date + shipment_batch +
##   Plate + WIKI + Reads + (1 | village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 4846.8
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -4.2706 -0.5307 -0.0004  0.5368  4.6040
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   building_id (Intercept) 0.2449   0.4949
##   village      (Intercept) 3.7268   1.9305
##   Residual                0.9638   0.9817
## Number of obs: 1554, groups:  building_id, 874; village, 18
##
## Fixed effects:
##               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      2.361e+01  4.687e+01  1.298e+02   0.504  0.61536
## between_c_all      3.104e+00  1.160e+00  1.489e+03   2.677  0.00751 **
## age_at_survey     -1.661e-03  1.759e-03  1.510e+03  -0.944  0.34511
## household_wealth_index_w3  1.467e-02  2.561e-02  8.055e+02   0.573  0.56702
## genderwoman        1.033e-01  5.729e-02  1.194e+03   1.802  0.07176 .
## DNA_conc          -1.996e-05  2.336e-04  1.474e+03  -0.085  0.93191
## BMI               -1.366e-02  6.848e-03  1.510e+03  -1.995  0.04623 *
## sampling_date     -8.355e-04  2.478e-03  1.300e+02  -0.337  0.73655
## shipment_batch    -1.614e-01  5.067e-02  1.523e+03  -3.185  0.00147 **
## Plate012023       -3.940e-01  2.583e-01  1.512e+03  -1.525  0.12738
## Plate012323        2.381e-01  2.875e-01  1.523e+03   0.828  0.40761
## Plate013023        5.039e-01  3.371e-01  1.495e+03   1.495  0.13514
## Plate021323        4.230e-01  3.350e-01  1.496e+03   1.263  0.20687
## Plate032322       -9.367e-01  3.699e-01  1.352e+03  -2.532  0.01145 *
## Plate032422       -8.985e-01  3.605e-01  1.347e+03  -2.493  0.01280 *
```

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## Plate110520          -4.246e+00  1.792e+00  9.767e+01  -2.370  0.01977 *
## Plate111020          -4.479e+00  1.763e+00  9.473e+01  -2.540  0.01271 *
## Reads                5.463e-09  1.009e-09  1.443e+03   5.415  7.18e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

Average strain-sharing rate to the rest of the village, eigenvector centrality

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ eigen_c_all + age_at_survey + household_wealth_index_w3 +
##   gender + DNA_conc + BMI + sampling_date + shipment_batch +
##   Plate + WIKI + Reads + (1 | village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 4815.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.7030 -0.5275  0.0067  0.4994  4.7625
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 0.2131   0.4616
## village      (Intercept) 3.4712   1.8631
## Residual                0.9633   0.9815
## Number of obs: 1554, groups: building_id, 874; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    1.559e+01  4.613e+01  1.222e+02  0.338  0.73595
## eigen_c_all     9.324e-01  1.419e-01  1.231e+03  6.570  7.41e-11 ***
## age_at_survey   -3.332e-03  1.728e-03  1.512e+03 -1.929  0.05398 .
## household_wealth_index_w3  1.227e-02  2.498e-02  8.057e+02  0.491  0.62331
## genderwoman     1.386e-01  5.728e-02  1.218e+03  2.419  0.01570 *
## DNA_conc        -2.043e-05  2.313e-04  1.486e+03 -0.088  0.92964
## BMI             -1.541e-02  6.768e-03  1.509e+03 -2.276  0.02296 *
## sampling_date   -4.128e-04  2.439e-03  1.223e+02 -0.169  0.86588
## shipment_batch  -1.636e-01  5.013e-02  1.528e+03 -3.263  0.00113 **
## Plate012023     -3.261e-01  2.561e-01  1.518e+03 -1.274  0.20296
## Plate012323     1.518e-01  2.844e-01  1.521e+03  0.534  0.59357
## Plate013023     4.226e-01  3.333e-01  1.488e+03  1.268  0.20503
## Plate021323     3.713e-01  3.311e-01  1.491e+03  1.122  0.26223
## Plate032322    -9.612e-01  3.647e-01  1.338e+03 -2.635  0.00850 **
## Plate032422    -9.125e-01  3.553e-01  1.336e+03 -2.568  0.01032 *
## Plate110520    -3.917e+00  1.760e+00  9.277e+01 -2.226  0.02847 *
## Plate111020    -4.189e+00  1.732e+00  8.993e+01 -2.419  0.01760 *
## Reads          5.527e-09  1.000e-09  1.459e+03  5.527  3.86e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

Average strain-sharing rate to the rest of the village, degree

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ degree_c_all + age_at_survey + household_wealth_index_w3 +
##   gender + DNA_conc + BMI + sampling_date + shipment_batch +
##   Plate + WIKI + Reads + (1 | village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 4826
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -4.4784 -0.5353 -0.0022  0.5109  4.8493
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 0.2091   0.4573
## village      (Intercept) 3.5514   1.8845
## Residual                0.9694   0.9846
## Number of obs: 1554, groups: building_id, 874; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    1.928e+01  4.632e+01  1.270e+02   0.416  0.67791
## degree_c_all    4.662e-02  7.469e-03  1.508e+03   6.241 5.63e-10 ***
## age_at_survey   -4.378e-03  1.791e-03  1.511e+03  -2.444  0.01464 *
## household_wealth_index_w3 -2.677e-04  2.518e-02  8.110e+02  -0.011  0.99152
## genderwoman     1.199e-01  5.718e-02  1.215e+03   2.096  0.03625 *
## DNA_conc        -9.337e-06  2.317e-04  1.487e+03  -0.040  0.96786
## BMI             -1.557e-02  6.779e-03  1.509e+03  -2.297  0.02177 *
## sampling_date   -6.085e-04  2.449e-03  1.272e+02  -0.248  0.80416
## shipment_batch  -1.627e-01  5.020e-02  1.529e+03  -3.242  0.00121 **
## Plate012023     -3.803e-01  2.561e-01  1.519e+03  -1.485  0.13775
## Plate012323      2.182e-01  2.846e-01  1.523e+03   0.767  0.44328
## Plate013023      4.542e-01  3.337e-01  1.493e+03   1.361  0.17370
## Plate021323      3.999e-01  3.316e-01  1.495e+03   1.206  0.22799
## Plate032322     -9.800e-01  3.652e-01  1.346e+03  -2.683  0.00738 **
## Plate032422     -9.470e-01  3.557e-01  1.342e+03  -2.662  0.00785 **
## Plate110520     -4.126e+00  1.767e+00  9.628e+01  -2.334  0.02165 *
## Plate111020     -4.370e+00  1.740e+00  9.337e+01  -2.512  0.01373 *
## Reads           5.402e-09  1.002e-09  1.460e+03   5.393 8.06e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, clustering coefficient

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ cluster_coef_all + age_at_survey + household_wealth_index_w3 +
##   gender + DNA_conc + BMI + sampling_date + shipment_batch +
##   Plate + WIKI + Reads + (1 | village_name) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 9163.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7335 -0.4635 -0.1249  0.3498  6.1423
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 10.9973  3.316
## village_name (Intercept)  0.1945  0.441
## Residual              12.2702  3.503
## Number of obs: 1554, groups:  building_id, 874; village_name, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      5.723e+01  5.904e+01  1.332e+01   0.969  0.34964
## cluster_coef_all    3.004e+00  4.917e-01  1.415e+03   6.109  1.30e-09 ***
## age_at_survey      -3.997e-02  6.817e-03  1.401e+03  -5.863  5.67e-09 ***
## household_wealth_index_w3 -7.260e-01  1.166e-01  7.641e+02  -6.227  7.83e-10 ***
## genderwoman         1.038e-01  2.167e-01  1.057e+03   0.479  0.63185
## DNA_conc           -3.132e-04  9.214e-04  1.288e+03  -0.340  0.73395
## BMI                -8.023e-02  2.784e-02  1.440e+03  -2.882  0.00401 **
## sampling_date       -2.028e-03  3.118e-03  1.337e+01  -0.650  0.52655
## shipment_batch      -3.301e-01  1.758e-01  1.268e+02  -1.878  0.06262 .
## Plate012023         2.627e-01  8.796e-01  1.461e+02   0.299  0.76567
## Plate012323         4.403e-01  8.950e-01  1.156e+02   0.492  0.62365
## Plate013023         2.629e-03  9.017e-01  3.477e+01   0.003  0.99769
## Plate021323         8.297e-01  9.363e-01  6.986e+01   0.886  0.37857
## Plate032322        -2.985e+00  9.550e-01  3.228e+01  -3.125  0.00374 **
## Plate032422        -3.132e+00  9.432e-01  3.280e+01  -3.320  0.00221 **
## Plate110520        -5.997e+00  2.657e+00  2.893e+01  -2.257  0.03173 *
## Plate111020        -4.952e+00  2.436e+00  1.981e+01  -2.033  0.05566 .
## Reads              7.128e-09  3.877e-09  8.619e+02   1.839  0.06633 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, eigenvector centrality

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ eigen_c_all + age_at_survey + household_wealth_index_w3 +
##   gender + DNA_conc + BMI + sampling_date + shipment_batch +
##   Plate + WIKI + Reads + (1 | village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 9168.3
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -2.7055 -0.4844 -0.1081  0.3621  6.3094
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 11.2685  3.3569
## village      (Intercept)  0.3027  0.5501
## Residual                12.1676  3.4882
## Number of obs: 1554, groups: building_id, 874; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      1.069e+02  6.306e+01  1.518e+01   1.695  0.110472
## eigen_c_all       -3.488e+00  6.172e-01  1.403e+03  -5.652  1.92e-08 ***
## age_at_survey     -3.474e-02  7.049e-03  1.430e+03  -4.928  9.27e-07 ***
## household_wealth_index_w3 -7.219e-01  1.177e-01  7.787e+02  -6.132  1.38e-09 ***
## genderwoman       -1.699e-02  2.177e-01  1.038e+03  -0.078  0.937812
## DNA_conc          -2.631e-04  9.211e-04  1.274e+03  -0.286  0.775180
## BMI               -7.840e-02  2.787e-02  1.428e+03  -2.813  0.004972 **
## sampling_date     -4.576e-03  3.330e-03  1.521e+01  -1.374  0.189283
## shipment_batch    -2.716e-01  1.787e-01  1.504e+02  -1.520  0.130638
## Plate012023        1.038e-01  8.967e-01  1.631e+02   0.116  0.907948
## Plate012323        4.542e-01  9.136e-01  1.194e+02   0.497  0.620026
## Plate013023       -4.010e-01  9.351e-01  3.826e+01  -0.429  0.670470
## Plate021323        4.745e-01  9.632e-01  6.891e+01   0.493  0.623880
## Plate032322       -3.636e+00  1.002e+00  3.629e+01  -3.629  0.000869 ***
## Plate032422       -3.708e+00  9.897e-01  3.780e+01  -3.747  0.000597 ***
## Plate110520       -7.489e+00  2.785e+00  3.173e+01  -2.689  0.011331 *
## Plate111020       -6.328e+00  2.574e+00  2.254e+01  -2.459  0.022065 *
## Reads             6.540e-09  3.888e-09  9.850e+02   1.682  0.092874 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, betweenness centrality

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ between_c_all + age_at_survey + household_wealth_index_w3 +
##   gender + DNA_conc + BMI + sampling_date + shipment_batch +
##   Plate + WIKI + Reads + (1 | village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 9173.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7858 -0.4731 -0.1213  0.3578  6.3638
##
## Random effects:
##   Groups             Name             Variance Std.Dev.
## building_id (Intercept) 11.2337   3.3517
## village      (Intercept)  0.1968   0.4436
## Residual                12.3169   3.5095
## Number of obs: 1554, groups: building_id, 874; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      9.366e+01  5.957e+01  1.459e+01   1.572  0.137305
## between_c_all     -2.167e+01  4.579e+00  1.329e+03  -4.732  2.46e-06 ***
## age_at_survey     -3.624e-02  7.098e-03  1.423e+03  -5.105  3.75e-07 ***
## household_wealth_index_w3 -7.186e-01  1.175e-01  7.568e+02  -6.114  1.56e-09 ***
## genderwoman        8.402e-02  2.174e-01  1.049e+03   0.386  0.699264
## DNA_conc          -1.845e-04  9.252e-04  1.281e+03  -0.199  0.841943
## BMI               -7.932e-02  2.799e-02  1.434e+03  -2.834  0.004668 **
## sampling_date     -3.888e-03  3.146e-03  1.465e+01  -1.236  0.235994
## shipment_batch    -2.760e-01  1.762e-01  1.349e+02  -1.566  0.119678
## Plate012023        2.188e-01  8.837e-01  1.572e+02   0.248  0.804803
## Plate012323        1.388e-01  9.001e-01  1.253e+02   0.154  0.877664
## Plate013023       -6.070e-01  9.078e-01  3.921e+01  -0.669  0.507620
## Plate021323        3.357e-01  9.441e-01  7.635e+01   0.356  0.723153
## Plate032322       -3.648e+00  9.703e-01  3.729e+01  -3.759  0.000584 ***
## Plate032422       -3.643e+00  9.567e-01  3.729e+01  -3.807  0.000508 ***
## Plate110520       -7.108e+00  2.684e+00  3.186e+01  -2.649  0.012461 *
## Plate111020       -6.092e+00  2.463e+00  2.198e+01  -2.474  0.021581 *
## Reads             6.719e-09  3.890e-09  8.893e+02   1.727  0.084457 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, degree

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ degree_c_all + age_at_survey + household_wealth_index_w3 +
##     gender + DNA_conc + BMI + l0400 + mb_m0300 + sampling_date +
##     shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |
##     building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 8069.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6382 -0.4873 -0.1054  0.3713  6.2280
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## building_id (Intercept) 10.4304  3.2296
## village      (Intercept)  0.0533  0.2309
## Residual                    12.4824  3.5330
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    7.887e+01  5.679e+01  1.214e+01   1.389  0.189860
## degree_c_all   -2.132e-01  3.248e-02  1.167e+03  -6.564  7.87e-11 ***
## age_at_survey  -3.218e-02  7.809e-03  1.227e+03  -4.121  4.03e-05 ***
## household_wealth_index_w3 -5.151e-01  1.236e-01  6.635e+02  -4.169  3.47e-05 ***
## genderwoman     3.867e-02  2.368e-01  9.465e+02   0.163  0.870338
## DNA_conc        -8.311e-05  9.910e-04  1.139e+03  -0.084  0.933181
## BMI             -6.921e-02  3.013e-02  1.273e+03  -2.297  0.021764 *
## l04002           2.209e+00  1.000e+00  6.869e+02   2.208  0.027567 *
## l04003           5.621e+00  1.331e+00  7.866e+02   4.224  2.68e-05 ***
## l04004           8.641e-01  7.562e-01  7.133e+02   1.143  0.253522
## l04005           2.250e+00  1.220e+00  7.573e+02   1.844  0.065517 .
## l04009          -1.149e+00  2.000e+00  8.988e+02  -0.574  0.565910
## l040010          6.075e-01  1.523e+00  9.151e+02   0.399  0.689982
## l040011          1.038e+00  2.057e+00  9.824e+02   0.505  0.613792
## mb_m03002       -1.863e-01  7.409e-01  1.200e+03  -0.251  0.801532
## mb_m03003        1.254e-01  7.151e-01  1.205e+03   0.175  0.860850
## mb_m03004       -3.254e-01  7.443e-01  1.209e+03  -0.437  0.662075
## mb_m03005       -1.788e-01  8.129e-01  1.218e+03  -0.220  0.825913
## mb_m03006        5.532e-01  7.579e-01  1.166e+03   0.730  0.465575
## mb_m03007       -2.419e-01  7.618e-01  1.211e+03  -0.318  0.750848
## sampling_date   -3.159e-03  2.999e-03  1.216e+01  -1.054  0.312592
## shipment_batch  -3.017e-01  1.777e-01  1.052e+02  -1.698  0.092485 .
## Plate012023      4.410e-01  9.455e-01  1.726e+02   0.466  0.641479
## Plate012323      3.248e-01  9.338e-01  1.187e+02   0.348  0.728554
## Plate013023     -1.381e-01  9.101e-01  3.905e+01  -0.152  0.880149
## Plate021323      6.565e-01  9.896e-01  9.402e+01   0.663  0.508680
## Plate032322     -3.376e+00  9.626e-01  3.898e+01  -3.507  0.001156 **
## Plate032422     -3.520e+00  9.458e-01  3.981e+01  -3.722  0.000611 ***
```

```

## Plate110520          -6.368e+00  2.626e+00  3.033e+01  -2.425  0.021462 *
## Plate111020          -5.359e+00  2.383e+00  1.888e+01  -2.249  0.036664 *
## Reads                7.703e-09  4.144e-09  6.461e+02   1.859  0.063504 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

Separate covariates

Average strain-sharing rate to the rest of the villages, betweenness centrality, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula:  
## strain_sim_all ~ between_c_all + age_at_survey + household_wealth_index_w3 +  
##   DDS + med_painkillers + med_antibiotics + med_antidiarrheal +  
##   med_antiparasite + med_vitamins + med_zinc + med_antifungal +  
##   med_antihypertensives + med_antidiabetics + med_antiacids +  
##   med_laxatives + l0400 + mb_m0300 + gender + DNA_conc + BMI +  
##   sampling_date + shipment_batch + Plate + WIKI + Reads + (1 |  
##   village) + (1 | building_id)  
## Data: centrality_sim_df_covars_all  
##  
## REML criterion at convergence: 4297.4  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -4.2110 -0.5401 -0.0003  0.5120  4.4252  
##  
## Random effects:  
## Groups      Name      Variance Std.Dev.  
## building_id (Intercept) 0.2460   0.4960  
## village      (Intercept) 2.9350   1.7132  
## Residual                0.9517   0.9755  
## Number of obs: 1371, groups:  building_id, 816; village, 18  
##  
## Fixed effects:  
##              Estimate Std. Error      df t value Pr(>|t|)  
## (Intercept)      3.568e+00  5.631e+01  4.995e+01   0.063  0.949726  
## between_c_all      2.957e+00  1.248e+00  1.266e+03   2.370  0.017948 *  
## age_at_survey     -2.831e-03  1.942e-03  1.294e+03  -1.458  0.145178  
## household_wealth_index_w3  2.310e-02  2.782e-02  7.398e+02   0.830  0.406661  
## DDS              -5.165e-03  2.401e-02  1.259e+03  -0.215  0.829706  
## med_painkillers    -1.033e-01  6.248e-02  1.271e+03  -1.653  0.098587 .  
## med_antibiotics    -2.994e-01  9.247e-02  1.289e+03  -3.238  0.001234 **  
## med_antidiarrheal   2.868e-01  1.672e-01  1.241e+03   1.715  0.086580 .  
## med_antiparasite   -4.220e-01  1.870e-01  1.268e+03  -2.256  0.024222 *  
## med_vitamins       -1.446e-01  7.970e-02  1.277e+03  -1.815  0.069785 .  
## med_zinc           9.342e-01  1.115e+00  1.236e+03   0.838  0.402202  
## med_antifungal      4.057e-02  2.832e-01  1.251e+03   0.143  0.886117  
## med_antihypertensives  8.946e-02  1.536e-01  1.286e+03   0.583  0.560262  
## med_antidiabetics   2.666e-02  2.133e-01  1.290e+03   0.125  0.900561  
## med_antiacids       6.648e-02  1.811e-01  1.301e+03   0.367  0.713546  
## med_laxatives       6.473e-01  5.470e-01  1.235e+03   1.183  0.236882  
## l04002              8.243e-02  2.147e-01  5.713e+02   0.384  0.701245  
## l04003              3.271e-01  2.869e-01  6.694e+02   1.140  0.254656  
## l04004              2.408e-01  1.612e-01  5.703e+02   1.494  0.135839  
## l04005              5.277e-01  2.667e-01  6.899e+02   1.979  0.048234 *  
## l04009             -5.151e-02  4.462e-01  8.940e+02  -0.115  0.908121  
## l040010             3.308e-01  3.375e-01  8.943e+02   0.980  0.327236
```

```

## 1040011          9.991e-01  4.633e-01  1.011e+03   2.157 0.031272 *
## mb_m03002       -1.965e-01  1.842e-01  1.271e+03  -1.067 0.286224
## mb_m03003       -8.580e-02  1.776e-01  1.269e+03  -0.483 0.629167
## mb_m03004       -2.043e-01  1.849e-01  1.275e+03  -1.105 0.269502
## mb_m03005       -4.167e-01  2.011e-01  1.287e+03  -2.072 0.038471 *
## mb_m03006       -1.821e-01  1.899e-01  1.244e+03  -0.959 0.337798
## mb_m03007       -4.611e-02  1.898e-01  1.280e+03  -0.243 0.808050
## genderwoman      1.468e-01  6.289e-02  1.083e+03   2.335 0.019751 *
## DNA_conc         4.452e-05  2.491e-04  1.280e+03   0.179 0.858149
## BMI              -1.280e-02  7.400e-03  1.306e+03  -1.729 0.084000 .
## sampling_date     2.220e-04  2.978e-03  4.998e+01   0.075 0.940875
## shipment_batch   -1.806e-01  5.364e-02  1.310e+03  -3.367 0.000783 ***
## Plate012023      -5.616e-01  2.822e-01  1.316e+03  -1.990 0.046844 *
## Plate012323       1.337e-01  3.146e-01  1.296e+03   0.425 0.670812
## Plate013023       4.616e-01  3.712e-01  1.240e+03   1.244 0.213831
## Plate021323       5.134e-01  3.816e-01  1.230e+03   1.346 0.178659
## Plate032322      -9.200e-01  3.970e-01  1.200e+03  -2.317 0.020668 *
## Plate032422      -9.288e-01  3.849e-01  1.192e+03  -2.413 0.015968 *
## Plate110520      -2.701e+00  2.065e+00  4.355e+01  -1.308 0.197702
## Plate111020      -2.939e+00  2.051e+00  4.246e+01  -1.433 0.159258
## Reads            5.815e-09  1.087e-09  1.219e+03   5.351 1.04e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

Average strain-sharing rate to the rest of the village, eigenvector centrality, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ eigen_c_all + age_at_survey + household_wealth_index_w3 +
##   DDS + med_painkillers + med_antibiotics + med_antidiarrheal +
##   med_antiparasite + med_vitamins + med_zinc + med_antifungal +
##   med_antihypertensives + med_antidiabetics + med_antiacids +
##   med_laxatives + 10400 + mb_m0300 + gender + DNA_conc + BMI +
##   sampling_date + shipment_batch + Plate + WIKI + Reads + (1 |
##   village) + (1 | building_id)
##   Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 4276.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.6525 -0.5418  0.0000  0.5107  4.5587
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   building_id (Intercept) 0.2164   0.4652
##   village      (Intercept) 2.7178   1.6486
##   Residual                0.9542   0.9769
## Number of obs: 1371, groups:  building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    -7.951e+00  5.503e+01  4.889e+01  -0.144  0.885710
## eigen_c_all      8.596e-01  1.525e-01  1.097e+03   5.635  2.23e-08 ***
## age_at_survey   -4.259e-03  1.907e-03  1.300e+03  -2.234  0.025684 *
## household_wealth_index_w3  1.858e-02  2.725e-02  7.420e+02   0.682  0.495521
## DDS             -3.840e-03  2.383e-02  1.269e+03  -0.161  0.872012
## med_painkillers  -1.110e-01  6.198e-02  1.281e+03  -1.791  0.073490 .
## med_antibiotics  -2.899e-01  9.173e-02  1.294e+03  -3.161  0.001611 **
## med_antidiarrheal  2.817e-01  1.660e-01  1.256e+03   1.697  0.090019 .
## med_antiparasite -4.372e-01  1.856e-01  1.277e+03  -2.356  0.018645 *
## med_vitamins     -1.134e-01  7.924e-02  1.281e+03  -1.430  0.152834
## med_zinc          9.824e-01  1.102e+00  1.249e+03   0.891  0.372925
## med_antifungal    1.684e-02  2.812e-01  1.263e+03   0.060  0.952248
## med_antihypertensives  7.034e-02  1.523e-01  1.291e+03   0.462  0.644354
## med_antidiabetics  2.362e-02  2.115e-01  1.294e+03   0.112  0.911059
## med_antiacids     4.393e-02  1.795e-01  1.303e+03   0.245  0.806671
## med_laxatives     6.117e-01  5.429e-01  1.249e+03   1.127  0.260128
## 104002            2.218e-02  2.107e-01  5.773e+02   0.105  0.916190
## 104003            2.745e-01  2.814e-01  6.788e+02   0.975  0.329671
## 104004            1.851e-01  1.583e-01  5.759e+02   1.170  0.242649
## 104005            3.841e-01  2.631e-01  7.053e+02   1.460  0.144729
## 104009           -2.188e-02  4.386e-01  9.085e+02  -0.050  0.960235
## 1040010           3.613e-01  3.319e-01  9.105e+02   1.089  0.276656
## 1040011           9.619e-01  4.566e-01  1.030e+03   2.106  0.035404 *
## mb_m03002        -2.490e-01  1.831e-01  1.277e+03  -1.360  0.174076
```

```

## mb_m03003      -1.433e-01  1.766e-01  1.274e+03  -0.811  0.417393
## mb_m03004      -2.547e-01  1.837e-01  1.280e+03  -1.386  0.165912
## mb_m03005      -4.658e-01  1.996e-01  1.292e+03  -2.333  0.019788 *
## mb_m03006      -2.190e-01  1.887e-01  1.253e+03  -1.161  0.246063
## mb_m03007      -8.858e-02  1.884e-01  1.285e+03  -0.470  0.638342
## genderwoman     1.807e-01  6.295e-02  1.106e+03   2.871  0.004171 **
## DNA_conc        6.362e-05  2.470e-04  1.290e+03   0.258  0.796809
## BMI            -1.452e-02  7.330e-03  1.306e+03  -1.981  0.047818 *
## sampling_date    8.354e-04  2.910e-03  4.891e+01   0.287  0.775246
## shipment_batch  -1.792e-01  5.317e-02  1.317e+03  -3.370  0.000774 ***
## Plate012023     -5.232e-01  2.800e-01  1.318e+03  -1.869  0.061869 .
## Plate012323      1.430e-02  3.121e-01  1.291e+03   0.046  0.963453
## Plate013023      3.507e-01  3.678e-01  1.228e+03   0.953  0.340539
## Plate021323      4.492e-01  3.778e-01  1.218e+03   1.189  0.234626
## Plate032322     -9.614e-01  3.916e-01  1.188e+03  -2.455  0.014239 *
## Plate032422     -9.583e-01  3.795e-01  1.181e+03  -2.525  0.011686 *
## Plate110520     -2.297e+00  2.016e+00  4.299e+01  -1.139  0.260870
## Plate111020     -2.568e+00  2.001e+00  4.187e+01  -1.283  0.206427
## Reads           5.864e-09  1.079e-09  1.238e+03   5.432  6.69e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

Average strain-sharing rate to the rest of the village, degree, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ degree_c_all + age_at_survey + household_wealth_index_w3 +
##   DDS + med_painkillers + med_antibiotics + med_antidiarrheal +
##   med_antiparasite + med_vitamins + med_zinc + med_antifungal +
##   med_antihypertensives + med_antidiabetics + med_antiacids +
##   med_laxatives + 10400 + mb_m0300 + gender + DNA_conc + BMI +
##   sampling_date + shipment_batch + Plate + WIKI + Reads + (1 |
##   village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 4285.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.4507 -0.5655 -0.0088  0.5109  4.6461
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   building_id (Intercept) 0.2085   0.4566
##   village      (Intercept) 2.7961   1.6721
##   Residual                0.9630   0.9813
## Number of obs: 1371, groups:  building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    -4.137e+00  5.538e+01  5.039e+01  -0.075  0.940749
## degree_c_all     4.308e-02  8.037e-03  1.309e+03   5.360  9.82e-08 ***
## age_at_survey   -5.241e-03  1.974e-03  1.303e+03  -2.655  0.008021 **
## household_wealth_index_w3  5.528e-03  2.750e-02  7.423e+02   0.201  0.840770
## DDS             -4.549e-03  2.387e-02  1.270e+03  -0.191  0.848891
## med_painkillers  -1.128e-01  6.210e-02  1.283e+03  -1.816  0.069648 .
## med_antibiotics  -2.925e-01  9.185e-02  1.295e+03  -3.184  0.001485 **
## med_antidiarrheal  2.717e-01  1.663e-01  1.257e+03   1.634  0.102575
## med_antiparasite  -4.158e-01  1.859e-01  1.278e+03  -2.237  0.025444 *
## med_vitamins     -1.099e-01  7.942e-02  1.283e+03  -1.384  0.166603
## med_zinc          9.540e-01  1.103e+00  1.251e+03   0.865  0.387078
## med_antifungal    3.146e-02  2.816e-01  1.264e+03   0.112  0.911072
## med_antihypertensives  1.026e-01  1.525e-01  1.292e+03   0.673  0.501109
## med_antidiabetics  7.281e-03  2.118e-01  1.294e+03   0.034  0.972583
## med_antiacids     3.641e-02  1.797e-01  1.303e+03   0.203  0.839475
## med_laxatives     6.386e-01  5.439e-01  1.251e+03   1.174  0.240568
## 104002            4.936e-02  2.100e-01  5.608e+02   0.235  0.814212
## 104003            3.297e-01  2.808e-01  6.644e+02   1.174  0.240795
## 104004            2.186e-01  1.576e-01  5.591e+02   1.387  0.165937
## 104005            4.645e-01  2.615e-01  6.880e+02   1.776  0.076176 .
## 104009           -1.329e-02  4.381e-01  8.987e+02  -0.030  0.975803
## 1040010           3.444e-01  3.316e-01  9.006e+02   1.039  0.299250
## 1040011           9.781e-01  4.563e-01  1.024e+03   2.144  0.032305 *
## mb_m03002       -2.660e-01  1.836e-01  1.277e+03  -1.449  0.147622
```

```

## mb_m03003      -1.422e-01  1.769e-01  1.275e+03  -0.804  0.421699
## mb_m03004      -2.627e-01  1.841e-01  1.281e+03  -1.427  0.153746
## mb_m03005      -4.632e-01  1.999e-01  1.294e+03  -2.317  0.020658 *
## mb_m03006      -2.415e-01  1.892e-01  1.253e+03  -1.276  0.202184
## mb_m03007      -1.073e-01  1.889e-01  1.286e+03  -0.568  0.570232
## genderwoman    1.575e-01  6.277e-02  1.102e+03   2.510  0.012221 *
## DNA_conc       5.149e-05  2.474e-04  1.291e+03   0.208  0.835152
## BMI            -1.487e-02  7.343e-03  1.306e+03  -2.025  0.043069 *
## sampling_date   6.332e-04  2.928e-03  5.041e+01   0.216  0.829674
## shipment_batch -1.786e-01  5.325e-02  1.317e+03  -3.354  0.000818 ***
## Plate012023    -5.681e-01  2.802e-01  1.318e+03  -2.028  0.042785 *
## Plate012323     8.972e-02  3.120e-01  1.295e+03   0.288  0.773720
## Plate013023     3.875e-01  3.681e-01  1.237e+03   1.053  0.292771
## Plate021323     4.676e-01  3.783e-01  1.227e+03   1.236  0.216742
## Plate032322    -9.780e-01  3.921e-01  1.194e+03  -2.494  0.012751 *
## Plate032422    -9.950e-01  3.798e-01  1.187e+03  -2.620  0.008908 **
## Plate110520    -2.524e+00  2.029e+00  4.414e+01  -1.244  0.220077
## Plate111020    -2.763e+00  2.015e+00  4.302e+01  -1.372  0.177329
## Reads          5.694e-09  1.081e-09  1.240e+03   5.266  1.64e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

First degree connections, clustering coefficient, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ cluster_coef_all + age_at_survey + household_wealth_index_w3 +
##   DDS + med_painkillers + med_antibiotics + med_antidiarrheal +
##   med_antiparasite + med_vitamins + med_zinc + med_antifungal +
##   med_antihypertensives + med_antidiabetics + med_antiacids +
##   med_laxatives + l0400 + mb_m0300 + gender + DNA_conc + BMI +
##   sampling_date + shipment_batch + Plate + WIKI + Reads + (1 |
##   village_name) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 8043.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4441 -0.4922 -0.1047  0.3430  5.9516
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 10.33190 3.2143
## village_name (Intercept)  0.08109 0.2848
## Residual              12.58598 3.5477
## Number of obs: 1371, groups:  building_id, 816; village_name, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      3.601e+01  5.852e+01  1.236e+01   0.615  0.54953
## cluster_coef_all    3.453e+00  5.396e-01  1.220e+03   6.400 2.21e-10 ***
## age_at_survey     -4.765e-02  7.563e-03  1.195e+03  -6.300 4.18e-10 ***
## household_wealth_index_w3 -5.863e-01  1.237e-01  6.933e+02  -4.740 2.59e-06 ***
## DDS               -6.639e-02  9.602e-02  1.148e+03  -0.691  0.48945
## med_painkillers     9.635e-02  2.514e-01  1.171e+03   0.383  0.70160
## med_antibiotics    -2.590e-01  3.745e-01  1.204e+03  -0.691  0.48941
## med_antidiarrheal    8.893e-01  6.667e-01  1.097e+03   1.334  0.18252
## med_antiparasite   -9.923e-01  7.533e-01  1.165e+03  -1.317  0.18802
## med_vitamins       -4.503e-01  3.217e-01  1.194e+03  -1.400  0.16192
## med_zinc            1.933e+00  4.840e+00  1.134e+03   0.399  0.68975
## med_antifungal      6.247e-01  1.137e+00  1.129e+03   0.549  0.58294
## med_antihypertensives 5.881e-02  6.218e-01  1.228e+03   0.095  0.92466
## med_antidiabetics   1.098e+00  8.667e-01  1.226e+03   1.267  0.20549
## med_antiacids       5.553e-01  7.427e-01  1.285e+03   0.748  0.45479
## med_laxatives       1.352e-01  2.180e+00  1.097e+03   0.062  0.95054
## l04002              1.929e+00  1.003e+00  6.962e+02   1.922  0.05496 .
## l04003              5.403e+00  1.335e+00  7.928e+02   4.048 5.66e-05 ***
## l04004              7.847e-01  7.583e-01  7.197e+02   1.035  0.30110
## l04005              2.019e+00  1.224e+00  7.620e+02   1.650  0.09928 .
## l04009             -7.203e-01  2.006e+00  9.053e+02  -0.359  0.71959
## l040010             9.681e-01  1.531e+00  9.233e+02   0.632  0.52724
## l040011             1.245e+00  2.072e+00  9.936e+02   0.601  0.54800
## mb_m03002          -4.927e-01  7.443e-01  1.202e+03  -0.662  0.50811
## mb_m03003          -1.642e-01  7.187e-01  1.205e+03  -0.229  0.81928
```

```

## mb_m03004      -5.107e-01  7.479e-01  1.207e+03  -0.683  0.49488
## mb_m03005      -3.548e-01  8.172e-01  1.218e+03  -0.434  0.66430
## mb_m03006       2.256e-01  7.617e-01  1.166e+03   0.296  0.76718
## mb_m03007      -5.374e-01  7.683e-01  1.211e+03  -0.699  0.48438
## genderwoman     1.097e-01  2.442e-01  9.729e+02   0.449  0.65351
## DNA_conc       -1.061e-04  9.965e-04  1.136e+03  -0.106  0.91524
## BMI            -8.288e-02  3.031e-02  1.257e+03  -2.734  0.00634 **
## sampling_date  -8.986e-04  3.091e-03  1.237e+01  -0.291  0.77604
## shipment_batch -4.282e-01  1.810e-01  1.078e+02  -2.365  0.01980 *
## Plate012023     3.015e-01  9.556e-01  1.691e+02   0.315  0.75278
## Plate012323     3.840e-01  9.493e-01  1.235e+02   0.405  0.68651
## Plate013023     1.666e-01  9.314e-01  3.912e+01   0.179  0.85898
## Plate021323     1.065e+00  1.008e+00  9.097e+01   1.056  0.29355
## Plate032322    -3.027e+00  9.788e-01  3.845e+01  -3.092  0.00369 **
## Plate032422    -3.224e+00  9.600e-01  3.889e+01  -3.358  0.00177 **
## Plate110520    -5.940e+00  2.683e+00  3.033e+01  -2.214  0.03447 *
## Plate111020    -4.904e+00  2.443e+00  1.918e+01  -2.007  0.05900 .
## Reads          8.018e-09  4.186e-09  6.854e+02   1.915  0.05586 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

First degree connections, eigenvector centrality, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ eigen_c_all + age_at_survey + household_wealth_index_w3 +
##   DDS + med_painkillers + med_antibiotics + med_antidiarrheal +
##   med_antiparasite + med_vitamins + med_zinc + med_antifungal +
##   med_antihypertensives + med_antidiabetics + med_antiacids +
##   med_laxatives + l0400 + mb_m0300 + gender + DNA_conc + BMI +
##   sampling_date + shipment_batch + Plate + WIKI + Reads + (1 |
##   village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 8054.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.3442 -0.4847 -0.1212  0.3485  6.0894
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## building_id (Intercept) 10.3648  3.2194
## village      (Intercept)  0.1241  0.3523
## Residual                12.7141  3.5657
## Number of obs: 1371, groups:  building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      9.402e+01  6.124e+01  1.387e+01   1.535  0.147218
## eigen_c_all      -3.567e+00  6.580e-01  1.182e+03  -5.421  7.17e-08 ***
## age_at_survey    -4.309e-02  7.811e-03  1.220e+03  -5.516  4.22e-08 ***
## household_wealth_index_w3 -5.771e-01  1.245e-01  7.044e+02  -4.634  4.27e-06 ***
## DDS              -9.935e-02  9.639e-02  1.144e+03  -1.031  0.302887
## med_painkillers    5.984e-02  2.523e-01  1.168e+03   0.237  0.812572
## med_antibiotics   -4.261e-01  3.759e-01  1.207e+03  -1.134  0.257191
## med_antidiarrheal  9.330e-01  6.698e-01  1.092e+03   1.393  0.163947
## med_antiparasite  -8.452e-01  7.569e-01  1.162e+03  -1.117  0.264387
## med_vitamins      -4.698e-01  3.236e-01  1.189e+03  -1.452  0.146813
## med_zinc           1.266e+00  4.859e+00  1.128e+03   0.261  0.794511
## med_antifungal     6.329e-01  1.142e+00  1.125e+03   0.554  0.579708
## med_antihypertensives 1.653e-01  6.247e-01  1.226e+03   0.265  0.791373
## med_antidiabetics  1.078e+00  8.705e-01  1.224e+03   1.239  0.215707
## med_antiacids      8.656e-01  7.454e-01  1.287e+03   1.161  0.245780
## med_laxatives      9.500e-01  2.186e+00  1.089e+03   0.435  0.663898
## l04002             2.308e+00  1.009e+00  6.972e+02   2.288  0.022465 *
## l04003             5.737e+00  1.339e+00  7.808e+02   4.283  2.07e-05 ***
## l04004             9.888e-01  7.626e-01  7.135e+02   1.297  0.195177
## l04005             2.634e+00  1.235e+00  7.734e+02   2.132  0.033301 *
## l04009            -1.182e+00  2.012e+00  8.952e+02  -0.588  0.556954
## l040010            4.243e-01  1.534e+00  9.113e+02   0.277  0.782182
## l040011            1.333e+00  2.080e+00  9.849e+02   0.641  0.521596
## mb_m03002         -3.294e-01  7.486e-01  1.196e+03  -0.440  0.660024
## mb_m03003          8.232e-02  7.227e-01  1.198e+03   0.114  0.909337
```

```

## mb_m03004          -3.726e-01  7.519e-01  1.202e+03  -0.495  0.620343
## mb_m03005          -1.886e-01  8.216e-01  1.214e+03  -0.230  0.818449
## mb_m03006           4.183e-01  7.658e-01  1.161e+03   0.546  0.585000
## mb_m03007          -3.626e-01  7.718e-01  1.206e+03  -0.470  0.638545
## genderwoman        -3.520e-02  2.473e-01  9.667e+02  -0.142  0.886843
## DNA_conc           -6.575e-05  1.001e-03  1.131e+03  -0.066  0.947655
## BMI                -7.967e-02  3.050e-02  1.255e+03  -2.612  0.009105 **
## sampling_date       -3.897e-03  3.234e-03  1.389e+01  -1.205  0.248330
## shipment_batch     -3.549e-01  1.833e-01  1.151e+02  -1.936  0.055289 .
## Plate012023         1.876e-01  9.687e-01  1.716e+02   0.194  0.846636
## Plate012323         3.563e-01  9.626e-01  1.247e+02   0.370  0.711884
## Plate013023        -3.195e-01  9.519e-01  4.093e+01  -0.336  0.738861
## Plate021323         7.022e-01  1.025e+00  8.870e+01   0.685  0.495051
## Plate032322        -3.815e+00  1.014e+00  4.179e+01  -3.763  0.000518 ***
## Plate032422        -3.933e+00  9.950e-01  4.292e+01  -3.953  0.000284 ***
## Plate110520        -7.650e+00  2.776e+00  3.306e+01  -2.756  0.009457 **
## Plate111020        -6.499e+00  2.541e+00  2.138e+01  -2.558  0.018187 *
## Reads              7.395e-09  4.217e-09  7.427e+02   1.754  0.079894 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

First degree connections, betweenness centrality, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ between_c_all + age_at_survey + household_wealth_index_w3 +
##   DDS + med_painkillers + med_antibiotics + med_antidiarrheal +
##   med_antiparasite + med_vitamins + med_zinc + med_antifungal +
##   med_antihypertensives + med_antidiabetics + med_antiacids +
##   med_laxatives + l0400 + mb_m0300 + gender + DNA_conc + BMI +
##   sampling_date + shipment_batch + Plate + WIKI + Reads + (1 |
##   village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 8062.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4240 -0.4789 -0.1124  0.3463  6.1808
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 10.4519  3.2329
## village      (Intercept)  0.1047  0.3236
## Residual                12.8365  3.5828
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      7.912e+01  6.045e+01  1.605e+01   1.309  0.209043
## between_c_all     -2.058e+01  4.944e+00  1.132e+03  -4.163  3.38e-05 ***
## age_at_survey     -4.492e-02  7.901e-03  1.215e+03  -5.685  1.63e-08 ***
## household_wealth_index_w3 -5.873e-01  1.250e-01  7.167e+02  -4.700  3.13e-06 ***
## DDS               -9.728e-02  9.682e-02  1.149e+03  -1.005  0.315208
## med_painkillers     4.024e-02  2.535e-01  1.170e+03   0.159  0.873885
## med_antibiotics    -3.994e-01  3.775e-01  1.211e+03  -1.058  0.290268
## med_antidiarrheal    9.006e-01  6.728e-01  1.098e+03   1.338  0.181032
## med_antiparasite   -8.562e-01  7.605e-01  1.168e+03  -1.126  0.260454
## med_vitamins       -3.558e-01  3.245e-01  1.197e+03  -1.097  0.273026
## med_zinc           1.610e+00  4.880e+00  1.134e+03   0.330  0.741534
## med_antifungal     5.510e-01  1.148e+00  1.130e+03   0.480  0.631240
## med_antihypertensives 7.447e-02  6.274e-01  1.229e+03   0.119  0.905540
## med_antidiabetics  1.190e+00  8.750e-01  1.228e+03   1.360  0.174011
## med_antiacids      7.314e-01  7.486e-01  1.288e+03   0.977  0.328761
## med_laxatives      7.139e-01  2.197e+00  1.096e+03   0.325  0.745256
## l04002             2.066e+00  1.012e+00  7.073e+02   2.042  0.041484 *
## l04003             5.448e+00  1.345e+00  7.910e+02   4.051  5.61e-05 ***
## l04004             7.375e-01  7.644e-01  7.222e+02   0.965  0.334977
## l04005             1.976e+00  1.234e+00  7.726e+02   1.602  0.109582
## l04009            -7.848e-01  2.024e+00  9.095e+02  -0.388  0.698249
## l040010            6.589e-01  1.542e+00  9.208e+02   0.427  0.669157
## l040011            1.200e+00  2.089e+00  9.929e+02   0.574  0.565907
## mb_m03002         -4.437e-01  7.513e-01  1.201e+03  -0.591  0.554894
## mb_m03003         -5.088e-02  7.253e-01  1.204e+03  -0.070  0.944086
```

```

## mb_m03004          -4.911e-01  7.548e-01  1.207e+03  -0.651  0.515401
## mb_m03005          -2.728e-01  8.250e-01  1.218e+03  -0.331  0.740968
## mb_m03006           3.468e-01  7.690e-01  1.166e+03   0.451  0.652084
## mb_m03007          -4.435e-01  7.751e-01  1.211e+03  -0.572  0.567276
## genderwoman         8.020e-02  2.468e-01  9.721e+02   0.325  0.745295
## DNA_conc            8.187e-05  1.006e-03  1.137e+03   0.081  0.935169
## BMI                -8.200e-02  3.065e-02  1.256e+03  -2.675  0.007562 **
## sampling_date       -3.104e-03  3.192e-03  1.607e+01  -0.972  0.345355
## shipment_batch      -3.568e-01  1.832e-01  1.335e+02  -1.947  0.053610 .
## Plate012023         2.618e-01  9.688e-01  2.028e+02   0.270  0.787236
## Plate012323         4.244e-02  9.637e-01  1.504e+02   0.044  0.964934
## Plate013023        -4.749e-01  9.511e-01  5.045e+01  -0.499  0.619749
## Plate021323         6.057e-01  1.026e+00  1.091e+02   0.590  0.556127
## Plate032322        -3.759e+00  1.015e+00  5.145e+01  -3.704  0.000519 ***
## Plate032422        -3.784e+00  9.922e-01  5.067e+01  -3.814  0.000373 ***
## Plate110520        -7.150e+00  2.760e+00  3.871e+01  -2.591  0.013428 *
## Plate111020        -6.165e+00  2.524e+00  2.508e+01  -2.443  0.021968 *
## Reads               7.525e-09  4.231e-09  7.672e+02   1.778  0.075721 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.00425046 (tol = 0.002, component 1)

```

First degree connections, degree, use separate covariates

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ degree_c_all + age_at_survey + household_wealth_index_w3 +
##     DDS + med_painkillers + med_antibiotics + med_antidiarrheal +
##     med_antiparasite + med_vitamins + med_zinc + med_antifungal +
##     med_antihypertensives + med_antidiabetics + med_antiacids +
##     med_laxatives + l0400 + mb_m0300 + gender + DNA_conc + BMI +
##     l0400 + mb_m0300 + sampling_date + shipment_batch + Plate +
##     WIKI + Reads + (1 | village) + (1 | building_id)
## Data: centrality_sim_df_covars_all
##
## REML criterion at convergence: 8045
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2554 -0.4875 -0.1006  0.3790  5.9664
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 10.41185 3.2267
## village      (Intercept)  0.04731 0.2175
## Residual                12.48725 3.5337
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      6.826e+01  5.681e+01  1.180e+01   1.202  0.253088
## degree_c_all      -2.204e-01  3.266e-02  1.152e+03  -6.747  2.38e-11 ***
## age_at_survey     -3.493e-02  8.019e-03  1.214e+03  -4.356  1.44e-05 ***
## household_wealth_index_w3 -5.159e-01  1.244e-01  6.809e+02  -4.148  3.77e-05 ***
## DDS               -9.466e-02  9.567e-02  1.139e+03  -0.989  0.322661
## med_painkillers      8.980e-02  2.506e-01  1.165e+03   0.358  0.720217
## med_antibiotics     -4.273e-01  3.731e-01  1.197e+03  -1.145  0.252310
## med_antidiarrheal    9.800e-01  6.651e-01  1.089e+03   1.473  0.140930
## med_antiparasite    -8.811e-01  7.515e-01  1.159e+03  -1.172  0.241288
## med_vitamins        -5.281e-01  3.215e-01  1.184e+03  -1.643  0.100710
## med_zinc             1.184e+00  4.838e+00  1.127e+03   0.245  0.806623
## med_antifungal       5.789e-01  1.134e+00  1.121e+03   0.510  0.609978
## med_antihypertensives 1.404e-02  6.205e-01  1.224e+03   0.023  0.981956
## med_antidiabetics    1.153e+00  8.648e-01  1.221e+03   1.333  0.182815
## med_antiacids        9.184e-01  7.404e-01  1.281e+03   1.240  0.215096
## med_laxatives       7.538e-01  2.170e+00  1.085e+03   0.347  0.728372
## l04002              2.278e+00  1.003e+00  6.826e+02   2.271  0.023431 *
## l04003              5.477e+00  1.334e+00  7.833e+02   4.104  4.48e-05 ***
## l04004              9.317e-01  7.585e-01  7.112e+02   1.228  0.219773
## l04005              2.369e+00  1.224e+00  7.526e+02   1.935  0.053322 .
## l04009             -1.341e+00  2.003e+00  8.919e+02  -0.670  0.503255
## l040010             6.521e-01  1.528e+00  9.117e+02   0.427  0.669706
## l040011             1.323e+00  2.071e+00  9.848e+02   0.639  0.522993
## mb_m03002          -1.817e-01  7.443e-01  1.192e+03  -0.244  0.807228
## mb_m03003           1.129e-01  7.178e-01  1.195e+03   0.157  0.875024
```

```

## mb_m03004          -3.025e-01  7.470e-01  1.198e+03  -0.405  0.685555
## mb_m03005          -1.618e-01  8.161e-01  1.211e+03  -0.198  0.842878
## mb_m03006           5.249e-01  7.608e-01  1.156e+03   0.690  0.490385
## mb_m03007          -2.493e-01  7.669e-01  1.202e+03  -0.325  0.745189
## genderwoman         4.644e-02  2.438e-01  9.625e+02   0.190  0.848987
## DNA_conc            -8.503e-05  9.938e-04  1.125e+03  -0.086  0.931832
## BMI                 -7.471e-02  3.032e-02  1.254e+03  -2.464  0.013881 *
## sampling_date       -2.558e-03  3.001e-03  1.182e+01  -0.852  0.410934
## shipment_batch      -3.241e-01  1.785e-01  1.003e+02  -1.816  0.072402 .
## Plate012023         4.286e-01  9.470e-01  1.702e+02   0.453  0.651458
## Plate012323         3.541e-01  9.396e-01  1.241e+02   0.377  0.706893
## Plate013023        -5.132e-02  9.142e-01  3.968e+01  -0.056  0.955513
## Plate021323         7.520e-01  9.963e-01  9.528e+01   0.755  0.452215
## Plate032322        -3.330e+00  9.630e-01  3.857e+01  -3.458  0.001342 **
## Plate032422        -3.540e+00  9.454e-01  3.902e+01  -3.745  0.000582 ***
## Plate110520        -6.054e+00  2.630e+00  2.962e+01  -2.302  0.028574 *
## Plate111020        -5.106e+00  2.384e+00  1.840e+01  -2.141  0.045856 *
## Reads               7.407e-09  4.164e-09  6.314e+02   1.779  0.075765 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling

```

Mahalanobis

Average strain-sharing rate to the rest of the villages, betweenness centrality, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula:  
## strain_sim_all ~ between_c_all + maha_social + DNA_conc + sampling_date +  
##   shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |  
##   building_id)  
## Data:  
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,  
##   FALSE, var(sub_covar_centrality, na.rm = TRUE)))  
##  
## REML criterion at convergence: 4293.6  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max   
## -4.3265 -0.5221  0.0011  0.5155  4.5525   
##  
## Random effects:  
## Groups      Name                Variance Std.Dev.  
## building_id (Intercept) 0.2422    0.4921  
## village      (Intercept) 2.9368    1.7137  
## Residual                        0.9785    0.9892  
## Number of obs: 1371, groups:  building_id, 816; village, 18  
##  
## Fixed effects:  
##              Estimate Std. Error      df t value Pr(>|t|)   
## (Intercept)   3.039e+01  5.606e+01  5.054e+01  0.542  0.59011  
## between_c_all  1.919e+00  1.184e+00  1.277e+03  1.622  0.10514  
## maha_social    5.257e-05  6.319e-04  1.324e+03  0.083  0.93371  
## DNA_conc       8.545e-05  2.473e-04  1.313e+03  0.346  0.72976  
## sampling_date -1.214e-03  2.964e-03  5.056e+01 -0.410  0.68376  
## shipment_batch -1.729e-01  5.343e-02  1.341e+03 -3.236  0.00124 **  
## Plate012023    -5.489e-01  2.831e-01  1.346e+03 -1.939  0.05273 .  
## Plate012323    1.917e-01  3.155e-01  1.321e+03  0.607  0.54364  
## Plate013023    4.633e-01  3.717e-01  1.264e+03  1.246  0.21293  
## Plate021323    4.266e-01  3.815e-01  1.254e+03  1.118  0.26371  
## Plate032322   -1.070e+00  3.959e-01  1.219e+03 -2.703  0.00696 **  
## Plate032422   -1.052e+00  3.844e-01  1.212e+03 -2.736  0.00632 **  
## Plate110520   -3.465e+00  2.059e+00  4.375e+01 -1.683  0.09957 .  
## Plate111020   -3.686e+00  2.044e+00  4.267e+01 -1.803  0.07847 .  
## Reads          5.678e-09  1.089e-09  1.249e+03  5.215  2.15e-07 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
## fit warnings:  
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients  
## Some predictor variables are on very different scales: consider rescaling
```

Average strain-sharing rate to the rest of the village, eigenvector centrality, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ eigen_c_all + maha_social + DNA_conc + sampling_date +
##   shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |
##   building_id)
## Data:
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,
##   FALSE, var(sub_covar_centrality, na.rm = TRUE)))
##
## REML criterion at convergence: 4276.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.5583 -0.5340  0.0020  0.5062  4.6814
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 0.2137   0.4622
## village      (Intercept) 2.7264   1.6512
## Residual                        0.9839   0.9919
## Number of obs: 1371, groups:  building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   2.026e+01  5.486e+01  4.940e+01   0.369  0.71350
## eigen_c_all    7.134e-01  1.444e-01  1.151e+03   4.941  8.94e-07 ***
## maha_social   -3.692e-05  6.263e-04  1.326e+03  -0.059  0.95301
## DNA_conc       9.574e-05  2.457e-04  1.321e+03   0.390  0.69685
## sampling_date -6.844e-04  2.901e-03  4.941e+01  -0.236  0.81446
## shipment_batch -1.713e-01  5.305e-02  1.347e+03  -3.229  0.00127 **
## Plate012023   -5.110e-01  2.813e-01  1.347e+03  -1.817  0.06951 .
## Plate012323    9.109e-02  3.135e-01  1.315e+03   0.291  0.77143
## Plate013023    3.640e-01  3.691e-01  1.250e+03   0.986  0.32422
## Plate021323    3.783e-01  3.783e-01  1.242e+03   1.000  0.31756
## Plate032322   -1.105e+00  3.915e-01  1.204e+03  -2.822  0.00485 **
## Plate032422   -1.075e+00  3.799e-01  1.199e+03  -2.831  0.00472 **
## Plate110520   -3.082e+00  2.013e+00  4.314e+01  -1.531  0.13295
## Plate111020   -3.332e+00  1.997e+00  4.202e+01  -1.668  0.10269
## Reads         5.728e-09  1.083e-09  1.267e+03   5.287  1.46e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

Average strain-sharing rate to the rest of the village, degree, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## strain_sim_all ~ degree_c_all + maha_social + DNA_conc + sampling_date +
## shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |
## building_id)
## Data:
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,
## FALSE, var(sub_covar_centrality, na.rm = TRUE)))
##
## REML criterion at convergence: 4286.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.3611 -0.5344 -0.0074  0.5109  4.7289
##
## Random effects:
## Groups      Name      Variance Std.Dev.
## building_id (Intercept) 0.2104   0.4587
## village      (Intercept) 2.7946   1.6717
## Residual                    0.9900   0.9950
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   2.249e+01  5.520e+01  5.090e+01   0.407  0.68538
## degree_c_all   3.292e-02  7.348e-03  1.341e+03   4.481  8.07e-06 ***
## maha_social    -6.667e-05  6.278e-04  1.325e+03  -0.106  0.91544
## DNA_conc       9.097e-05  2.461e-04  1.321e+03   0.370  0.71171
## sampling_date  -8.058e-04  2.918e-03  5.092e+01  -0.276  0.78359
## shipment_batch -1.710e-01  5.314e-02  1.347e+03  -3.218  0.00132 **
## Plate012023    -5.479e-01  2.816e-01  1.347e+03  -1.946  0.05186 .
## Plate012323     1.691e-01  3.135e-01  1.319e+03   0.539  0.58975
## Plate013023     4.104e-01  3.694e-01  1.259e+03   1.111  0.26683
## Plate021323     4.040e-01  3.790e-01  1.250e+03   1.066  0.28672
## Plate032322    -1.112e+00  3.922e-01  1.211e+03  -2.834  0.00467 **
## Plate032422    -1.097e+00  3.805e-01  1.205e+03  -2.884  0.00399 **
## Plate110520    -3.224e+00  2.025e+00  4.433e+01  -1.592  0.11857
## Plate111020    -3.449e+00  2.010e+00  4.320e+01  -1.716  0.09341 .
## Reads          5.572e-09  1.085e-09  1.266e+03   5.135  3.26e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, clustering coefficient, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ cluster_coef_all + maha_social + DNA_conc + sampling_date +
## shipment_batch + Plate + WIKI + Reads + (1 | village_name) +
## (1 | building_id)
## Data:
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,
## FALSE, var(sub_covar_centrality, na.rm = TRUE)))
##
## REML criterion at convergence: 8169.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.8932 -0.4882 -0.1116  0.3423  5.8028
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## building_id (Intercept) 11.4132  3.3783
## village_name (Intercept)  0.2496  0.4996
## Residual              13.0027  3.6059
## Number of obs: 1371, groups: building_id, 816; village_name, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    1.013e+02  6.574e+01  1.872e+01   1.540  0.14020
## cluster_coef_all  4.275e+00  5.381e-01  1.225e+03   7.946 4.35e-15 ***
## maha_social     -3.839e-03  2.703e-03  1.349e+03  -1.420  0.15573
## DNA_conc        2.927e-04  1.003e-03  1.156e+03   0.292  0.77050
## sampling_date   -4.700e-03  3.470e-03  1.869e+01  -1.355  0.19172
## shipment_batch  -3.469e-01  1.896e-01  1.815e+02  -1.830  0.06892 .
## Plate012023      9.137e-01  1.002e+00  2.187e+02   0.912  0.36289
## Plate012323      9.486e-01  9.980e-01  1.532e+02   0.951  0.34335
## Plate013023      3.780e-01  1.009e+00  5.259e+01   0.375  0.70943
## Plate021323      9.195e-01  1.071e+00  1.051e+02   0.859  0.39248
## Plate032322     -3.113e+00  1.056e+00  4.987e+01  -2.947  0.00486 **
## Plate032422     -3.357e+00  1.039e+00  5.218e+01  -3.230  0.00214 **
## Plate110520     -6.732e+00  2.909e+00  4.092e+01  -2.314  0.02578 *
## Plate111020     -5.688e+00  2.696e+00  2.830e+01  -2.110  0.04385 *
## Reads           8.621e-09  4.270e-09  8.991e+02   2.019  0.04379 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, eigenvector centrality, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: sim_deg_one ~ eigen_c_all + maha_social + DNA_conc + sampling_date +
## shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |
## building_id)
## Data:
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,
## FALSE, var(sub_covar_centrality, na.rm = TRUE)))
##
## REML criterion at convergence: 8178.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.8444 -0.4823 -0.1099  0.3433  6.0670
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
## building_id (Intercept) 11.6479  3.4129
## village      (Intercept)  0.4967  0.7047
## Residual                12.9563  3.5995
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.668e+02  7.358e+01  1.866e+01   2.267 0.035462 *
## eigen_c_all   -4.651e+00  6.342e-01  1.290e+03  -7.334 3.94e-13 ***
## maha_social    -3.250e-03  2.716e-03  1.348e+03  -1.197 0.231558
## DNA_conc       3.176e-04  1.006e-03  1.143e+03   0.316 0.752191
## sampling_date  -8.052e-03  3.883e-03  1.860e+01  -2.074 0.052262 .
## shipment_batch -2.592e-01  1.955e-01  2.133e+02  -1.326 0.186380
## Plate012023    6.989e-01  1.036e+00  2.302e+02   0.675 0.500529
## Plate012323    1.013e+00  1.038e+00  1.404e+02   0.976 0.330841
## Plate013023   -1.118e-01  1.077e+00  5.227e+01  -0.104 0.917708
## Plate021323    4.535e-01  1.126e+00  8.559e+01   0.403 0.688170
## Plate032322   -3.959e+00  1.139e+00  4.863e+01  -3.476 0.001082 **
## Plate032422   -4.073e+00  1.120e+00  5.164e+01  -3.637 0.000637 ***
## Plate110520   -8.545e+00  3.156e+00  3.774e+01  -2.708 0.010123 *
## Plate111020   -7.397e+00  2.964e+00  2.782e+01  -2.495 0.018801 *
## Reads         7.865e-09  4.299e-09  9.688e+02   1.829 0.067633 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, betweenness centrality, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## sim_deg_one ~ between_c_all + maha_social + DNA_conc + sampling_date +
## shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |
## building_id)
## Data:
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,
## FALSE, var(sub_covar_centrality, na.rm = TRUE)))
##
## REML criterion at convergence: 8182.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.9432 -0.4803 -0.1198  0.3752  6.1148
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## building_id (Intercept) 11.5556  3.3993
## village      (Intercept)  0.4601  0.6783
## Residual                13.1307  3.6236
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.558e+02  7.260e+01  2.074e+01   2.146  0.043828 *
## between_c_all -3.202e+01  4.759e+00  1.167e+03  -6.729  2.66e-11 ***
## maha_social   -3.101e-03  2.725e-03  1.348e+03  -1.138  0.255273
## DNA_conc       5.080e-04  1.010e-03  1.155e+03   0.503  0.615204
## sampling_date -7.477e-03  3.831e-03  2.069e+01  -1.952  0.064658 .
## shipment_batch -2.657e-01  1.955e-01  2.265e+02  -1.359  0.175452
## Plate012023    7.621e-01  1.035e+00  2.470e+02   0.736  0.462179
## Plate012323    4.919e-01  1.037e+00  1.586e+02   0.474  0.636028
## Plate013023   -4.917e-01  1.073e+00  5.937e+01  -0.458  0.648473
## Plate021323    2.323e-01  1.124e+00  9.789e+01   0.207  0.836661
## Plate032322   -4.093e+00  1.135e+00  5.494e+01  -3.606  0.000671 ***
## Plate032422   -4.107e+00  1.114e+00  5.729e+01  -3.686  0.000508 ***
## Plate110520   -8.374e+00  3.132e+00  4.231e+01  -2.674  0.010610 *
## Plate111020   -7.425e+00  2.939e+00  3.111e+01  -2.527  0.016815 *
## Reads          8.068e-09  4.316e-09  9.788e+02   1.869  0.061884 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```

First degree connections, degree, use Mahalanobis distance

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: sim_deg_one ~ degree_c_all + maha_social + DNA_conc + sampling_date +
## shipment_batch + Plate + WIKI + Reads + (1 | village) + (1 |
## building_id)
## Data:
## dplyr::bind_cols(centrality_sim_df_covars_all, maha_social = mahalanobis(sub_covar_centrality,
## FALSE, var(sub_covar_centrality, na.rm = TRUE)))
##
## REML criterion at convergence: 8149.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7812 -0.4675 -0.1102  0.3827  5.9672
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## building_id (Intercept) 11.4621  3.3856
## village      (Intercept)  0.3479  0.5898
## Residual                12.5927  3.5486
## Number of obs: 1371, groups: building_id, 816; village, 18
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.214e+02  6.852e+01  1.710e+01   1.771  0.09437 .
## degree_c_all  -2.853e-01  3.005e-02  1.227e+03  -9.494 < 2e-16 ***
## maha_social    -2.608e-03  2.684e-03  1.348e+03  -0.972  0.33140
## DNA_conc       2.926e-04  9.918e-04  1.141e+03   0.295  0.76801
## sampling_date  -5.620e-03  3.617e-03  1.706e+01  -1.554  0.13854
## shipment_batch -2.297e-01  1.900e-01  1.802e+02  -1.209  0.22834
## Plate012023    9.159e-01  1.006e+00  2.069e+02   0.910  0.36372
## Plate012323    9.187e-01  1.006e+00  1.370e+02   0.914  0.36258
## Plate013023    8.917e-02  1.029e+00  4.862e+01   0.087  0.93128
## Plate021323    5.124e-01  1.085e+00  8.773e+01   0.472  0.63777
## Plate032322   -3.388e+00  1.081e+00  4.429e+01  -3.134  0.00306 **
## Plate032422   -3.565e+00  1.063e+00  4.689e+01  -3.354  0.00159 **
## Plate110520   -6.381e+00  2.986e+00  3.582e+01  -2.137  0.03952 *
## Plate111020   -5.430e+00  2.787e+00  2.567e+01  -1.948  0.06239 .
## Reads         8.030e-09  4.229e-09  9.244e+02   1.899  0.05789 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
```