Component response rate variation drives stability in large complex systems

Supporting information

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Note: All text, code, and data underlying this manuscript are publicly available on GitHub as part of the RandomMatrixStability package. The text below explains how all results from the main manuscript can be recreated using the RandomMatrixStability package available on GitHub. To download this package, which includes all functions and tools for recreating the text, this supplemental information, and running all code, the `devtools` library is needed.

```
install.packages("devtools");
library(devtools);
```

The code below installs the RandomMatrixStability package using devtools.

```
install_github("bradduthie/random_matrix_stability")
```

While downloading this package is recommended, all relevant code is also reproduced below with explanation.

Contents

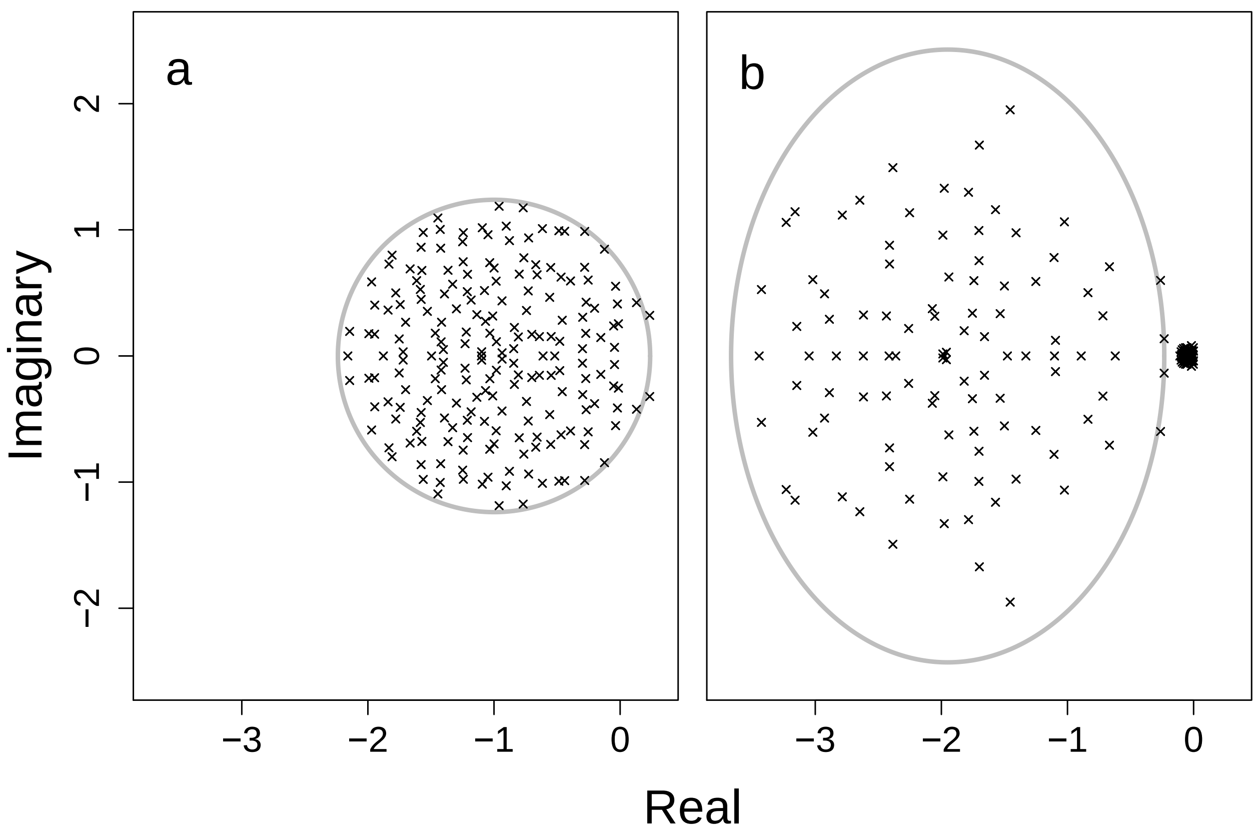
Code and simulations underlying Fig. 1

The sample M used for the eigenvalue distributions in Fig. 1 of the text is available on GitHub, and was produced by running the following function.

```
find_bgamma <- function(S = 200, C = 0.05, Osd = 0.4, iters = 10000){
    while(iters > 0){
        A_dat  <- rnorm(n = S * S, mean = 0, sd = Osd);
        A_mat  <- matrix(data = A_dat, nrow = S);
        C_dat  <- rbinom(n = S * S, size = 1, prob = C);
        C_mat  <- matrix(data = C_dat, nrow = S, ncol = S);
```

```
        A_mat  <- A_mat * C_mat;
        gammas <- c(rep(1.95, S/2), rep(0.05, S/2))
        mu_gam <- mean(gammas);
        diag(A_mat) <- -1;
        A1     <- gammas * A_mat;
        A0     <- mu_gam * A_mat;
        A0_e   <- eigen(A0)$values;
        A0_r   <- Re(A0_e);
        A0_i   <- Im(A0_e);
        A1_e   <- eigen(A1)$values;
        A1_r   <- Re(A1_e);
        A1_i   <- Im(A1_e);
        if(max(A0_r) >= 0 & max(A1_r) < 0){
            return(list(A0 = A0, A1 = A1));
            break;
        }
        print(iters);
        iters <- iters - 1;
    }
}
```

The above function terminates when a matrix M is found that is not stable when all component response rates are set to $\gamma = 1$, but is stable when half of component response rates are 1.95 and half are 0.05. The function is used to illustrate the concept of how fast versus slow component responses can cause a system to become stable. Simulations were run for `iter = 1000000`, but terminated once an acceptable `A0` and `A1` were found. The code below plots the eigenvalue distributions of `A0` and `A1` in panels **a** and **b**, respectively. The plot itself can be recreated with the function and code below.



To find out how frequently M was stable given that all $\gamma = 1$ versus $\gamma = \{1.95, 0.05\}$, the function below was created.

```
stab_bgamma <- function(S = 200, C = 0.05, Osd = 0.4, iters = 10000){
    ress     <- matrix(data = 0, nrow = iters, ncol = 2);
    A0_count <- 0;
    A1_count <- 0;
    while(iters > 0){
        A_dat  <- rnorm(n = S * S, mean = 0, sd = Osd);
        A_mat  <- matrix(data = A_dat, nrow = S);
        C_dat  <- rbinom(n = S * S, size = 1, prob = C);
        C_mat  <- matrix(data = C_dat, nrow = S, ncol = S);
        A_mat  <- A_mat * C_mat;
        gammas <- c(rep(1.95, S/2), rep(0.05, S/2))
        mu_gam <- mean(gammas);
        diag(A_mat) <- -1;
        A1     <- gammas * A_mat;
        A0     <- mu_gam * A_mat;
        A0_e   <- eigen(A0)$values;
        A0_r   <- Re(A0_e);
        A0_i   <- Im(A0_e);
        A1_e   <- eigen(A1)$values;
        A1_r   <- Re(A1_e);
        A1_i   <- Im(A1_e);
        if(max(A0_r) < 0){
            ress[iters, 1] <- 1;
            A0_count       <- A0_count + 1;
            }
        if(max(A1_r) < 0){
            ress[iters, 2] <- 1;
            A1_count       <- A1_count + 1;
        }
        print(c(iters, A0_count, A1_count));
        iters <- iters - 1;
    }
    return(ress);
}
```

The above functions produced the `bi_pr_st` data.

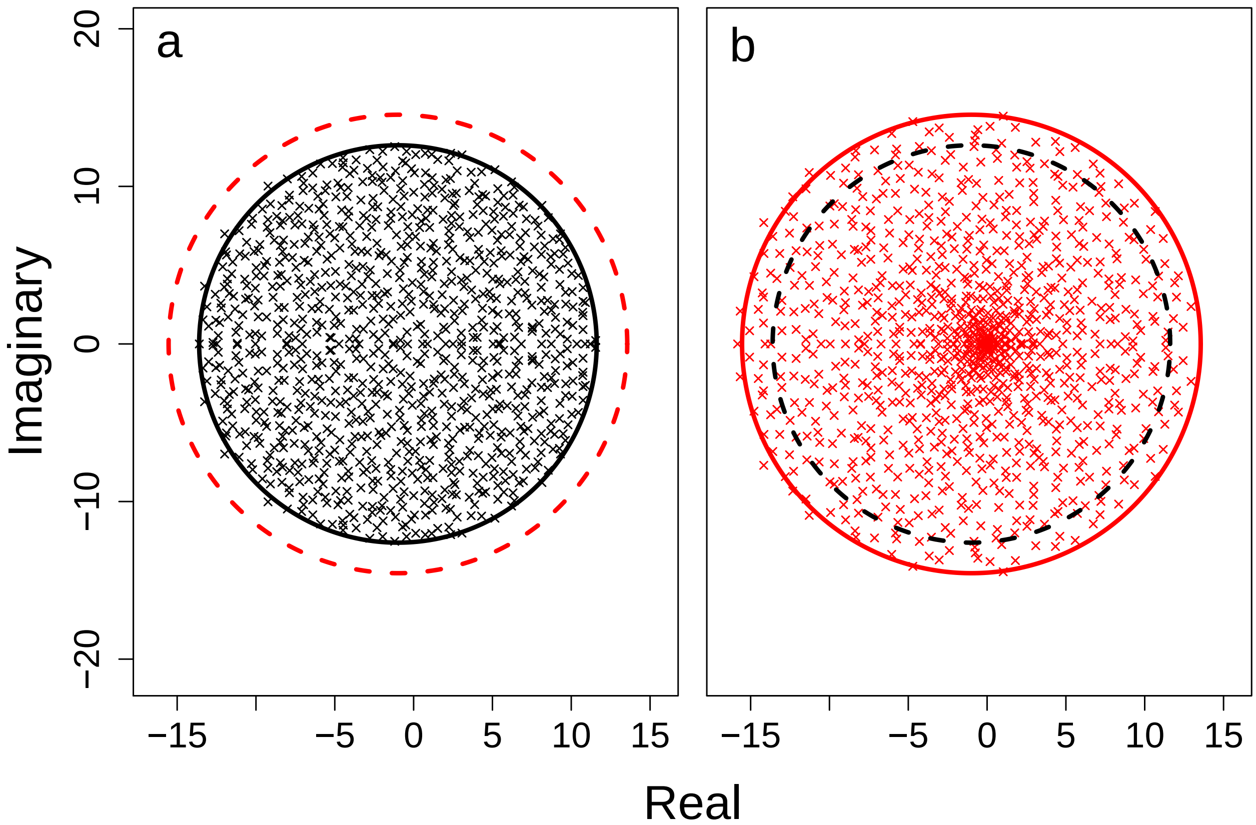
```
bi_pr_st <- read.csv("sim_results/bi_gamma/bi_pr_st.csv");
pr_st    <- bi_pr_st[,-1];
```

The function above was run for `iters = 1000000`, and the resulting matrix `ress` was returned. Each row of `ress` represents a single M given $\gamma = 1$ (column 1) versus $\gamma = \{1.95, 0.05\}$ (column 2). Values of 0 indicate that M was found to be unstable (at least one real component of its eigenvalues greater than or equal to zero), whereas values of 1 indicate that M was found to be stable (all real components of eigenvalues are negative). The frequencies of stable M were 1 given $\gamma = 1$ and 32 given $\gamma = \{1.95, 0.05\}$, as reported in the main text and legend of Fig. 1 (raw data are available on GitHub).

Code and simulations underlying Fig. 2

Figure 2 of the main text shows eigenvalue distributions in a system where $S = 1000$, $C = 1$, and $\sigma = 0.4$. Eigenvalues can be reproduced using the code below for when $\gamma = 1$ (panel a) and $\gamma \sim \mathcal{U}(0, 2)$ (panel b). The function below reproduces the figure.

```
plot_Fig_2 <- function(){
    A_comp <- NULL;
    A_dat  <- rnorm(n = 1000000, mean = 0, sd = 0.4);
    A_mat  <- matrix(data = A_dat, nrow = 1000);
    C_dat  <- rbinom(n = 1000 * 1000, size = 1, prob = 1);
    C_mat  <- matrix(data = C_dat, nrow = 1000, ncol = 1000);
    A_mat     <- A_mat * C_mat;
    gammas <- runif(n = 1000, min = 0, max = 2);
    mu_gam <- mean(gammas);
    diag(A_mat) <- -1;
    A1     <- gammas * A_mat;
    A0     <- mu_gam * A_mat;
    A0_e   <- eigen(A0)$values;
    A0_r   <- Re(A0_e);
    A0_i   <- Im(A0_e);
    A1_e   <- eigen(A1)$values;
    A1_r   <- Re(A1_e);
    A1_i   <- Im(A1_e);
    A0_vm       <- A0;
    diag(A0_vm) <- NA;
    A0vec       <- as.vector(A0_vm);
    A0vec       <- A0vec[is.na(A0vec) == FALSE];
    A1_vm       <- A1;
    diag(A1_vm) <- NA;
    A1vec       <- as.vector(A1_vm);
    A1vec       <- A1vec[is.na(A1vec) == FALSE];
    par(mfrow = c(1, 2), mar = c(0.5, 0.5, 0.5, 0.5), oma = c(5, 5, 0, 0));
    plot(A0_r, A0_i, xlim = c(-16.5, 15.5), ylim = c(-16.5,15.5), pch = 4,
         cex = 0.7, xlab = "", ylab = "", cex.lab = 1.5, cex.axis = 1.5,
         asp = 1);
    vl <- seq(from = 0, to = 2*pi, by = 0.001);
    x0 <- sqrt(1000) * sd(A0vec) * cos(vl) + mean(diag(A0));
    y0 <- sqrt(1000) * sd(A0vec) * sin(vl);
    x1 <- sqrt(1000) * sd(A1vec) * cos(vl) + mean(diag(A1));
    y1 <- sqrt(1000) * sd(A1vec) * sin(vl);
    text(x = -15.5, y = 19, labels = "a", cex = 2);
    points(x = x0, y = y0, type = "l", lwd = 3);
    points(x = x1, y = y1, type = "l", col = "red", lwd = 3, lty = "dashed");
    plot(A1_r, A1_i, xlim = c(-16.5, 15.5), ylim = c(-16.5,15.5), pch = 4, cex = 0.7,
         xlab = "", ylab = "", cex.lab = 1.5, cex.axis = 1.5, asp = 1, col = "red",
         yaxt = "n");
    text(x = -15.5, y = 19, labels = "b", cex = 2);
    points(x = x1, y = y1, type = "l", col = "red", lwd = 3)
    points(x = x0, y = y0, type = "l", lwd = 3, lty = "dashed");
    mtext(side = 1, "Real", outer = TRUE, line = 3, cex = 2);
    mtext(side = 2, "Imaginary", outer = TRUE, line = 2.5, cex = 2);
}
plot_Fig_2();
```



Stability across increasing S

Figure 3 of the main text reports the number of stable random complex systems found over 1 million iterations. The data used to make this figure is read into R below.

```
dat <- read.csv(file = "sim_results/C_1/random_all.csv");
dat <- dat[,-1]; # Extra row indicating column removed
```

The table below shows the results for all simulations of random M matrices at $\sigma = 0.4$ and $C = 1$ given a range of $S = \{2, 3, ..., 49, 50\}$. In this table, the `A0` refers to matrices where $\gamma = 1$, while `A1` refers to matrices after $Var(\gamma)$ is added and $\gamma \sim \mathcal{U}(0, 2)$. Each row summarises data for a given S over 1 million randomly simulated M (`A0` and `A1`). The column `A0_unstable` shows the number of `A0` matrices that are unstable, and the column `A0_stable` shows the number of `A0` matrices that are stable (these two columns sum to 1 million). Similarly, the column `A1_unstable` shows the number of `A1` matrices that are unstable and `A1_stable` shows the number that are stable. The columns `A1_stabilised` and `A1_destabilised` show how many `A0` matrices were stabilised or destabilised, respectively, by $Var(\gamma)$.

S	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
2	293	999707	293	999707	0	0
3	3602	996398	3609	996391	0	7
4	14937	985063	15008	984992	0	71
5	39289	960711	39783	960217	36	530
6	78845	921155	80207	919793	389	1751
7	133764	866236	136904	863096	1679	4819
8	204112	795888	208241	791759	5391	9520
9	288041	711959	291775	708225	12619	16353

S	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
10	384024	615976	384931	615069	23153	24060
11	485975	514025	481019	518981	35681	30725
12	590453	409547	577439	422561	48302	35288
13	689643	310357	669440	330560	57194	36991
14	777496	222504	751433	248567	60959	34896
15	850159	149841	821613	178387	58567	30021
16	905057	94943	877481	122519	51255	23679
17	943192	56808	919536	80464	40854	17198
18	969018	30982	949944	50056	30102	11028
19	984301	15699	970703	29297	20065	6467
20	992601	7399	983507	16493	12587	3493
21	996765	3235	991532	8468	7030	1797
22	998693	1307	995567	4433	3884	758
23	999503	497	997941	2059	1883	321
24	999861	139	999059	941	899	97
25	999964	36	999617	383	380	33
26	999993	7	999878	122	121	6
27	999995	5	999946	54	53	4
28	1000000	0	999975	25	25	0
29	1000000	0	999997	3	3	0
30	1000000	0	999999	1	1	0
31	1000000	0	999999	1	1	0
32	1000000	0	1000000	0	0	0
33	1000000	0	1000000	0	0	0
34	1000000	0	1000000	0	0	0
35	1000000	0	1000000	0	0	0
36	1000000	0	1000000	0	0	0
37	1000000	0	1000000	0	0	0
38	1000000	0	1000000	0	0	0
39	1000000	0	1000000	0	0	0
40	1000000	0	1000000	0	0	0
41	1000000	0	1000000	0	0	0
42	1000000	0	1000000	0	0	0
43	1000000	0	1000000	0	0	0
44	1000000	0	1000000	0	0	0
45	1000000	0	1000000	0	0	0
46	1000000	0	1000000	0	0	0
47	1000000	0	1000000	0	0	0
48	1000000	0	1000000	0	0	0
49	1000000	0	1000000	0	0	0
50	1000000	0	1000000	0	0	0

The results underlying this table were produced with the `rand_gen_var` function below.

```
rand_gen_var <- function(max_sp, iters, int_type = 0, rmx = 0.4, C = 1){
    tot_res <- NULL;
    fea_res <- NULL;
    for(i in 2:max_sp){
        iter           <- iters;
        tot_res[[i-1]] <- matrix(data = 0, nrow = iter, ncol = 7);
        fea_res[[i-1]] <- matrix(data = 0, nrow = iter, ncol = 7);
        while(iter > 0){
```

```
            r_vec    <- rnorm(n = i, mean = 0, sd = rmx);
            A0_dat   <- rnorm(n = i * i, mean = 0, sd = 0.4);
            A0       <- matrix(data = A0_dat, nrow = i, ncol = i);
            A0       <- species_interactions(mat = A0, type = int_type);
            C_dat    <- rbinom(n = i * i, size = 1, prob = C);
            C_mat    <- matrix(data = C_dat, nrow = i, ncol = i);
            A0       <- A0 * C_mat;
            diag(A0) <- -1;
            gam1     <- runif(n = i, min = 0, max = 2);
            A1       <- A0 * gam1;
            A0       <- A0 * mean(gam1);
            A0_stb   <- max(Re(eigen(A0)$values)) < 0;
            A1_stb   <- max(Re(eigen(A1)$values)) < 0;
            A0_fea   <- min(-1*solve(A0) %*% r_vec) > 0;
            A1_fea   <- min(-1*solve(A1) %*% r_vec) > 0;
            if(A0_stb == TRUE){
                tot_res[[i-1]][iter, 1] <- 1;
            }
            if(A1_stb == TRUE){
                tot_res[[i-1]][iter, 2] <- 1;
            }
            if(A0_fea == TRUE){
                fea_res[[i-1]][iter, 1] <- 1;
            }
            if(A1_fea == TRUE){
                fea_res[[i-1]][iter, 2] <- 1;
            }
            iter    <- iter - 1;
        }
        print(i);
    }
    all_res <- summarise_randmat(tot_res = tot_res, fea_res = fea_res);
    return(all_res);
}
```

The above function calls the two functions species_interactions and summarise_randmat, which are provided below.

```
species_interactions <- function(mat, type = 0){
    if(type == 1){
        mat[mat > 0] <- -1*mat[mat > 0];
    }
    if(type == 2){
        mat[mat < 0] <- -1*mat[mat < 0];
    }
    if(type == 3){
        for(i in 1:dim(mat)[1]){
            for(j in 1:dim(mat)[2]){
                if(mat[i, j] * mat[j, i] > 0){
                    mat[j, i] <- -1 * mat[j, i];
                }
            }
        }
    }
```

```r
    return(mat);
}

summarise_randmat <- function(tot_res, fea_res){
    sims    <- length(tot_res);
    all_res <- matrix(data = 0, nrow = sims, ncol = 13);
    for(i in 1:sims){
        all_res[i, 1]  <- i + 1;
        # Stable and unstable
        all_res[i, 2]  <- sum(tot_res[[i]][,1] == FALSE);
        all_res[i, 3]  <- sum(tot_res[[i]][,1] == TRUE);
        all_res[i, 4]  <- sum(tot_res[[i]][,2] == FALSE);
        all_res[i, 5]  <- sum(tot_res[[i]][,2] == TRUE);
        # Stabilised and destabilised
        all_res[i, 6] <- sum(tot_res[[i]][,1] == FALSE &
                                 tot_res[[i]][,2] == TRUE);
        all_res[i, 7] <- sum(tot_res[[i]][,1] == TRUE &
                                 tot_res[[i]][,2] == FALSE);
        # Feasible and infeasible
        all_res[i, 8]  <- sum(fea_res[[i]][,1] == FALSE);
        all_res[i, 9]  <- sum(fea_res[[i]][,1] == TRUE);
        all_res[i, 10]  <- sum(fea_res[[i]][,2] == FALSE);
        all_res[i, 11]  <- sum(fea_res[[i]][,2] == TRUE);
        # Feased and defeased
        all_res[i, 12] <- sum(fea_res[[i]][,1] == FALSE &
                                 fea_res[[i]][,2] == TRUE);
        all_res[i, 13] <- sum(fea_res[[i]][,1] == TRUE &
                                 fea_res[[i]][,2] == FALSE);
    }
    cnames <- c("N", "A0_unstable", "A0_stable", "A1_unstable", "A1_stable",
                "A1_stabilised", "A1_destabilised", "A0_infeasible",
                "A0_feasible", "A1_infeasible", "A1_feasible",
                "A1_made_feasible", "A1_made_infeasible");
    colnames(all_res) <- cnames;
    return(all_res);
}
```

Note that feasibility results were ommited for the table above, but are reported below.

Stability of ecological networks

While the foundational work of May[1] applies broadly to complex networks, much attention has been given specifically to ecological networks of interacting species. In these networks, the matrix M is interpreted as a community matrix and each row and column is interpreted as a single species. The effect that the density of any species i has on the population dynamics of species j is found in M_{ij}, meaning that M holds the effects of pair-wise interactions between S species[2–4]. While May's original work[1] considered only randomly assembled communities, recent work has specifically looked at more restricted ecological communities including competitive networks (all off-diagonal elements of M are negative), mutualist networks (all off-diagonal elements of M are positive), and predator-prey networks (for any pair of i and j, the effect of i on j is negative and j on i is positive, or vice versa)[2–5]. In general, competitor and mutualist networks tend to be unstable, while predator-prey networks tend to be highly stabilising.

I investigate competitor, mutualist, and predator-prey networks following Allesina et al.[2]. To create these networks, I first generated a random matrix M, then changed the elements of M accordingly. If M was a competitive network, then the sign of any positive off-diagonal elements was reversed to be negative. If M was a mutualist network, then the sign of any positive off-diagonal elements was reversed to be positive. And if M was a predator-prey network, then all i and j pairs of elements were checked; any pairs of the same sign were changed so that one was negative and the other was positive. The `species_interaction` function used to do this is below.

```
species_interactions <- function(mat, type = 0){
    if(type == 1){
        mat[mat > 0] <- -1*mat[mat > 0];
    }
    if(type == 2){
        mat[mat < 0] <- -1*mat[mat < 0];
    }
    if(type == 3){
        for(i in 1:dim(mat)[1]){
            for(j in 1:dim(mat)[2]){
                if(mat[i, j] * mat[j, i] > 0){
                    mat[j, i] <- -1 * mat[j, i];
                }
            }
        }
    }
    return(mat);
} # Note: -1 values are added in the diagonal later
```

This function was applied to all created matrices M, then the number of stable M matrices was estimated exactly as it was in the main text for random matrices for values of S from 2 to 50 (100 in the case of the relatively more stable predator-prey interactions), except that only 100000 random M were generated instead of 1 million. This produced the data set below.

```
cdat <- read.csv(file = "sim_results/ecology/competition_C_1.csv");
mdat <- read.csv(file = "sim_results/ecology/mutualism_C_1.csv");
pdat <- read.csv(file = "sim_results/ecology/pred-prey_C_1.csv");
```

The following tables for restricted ecological communities can therefore be compared with the random M results above. As with the results above, in the tables below, `A0` refers to matrices when $\gamma = 1$ and `A1` refers to matrices after $Var(\gamma)$ is added. The column `A0_unstable` shows the number of `A0` matrices that are unstable, and the column `A0_stable` shows the number of `A0` matrices that are stable (these two columns sum to 100000). Similarly, the column `A1_unstable` shows the number of `A1` matrices that are unstable and `A1_stable` shows the number that are stable. The columns `A1_stabilised` and `A1_destabilised` show how many `A0` matrices were stabilised or destabilised, respectively, by $Var(\gamma)$.

Competition

Results for competitor interaction networks are shown below

X	N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised
1	2	48	99952	48	99952	0
2	3	229	99771	231	99769	0
3	4	701	99299	704	99296	0
4	5	1579	98421	1587	98413	0
5	6	3218	96782	3253	96747	6
6	7	5519	94481	5619	94381	23
7	8	9062	90938	9237	90763	77
8	9	13436	86564	13729	86271	230

X	N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised
9	10	18911	81089	19303	80697	505
10	11	25594	74406	25961	74039	1011
11	12	33207	66793	33382	66618	1724
12	13	41160	58840	41089	58911	2655
13	14	50575	49425	49894	50106	3777
14	15	59250	40750	57892	42108	4824
15	16	67811	32189	65740	34260	5634
16	17	75483	24517	73056	26944	5943
17	18	82551	17449	79878	20122	5780
18	19	88030	11970	85204	14796	5417
19	20	92254	7746	89766	10234	4544
20	21	95233	4767	93002	6998	3695
21	22	97317	2683	95451	4549	2803
22	23	98508	1492	97122	2878	1991
23	24	99240	760	98407	1593	1216
24	25	99669	331	99082	918	739
25	26	99871	129	99490	510	452
26	27	99938	62	99732	268	240
27	28	99985	15	99888	112	108
28	29	99990	10	99951	49	46
29	30	100000	0	99981	19	19
30	31	100000	0	99993	7	7
31	32	100000	0	99996	4	4
32	33	100000	0	99998	2	2
33	34	100000	0	100000	0	0
...	...	...	...	...	...	...
49	50	100000	0	100000	0	0

Mutualism

Results for mutualist interaction networks are shown below

X	N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised
1	2	56	99944	56	99944	0
2	3	3301	96699	3301	96699	0
3	4	34446	65554	34446	65554	0
4	5	86520	13480	86520	13480	0
5	6	99683	317	99683	317	0
6	7	99998	2	99998	2	0
7	8	100000	0	100000	0	0
8	9	100000	0	100000	0	0
9	10	100000	0	100000	0	0
10	11	100000	0	100000	0	0
11	12	100000	0	100000	0	0
...	...	...	...	...	...	...
49	50	100000	0	100000	0	0

Predator-prey

Results for predator-prey interaction networks are shown below

X	N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised
1	2	0	100000	0	100000	0
2	3	0	100000	0	100000	0
3	4	0	100000	0	100000	0
4	5	1	99999	1	99999	0
5	6	4	99996	4	99996	0
6	7	2	99998	2	99998	0
7	8	5	99995	5	99995	0
8	9	20	99980	21	99979	0
9	10	20	99980	22	99978	0
10	11	38	99962	39	99961	0
11	12	64	99936	66	99934	0
12	13	87	99913	91	99909	0
13	14	157	99843	159	99841	0
14	15	215	99785	227	99773	0
15	16	293	99707	310	99690	0
16	17	383	99617	408	99592	0
17	18	443	99557	473	99527	3
18	19	642	99358	675	99325	4
19	20	836	99164	887	99113	7
20	21	1006	98994	1058	98942	10
21	22	1153	98847	1228	98772	20
22	23	1501	98499	1593	98407	30
23	24	1841	98159	1996	98004	40
24	25	2146	97854	2316	97684	58
25	26	2643	97357	2809	97191	119
26	27	3034	96966	3258	96742	158
27	28	3690	96310	3928	96072	201
28	29	4257	95743	4532	95468	290
29	30	4964	95036	5221	94779	424
30	31	5627	94373	5978	94022	452
31	32	6543	93457	6891	93109	666
32	33	7425	92575	7777	92223	818
33	34	8540	91460	8841	91159	1071
34	35	9526	90474	9842	90158	1337
35	36	10617	89383	10891	89109	1624
36	37	12344	87656	12508	87492	2021
37	38	13675	86325	13877	86123	2442
38	39	15264	84736	15349	84651	2870
39	40	17026	82974	17053	82947	3363
40	41	18768	81232	18614	81386	3905
41	42	20791	79209	20470	79530	4579
42	43	23150	76850	22754	77246	5217
43	44	25449	74551	24184	75816	6285
44	45	27702	72298	26464	73536	6754
45	46	30525	69475	28966	71034	7646
46	47	32832	67168	31125	68875	8487
47	48	36152	63848	33865	66135	9479
48	49	38714	61286	36242	63758	10125
49	50	41628	58372	38508	61492	11036
50	51	44483	55517	41023	58977	11704
51	52	48134	51866	44287	55713	12573
52	53	51138	48862	46721	53279	13223

X	N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised
53	54	54261	45739	49559	50441	13757
54	55	57647	42353	52403	47597	14324
55	56	60630	39370	55293	44707	14669
56	57	63647	36353	57787	42213	15103
57	58	66961	33039	60439	39561	15450
58	59	69968	30032	63708	36292	15246
59	60	72838	27162	66270	33730	15177
60	61	75609	24391	68873	31127	15006
61	62	77999	22001	71318	28682	14538
62	63	80616	19384	73517	26483	14510
63	64	83089	16911	76209	23791	13784
64	65	85150	14850	78086	21914	13412
65	66	86908	13092	80437	19563	12477
66	67	88671	11329	82379	17621	11718
67	68	90537	9463	84483	15517	10878
68	69	91969	8031	86233	13767	10033
69	70	93181	6819	87914	12086	9070
70	71	94330	5670	89200	10800	8401
71	72	95324	4676	90833	9167	7359
72	73	96143	3857	91805	8195	6726
73	74	96959	3041	93065	6935	5900
74	75	97543	2457	93987	6013	5222
75	76	97969	2031	94900	5100	4481
76	77	98497	1503	95756	4244	3809
77	78	98744	1256	96442	3558	3269
78	79	99045	955	96942	3058	2837
79	80	99276	724	97528	2472	2329
80	81	99481	519	97996	2004	1894
81	82	99556	444	98321	1679	1597
82	83	99691	309	98722	1278	1227
83	84	99752	248	98943	1057	1015
84	85	99833	167	99144	856	837
85	86	99895	105	99346	654	642
86	87	99925	75	99461	539	530
87	88	99945	55	99566	434	428
88	89	99976	24	99675	325	324
89	90	99977	23	99756	244	243
90	91	99982	18	99839	161	155
91	92	99988	12	99865	135	135
92	93	99994	6	99885	115	115
93	94	99993	7	99911	89	88
94	95	99998	2	99953	47	47
95	96	99999	1	99965	35	35
96	97	99999	1	99979	21	21
97	98	100000	0	99973	27	27
98	99	100000	0	99984	16	16
99	100	100000	0	99989	11	11

Overall, as expected[2], predator-prey communities are relatively stable while mutualist communties are highly unstable. But interestingly, while $Var(\gamma)$ stabilises predator-prey and competitor communities, it does not stabilise mutualist communities. This is unsurprising because purely mutualist communities are characterised by a very positive[2] leading $\Re(\lambda)$, and it is highly unlikely that $Var(\gamma)$ alone will shift all real parts of eigenvalues to negative values.

Different connectance (C) values

In the main text, for simplicity, I assumed connectance values of $C = 1$, meaning that all off-diagonal elements of a matrix M were potentially nonzero and sampled from a normal distribution $\mathcal{N}(0, \sigma^2)$ where $\sigma = 0.4$. Here I present four tables showing the number of stable communities given $C = \{0.3, 0.5, 0.7, 0.9\}$. In all cases, uniform variation in component response time ($\gamma \sim \mathcal{U}(0, 2)$) led to a higher number of stable communities than when γ did not vary ($\gamma = 1$). In contrast to the main text, 100000 rather than 1 million M were simulated. As with the results on stability with increasing S shown above, in the tables below `A0` refers to matrices when $\gamma = 1$, and `A1` refers to matrices after $Var(\gamma)$ is added. The column `A0_unstable` shows the number of `A0` matrices that are unstable, and the column `A0_stable` shows the number of `A0` matrices that are stable (these two columns sum to 100000). Similarly, the column `A1_unstable` shows the number of `A1` matrices that are unstable and `A1_stable` shows the number that are stable. The columns `A1_stabilised` and `A1_destabilised` show how many `A0` matrices were stabilised or destabilised, respectively, by $Var(\gamma)$.

All data reported below for various values of C are accessible using the below.

```
C3dat <- read.csv(file = "sim_results/C_other/rand_c-0pt3.csv");
C5dat <- read.csv(file = "sim_results/C_other/rand_c-0pt5.csv");
C7dat <- read.csv(file = "sim_results/C_other/rand_c-0pt7.csv");
C9dat <- read.csv(file = "sim_results/C_other/rand_c-0pt9.csv");
```

This includes the objects `C3dat`, `C5dat`, `C7dat`, and `C9dat`, which includes the results for $C = 0.3$, $C = 0.5$, $C = 0.7$, and $C = 0.9$, respectively.

Connectance $C = 0.3$

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
2	5	99995	5	99995	0	0
3	6	99994	6	99994	0	0
4	24	99976	24	99976	0	0
5	59	99941	59	99941	0	0
6	98	99902	98	99902	0	0
7	160	99840	161	99839	0	1
8	290	99710	293	99707	0	3
9	430	99570	434	99566	0	4
10	648	99352	653	99347	1	6
11	946	99054	957	99043	0	11
12	1392	98608	1415	98585	4	27
13	2032	97968	2065	97935	5	38
14	2627	97373	2688	97312	10	71
15	3588	96412	3647	96353	35	94
16	5019	94981	5124	94876	51	156
17	6512	93488	6673	93327	79	240
18	8444	91556	8600	91400	165	321
19	10416	89584	10667	89333	244	495
20	13254	86746	13477	86523	425	648
21	16248	83752	16481	83519	642	875
22	19497	80503	19719	80281	929	1151
23	23654	76346	23776	76224	1368	1490
24	28485	71515	28389	71611	1914	1818
25	32774	67226	32483	67517	2428	2137
26	38126	61874	37411	62589	3221	2506

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
27	43435	56565	42418	57582	3828	2811
28	49333	50667	47840	52160	4565	3072
29	55389	44611	53381	46619	5329	3321
30	60826	39174	58388	41612	5918	3480
31	66820	33180	64043	35957	6345	3568
32	72190	27810	69036	30964	6685	3531
33	77053	22947	73587	26413	6826	3360
34	81816	18184	78157	21843	6673	3014
35	85651	14349	82041	17959	6383	2773
36	88985	11015	85657	14343	5721	2393
37	92072	7928	88805	11195	5180	1913
38	94329	5671	91444	8556	4451	1566
39	95912	4088	93295	6705	3804	1187
40	97232	2768	95201	4799	2967	936
41	98179	1821	96506	3494	2356	683
42	98826	1174	97489	2511	1786	449
43	99275	725	98312	1688	1251	288
44	99583	417	98872	1128	903	192
45	99776	224	99339	661	576	139
46	99865	135	99518	482	413	66
47	99938	62	99744	256	226	32
48	99956	44	99824	176	151	19
49	99980	20	99914	86	85	19
50	99993	7	99950	50	46	3
51	99998	2	99971	29	28	1
52	99998	2	99986	14	14	2
53	99999	1	99992	8	7	0
54	100000	0	99997	3	3	0
55	100000	0	99999	1	1	0
56	100000	0	99998	2	2	0
57	100000	0	99999	1	1	0
58	100000	0	100000	0	0	0
...	...	...	...	...	...	...
100	100000	0	100000	0	0	0

Connectance $C = 0.5$

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
2	7	99993	7	99993	0	0
3	32	99968	32	99968	0	0
4	122	99878	122	99878	0	0
5	320	99680	321	99679	0	1
6	667	99333	673	99327	0	6
7	1233	98767	1252	98748	0	19
8	2123	97877	2156	97844	3	36
9	3415	96585	3471	96529	16	72
10	5349	94651	5450	94550	30	131
11	7990	92010	8185	91815	81	276
12	11073	88927	11301	88699	219	447
13	14971	85029	15204	84796	445	678
14	19754	80246	19992	80008	764	1002

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
15	25020	74980	25239	74761	1185	1404
16	30860	69140	30938	69062	1902	1980
17	37844	62156	37562	62438	2758	2476
18	44909	55091	44251	55749	3595	2937
19	52322	47678	51011	48989	4573	3262
20	60150	39850	58295	41705	5382	3527
21	67147	32853	64895	35105	5925	3673
22	74177	25823	71358	28642	6310	3491
23	80297	19703	77034	22966	6507	3244
24	85372	14628	82039	17961	6209	2876
25	89719	10281	86539	13461	5562	2382
26	92947	7053	90141	9859	4707	1901
27	95436	4564	92950	7050	3844	1358
28	97196	2804	95171	4829	2999	974
29	98300	1700	96842	3158	2115	657
30	99103	897	98033	1967	1466	396
31	99502	498	98665	1335	1068	231
32	99745	255	99185	815	696	136
33	99881	119	99572	428	375	66
34	99955	45	99788	212	191	24
35	99979	21	99900	100	95	16
36	99995	5	99950	50	50	5
37	99997	3	99970	30	28	1
38	99998	2	99986	14	13	1
39	99999	1	99991	9	9	1
40	100000	0	100000	0	0	0
41	100000	0	99999	1	1	0
42	100000	0	99999	1	1	0
43	100000	0	100000	0	0	0
...	...	...	...	...	...	...
50	100000	0	100000	0	0	0

124 **Connectance $C = 0.7$**

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
2	7	99993	7	99993	0	0
3	106	99894	106	99894	0	0
4	395	99605	397	99603	0	2
5	1117	98883	1123	98877	0	6
6	2346	97654	2367	97633	6	27
7	4314	95686	4388	95612	16	90
8	7327	92673	7456	92544	61	190
9	11514	88486	11792	88208	150	428
10	16247	83753	16584	83416	415	752
11	22481	77519	22759	77241	884	1162
12	29459	70541	29729	70271	1548	1818
13	37631	62369	37567	62433	2419	2355
14	46317	53683	45696	54304	3548	2927
15	54945	45055	53695	46305	4671	3421
16	63683	36317	61643	38357	5567	3527
17	72004	27996	69375	30625	6124	3495

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
18	79220	20780	76158	23842	6413	3351
19	85286	14714	82283	17717	5982	2979
20	90240	9760	87181	12819	5398	2339
21	93676	6324	91077	8923	4468	1869
22	96203	3797	94045	5955	3425	1267
23	97866	2134	96161	3839	2496	791
24	98842	1158	97633	2367	1713	504
25	99433	567	98630	1370	1079	276
26	99760	240	99259	741	655	154
27	99895	105	99576	424	377	58
28	99950	50	99790	210	194	34
29	99981	19	99915	85	80	14
30	99994	6	99952	48	47	5
31	99998	2	99972	28	28	2
32	99999	1	99992	8	8	1
33	100000	0	99997	3	3	0
34	100000	0	99999	1	1	0
35	100000	0	100000	0	0	0
...	...	...	...	...	...	...
50	100000	0	100000	0	0	0

Connectance $C = 0.9$

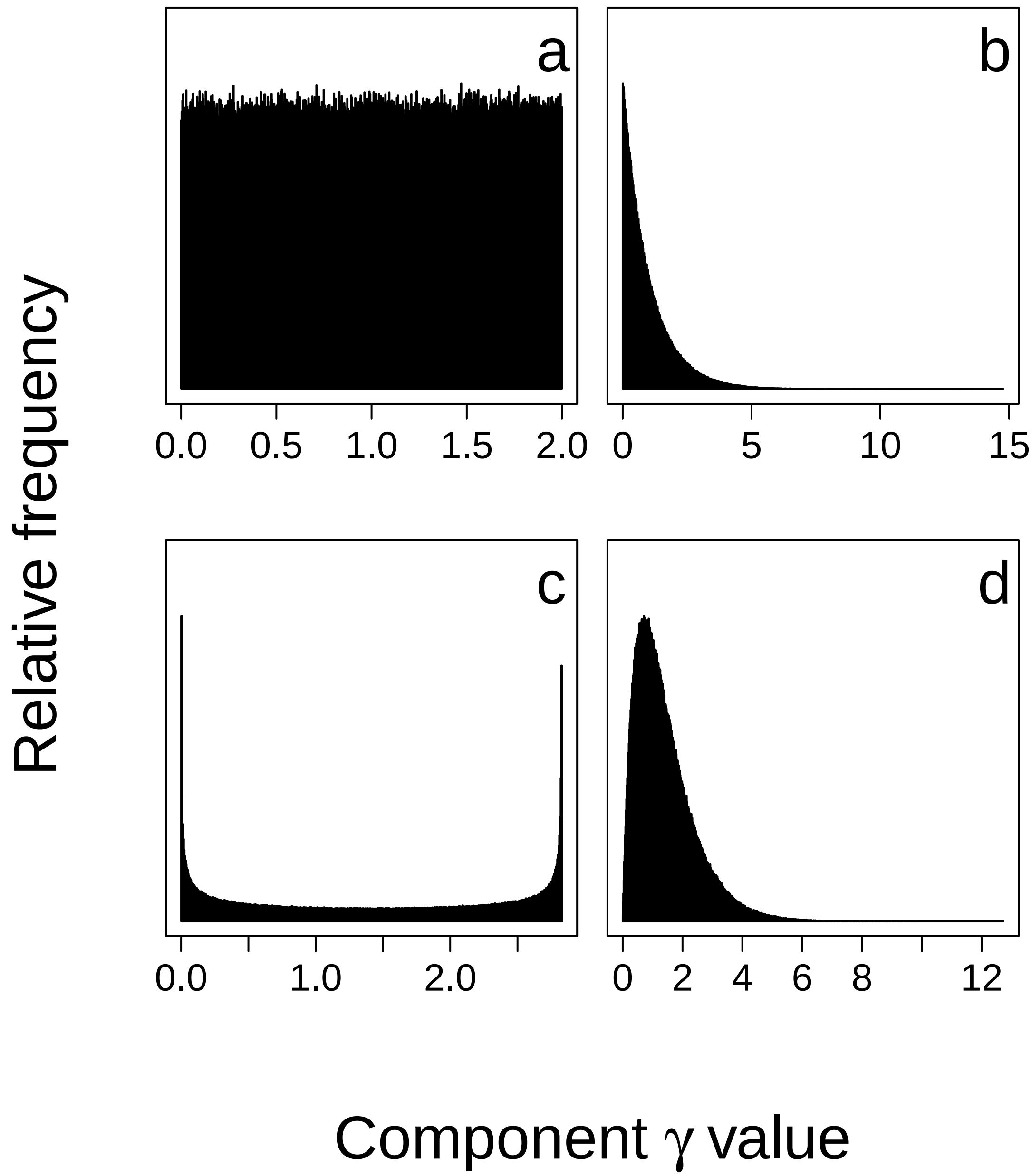
N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
2	14	99986	14	99986	0	0
3	240	99760	240	99760	0	0
4	1008	98992	1016	98984	0	8
5	2708	97292	2729	97271	2	23
6	5669	94331	5755	94245	13	99
7	9848	90152	10057	89943	91	300
8	15903	84097	16201	83799	336	634
9	22707	77293	23110	76890	765	1168
10	30796	69204	31122	68878	1526	1852
11	40224	59776	40082	59918	2649	2507
12	49934	50066	49288	50712	3773	3127
13	60138	39862	58803	41197	4984	3649
14	69100	30900	67110	32890	5755	3765
15	77607	22393	74884	25116	6273	3550
16	84663	15337	81780	18220	5975	3092
17	90075	9925	87290	12710	5209	2424
18	93944	6056	91419	8581	4271	1746
19	96650	3350	94530	5470	3287	1167
20	98160	1840	96698	3302	2191	729
21	99111	889	98133	1867	1389	411
22	99588	412	98905	1095	903	220
23	99837	163	99480	520	452	95
24	99932	68	99744	256	228	40
25	99976	24	99863	137	133	20
26	99995	5	99950	50	49	4
27	99996	4	99986	14	13	3
28	100000	0	99993	7	7	0

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
29	100000	0	99996	4	4	0
30	100000	0	99998	2	2	0
31	100000	0	100000	0	0	0
…	…	…	…	…	…	…
50	100000	0	100000	0	0	0

Different distributions of γ

In the main text, I considered a uniform distribution of component response rates $\gamma \sim \mathcal{U}(0, 2)$. The number of unstable and stable M matrices are reported in a table above across different values of S. Here I show complementary results for three different distributions including an exponential, beta, and gamma distribution of γ values. The shape of these distributions is shown in the figure below.

Distributions of component response rate (γ) values in complex systems. The stabilities of simulated complex systems with these γ distributions are compared to otherwise identical complex systems with a fixed component response rate of $\gamma = 1$ across different system sizes (S; i.e., component numbers) given a unit γ standard deviation ($\sigma_\gamma = 1$) for b-d. Distributions are as follows: (a) uniform, (b) exponential, (c) beta ($\alpha = 0.5$ and $\beta = 0.5$), and (d) gamma ($k = 2$ and $\theta = 2$). Each panel shows 1 million randomly generated γ values.



The same 100000 M matrices were used to investigate stability when applying each of these different distributions of γ values. The table below shows the number of M that were unstable (_unst) and stable (_stbl) for the exponential (Exp), beta, and gamma distributions.

```
fourdists <- read.csv(file = "sim_results/different_distr/four_distr_rand.csv");
kable(fourdists);
```

S	Exp_unst	Exp_stbl	beta_unst	beta_stbl	gamma_unst	gamma_stbl
2	30	99970	30	99970	30	99970
3	355	99645	355	99645	355	99645
4	1506	98494	1512	98488	1516	98484
5	3930	96070	3971	96029	4006	95994
6	7738	92262	7844	92156	7918	92082

S	Exp_unst	Exp_stbl	beta_unst	beta_stbl	gamma_unst	gamma_stbl
7	13606	86394	13889	86111	13990	86010
8	20535	79465	21002	78998	21114	78886
9	28614	71386	29060	70940	29110	70890
10	38375	61625	38388	61612	38441	61559
11	48616	51384	48211	51789	47957	52043
12	59254	40746	58025	41975	57473	42527
13	68816	31184	66753	33247	66127	33873
14	77721	22279	75149	24851	74222	25778
15	84842	15158	82030	17970	81040	18960
16	90365	9635	87809	12191	86600	13400
17	94171	5829	91756	8244	90668	9332
18	96978	3022	94977	5023	94176	5824
19	98376	1624	97018	2982	96268	3732
20	99218	782	98357	1643	97765	2235
21	99678	322	99124	876	98746	1254
22	99864	136	99599	401	99323	677
23	99954	46	99783	217	99668	332
24	99978	22	99920	80	99821	179
25	99996	4	99967	33	99911	89
26	99999	1	99979	21	99960	40
27	99999	1	99990	10	99983	17
28	100000	0	99999	1	99991	9
29	100000	0	99999	1	99999	1
30	100000	0	100000	0	100000	0
31	100000	0	100000	0	99999	1
32	100000	0	100000	0	100000	0
...	...	...	...	...	...	...
50	100000	0	100000	0	100000	0

In comparison to the uniform distribution (a), proportionally fewer random systems are found with the exponential distribution (b), while more are found with the beta (c) and gamma (d) distributions.

Genetic algorithm

Ideally, to investigate the potential of $Var(\gamma)$ for increasing the proportion of stable complex systems, the search space of all possible γ vectors would be evaluate for each unique M. This is technically impossible because any γ_i can take any real value between $0 - 2$, but even rounding γ to reasonable values would result in a search space too large to practically explore. Under these conditions, genetic algorithms are highly useful tools for finding practical solutions by mimicking the process of biological evolution[6]. In this case, the practical solution is finding vectors of γ that decrease the most positive real eigenvalue of M. The genetic algorithm below achieves this by initialising a large population of 1000 different potential γ vectors and allowing this population to evolve through a process of mutation, crossover (swaping γ_i values between vectors), selection, and reproduction until either a γ vector is found where all $\Re(\lambda) < 0$ or some "giving up" critiera is met (in the below 20 generations pass or the fitness increase from one generation to the next is below a certain criteria). The genetic algorithm relies on five functions. The first outer function `Evo_rand_gen_var` runs all of the simulations (`from` and `to` refer to S values, and `iters` refers to the number of M to try for each S).

```
Evo_rand_gen_var <- function(from, to, iters, int_type = 0, rmx = 0.4, C = 1){
    tot_res <- NULL;
```

```
    fea_res <- NULL;
    if(from >= to){
        stop("Argument 'from' must be less than argument 'to'");
    }
    for(i in from:to){
        nn              <- i;
        A1_stt          <- 0;
        A2_stt          <- 0;
        A1_fet          <- 0;
        A2_fet          <- 0;
        iter            <- iters;
        tot_res[[i-1]] <- matrix(data = 0, nrow = iter, ncol = 3);
        fea_res[[i-1]] <- matrix(data = 0, nrow = iter, ncol = 2);
        while(iter > 0){
            r_vec    <- rnorm(n = i, mean = 0, sd = rmx);
            A0_dat   <- rnorm(n = i * i, mean = 0, sd = 0.4);
            A0       <- matrix(data = A0_dat, nrow = i, ncol = i);
            A0       <- species_interactions(mat = A0, type = int_type);
            C_dat    <- rbinom(n = i * i, size = 1, prob = C);
            C_mat    <- matrix(data = C_dat, nrow = i, ncol = i);
            A0       <- A0 * C_mat;
            diag(A0) <- -1;
            gam1     <- runif(n = i, min = 0, max = 2);
            A1       <- A0 * gam1;
            A0_stb   <- max(Re(eigen(A0)$values)) < 0;
            A1_stb   <- rand_mat_ga(A1);
            A0_fea   <- min(-1*solve(A0) %*% r_vec) > 0;
            A1_fea   <- min(-1*solve(A1) %*% r_vec) > 0;
            if(A0_stb == TRUE){
                tot_res[[i-1]][iter, 1] <- 1;
            }
            if(A1_stb == TRUE){
                tot_res[[i-1]][iter, 2] <- 1;
            }
            if(A0_fea == TRUE){
                fea_res[[i-1]][iter, 1] <- 1;
            }
            if(A1_fea == TRUE){
                fea_res[[i-1]][iter, 2] <- 1;
            }
            iter    <- iter - 1;
        }
        print(i);
    }
    all_res <- summarise_randmat(tot_res = tot_res, fea_res = fea_res);
    return(all_res);
}
```

Note that `Evo_rand_gen_var` calls three custom sub-functions, `species_interactions`, `rand_mat_ga`, and `summarise_randmat`. The first simply allows for non-random interactions between components (e.g., modelling ecological interactions of random, competition, mutualism, or predator-prey).

```
species_interactions <- function(mat, type = 0){
    if(type == 1){
```

```
        mat[mat > 0] <- -1*mat[mat > 0];
    }
    if(type == 2){
        mat[mat < 0] <- -1*mat[mat < 0];
    }
    if(type == 3){
        for(i in 1:dim(mat)[1]){
            for(j in 1:dim(mat)[2]){
                if(mat[i, j] * mat[j, i] > 0){
                    mat[j, i] <- -1 * mat[j, i];
                }
            }
        }
    }
    return(mat);
}
```

The sub-function **rand_mat_ga** does the work of the genetic algorithm, searching for γ vectors that are stabilising.

```
rand_mat_ga <- function(A1, max_it = 20, converg = 0.01){
    nn        <- dim(A1)[1];
    rind      <- runif(n = nn*1000, min = 0, max = 1);
    inds      <- matrix(data = rind, nrow = 1000, ncol = nn);
    lastf     <- -10;
    ccrit     <- 10;
    find_st   <- 0;
    iter      <- max_it;
    while(iter > 0 & find_st < 1 & ccrit > converg){
        ivar  <- rep(x = 0, length = dim(inds)[1]);
        ifit  <- rep(x = 0, length = dim(inds)[1]);
        isst  <- rep(x = 0, length = dim(inds)[1]);
        for(i in 1:dim(inds)[1]){
            ifit[i] <- -1*max(Re(eigen(inds[i,]*A1)$values));
            ivar[i] <- var(inds[i,]);
            isst[i] <- max(Re(eigen(inds[i,]*A1)$values)) < 0;
        }
        most_fit <- order(ifit, decreasing = TRUE)[1:20];
        parents  <- inds[most_fit,];
        new_gen  <- matrix(data = t(parents), nrow = 1000, ncol = nn,
                           byrow = TRUE);
        mu_dat   <- rbinom(n = nn*1000, size = 1, prob = 0.2);
        mu_dat2  <- rnorm(n = nn*1000, mean = 0, sd = 0.02);
        mu_dat2[mu_dat2 < 0] <- -mu_dat2[mu_dat2 < 0];
        mu_dat2[mu_dat2 > 2] <- 2;
        mu_dat3  <- mu_dat * mu_dat2;
        mu_mat   <- matrix(data = mu_dat3, nrow = 1000, ncol = nn);
        new_gen  <- new_gen + mu_mat;
        new_gen  <- crossover(inds = new_gen, pr = 0.1);
        inds     <- new_gen;
        find_st  <- max(isst);
        newf     <- mean(ifit);
        ccrit    <- newf - lastf;
        lastf    <- newf;
```

```
        iter     <- iter - 1;
    }
    if(find_st == 1){
        s_row <- which(isst == 1)[1];
        writt <- c(nn, inds[s_row,]);
        cat(writt, file = "evo_out.txt", append = TRUE);
        cat("\n", file = "evo_out.txt", append = TRUE);
    }
    return(find_st);
}
```

The while loop continues until either `iter` generations have occured, a solution γ vector is found that results in all $\Re(\lambda) < 0$, or some criteria of minimum fitness increase is observed. Within the genetic algorithm, γ values are mutated, crossover occurs between γ vectors, and there is selection occurs in each generation such that the 20 γ vectors that produce the lowest maximum $\Re(\lambda)$ are allowed to have 50 offspring each. In mutation, any values that mutate below zero are multiplied by -1, and any values that mutate above 2 are set to 2. Note also that if a solution is found, then one such γ vector causing stability is printed to a file.

Crossover occurs in the `crossover` function below.

```
crossover <- function(inds, pr = 0.1){
    crossed <- floor(dim(inds)[1] * pr);
    cross1  <- sample(x = 1:dim(inds)[1], size = crossed);
    cross2  <- sample(x = 1:dim(inds)[1], size = crossed);
    for(i in 1:length(cross1)){
        fromv   <- sample(x = 1:dim(inds)[2], size = 1);
        tov     <- sample(x = 1:dim(inds)[2], size = 1);
        temp                   <- inds[cross1[i],fromv:tov];
        inds[cross1[i],fromv:tov] <- inds[cross2[i],fromv:tov];
        inds[cross2[i],fromv:tov] <- temp;
    }
    return(inds);
}
```

After all M are simulated in `Evo_rand_gen_var`, the `summarise_randmat` formats the data into a table.

```
summarise_randmat_ga <- function(tot_res, fea_res){
    sims    <- length(tot_res);
    all_res <- matrix(data = 0, nrow = sims, ncol = 10);
    for(i in 1:sims){
        unstables <- tot_res[[i]][,1] == FALSE & tot_res[[i]][,2] == FALSE;
        stables   <- tot_res[[i]][,1] == TRUE  & tot_res[[i]][,2] == TRUE;
        unstabled <- tot_res[[i]][,1] == TRUE  & tot_res[[i]][,2] == FALSE;
        stabled   <- tot_res[[i]][,1] == FALSE & tot_res[[i]][,2] == TRUE;
        non_feas  <- fea_res[[i]][,1] == FALSE & fea_res[[i]][,2] == FALSE;
        feasibl   <- fea_res[[i]][,1] == TRUE  & fea_res[[i]][,2] == TRUE;
        unfeased  <- fea_res[[i]][,1] == TRUE  & fea_res[[i]][,2] == FALSE;
        feased    <- fea_res[[i]][,1] == FALSE & fea_res[[i]][,2] == TRUE;
        foundd    <- tot_res[[i]][,3] == TRUE;
        all_res[i, 1]  <- i + 1;
        all_res[i, 2]  <- sum(unstables);
        all_res[i, 3]  <- sum(stables);
        all_res[i, 4]  <- sum(unstabled);
        all_res[i, 5]  <- sum(stabled);
        all_res[i, 6]  <- sum(non_feas);
        all_res[i, 7]  <- sum(feasibl);
```

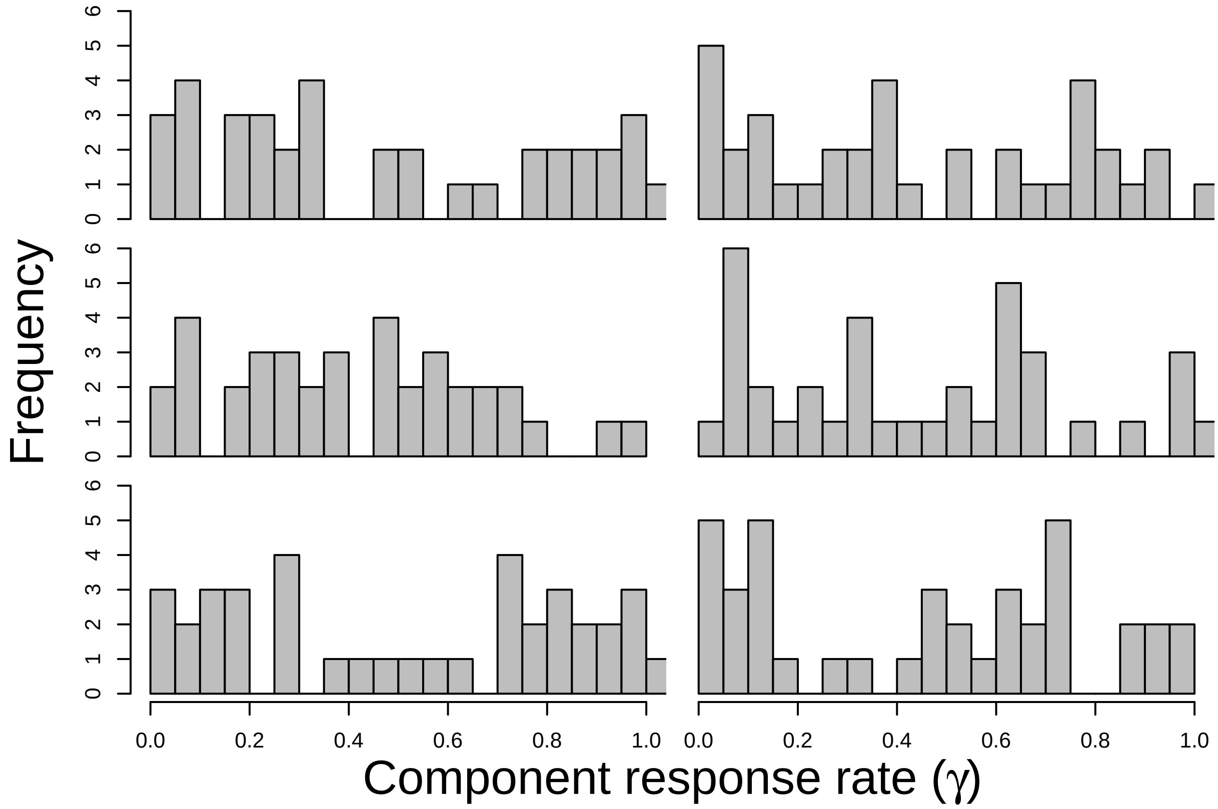
```
        all_res[i, 8]  <- sum(unfeased);
        all_res[i, 9]  <- sum(feased);
        all_res[i, 10] <- sum(foundd);
    }
    return(all_res);
}
```

Stability results from this table are shown below.

N	A0_unstable	A0_stable	A1_unstable	A1_stable	A1_stabilised	A1_destabilised
2	4	9996	4	9996	0	0
3	42	9958	42	9958	0	0
4	133	9867	133	9867	0	0
5	414	9586	411	9589	3	0
6	809	9191	799	9201	10	0
7	1380	8620	1339	8661	41	0
8	2074	7926	1927	8073	147	0
9	2885	7115	2503	7497	382	0
10	3842	6158	3158	6842	684	0
11	4867	5133	3613	6387	1255	1
12	5932	4068	4148	5852	1784	0
13	6937	3063	4470	5530	2468	1
14	7784	2216	4724	5276	3060	0
15	8519	1481	5086	4914	3433	0
16	9081	919	5262	4738	3819	0
17	9431	569	5368	4632	4063	0
18	9671	329	5571	4429	4100	0
19	9844	156	5807	4193	4037	0
20	9934	66	6133	3867	3801	0
21	6387	34	6421	3579	3545	0
22	6634	11	6645	3355	3344	0
23	7037	8	7045	2955	2947	0
24	7468	3	7471	2529	2526	0
25	7816	0	7816	2184	2184	0
26	8192	0	8192	1808	1808	0
27	8680	0	8680	1320	1320	0
28	8936	0	8936	1064	1064	0
29	9296	0	9296	704	704	0
30	9523	0	9523	477	477	0
31	9705	0	9705	295	295	0
32	9816	0	9816	184	184	0
33	9894	0	9894	106	106	0
34	9941	0	9941	59	59	0
35	9968	0	9968	32	32	0
36	9991	0	9991	9	9	0
37	9993	0	9993	7	7	0
38	9999	0	9999	1	1	0
39	9999	0	9999	1	1	0
40	10000	0	10000	0	0	0

The distribution of one of the γ vectors at $S = 39$ is shown below (all are available on GitHub). Distributions of γ values in vectors for the highest values of S are shown below.

```r
evo_out <- scan(file = "sim_results/evolved/Evo_out.txt");
plot_evo_out(evo_out);
```



The distribution of γ values found by the genetic algorithm is uniform.

Work in progress

Feasilbility of complex systems

Work in progress

It also would be useful to look at feasibility criteria established by 7, who very recently made the point that some of May and Allesina's criteria allows for negative species densities when stable. Feasibility criteria are as follows,

$$x^* = -\left(\theta I + (CS)^{-\delta} A\right)^{-1} r.$$

The above is not nearly as nasty as it looks, especially because it is entirely reasonable to simply use convenient values to parameterise it. The variable x^* is just the vector of species abundances at equilibrium (we need all of them to be positive). The matrix I is just the identity matrix (1s on the diagonal, 0s on the off-diagonal elements), and the value θ is just the strength of intraspecific competition – we can just set this to $\theta = -1$ (as others have). The variable C is just the connectance of the community, which we will also set to 1 for convenience (lower values would mean that some species don't interact with one another, corresponding to an off-diagonal matrix element of 0). And δ just affects the strength of interactions – which we can set to $\delta = 0$ for strong interactions. Hence, the whole $(CS)^{-\delta} = 1$, so we're just adding the diagonal matrix of -1s (θI) to A, which has a diagonal of all zeros and an off-diagonal effecting species interactions,

$$x^{*} = -\left(\theta I + A\right)^{-1} r.$$

To check the feasibility criteria, all that needs to be done is to invert $(\theta I + A)$ and multiply the matrix by the vector of growth rates r, which we can also just set to 1. So really, we're just multiplying $-(\theta I + A)$ by a vector of ones and checking to make sure that all the values are positive. This isn't much extra work, but it will probably go a long way toward satisfying any reviewers familiar with 7.

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