

Teyssède, A. and Robert, A. 2014. Contrasting effects of habitat reduction, conversion and alteration on neutral and non neutral biological communities. – *Oikos* doi: 10.1111/j.1600-0706.2013.00928.x

Appendix 1

Methodological details

1) Protocol used to model habitat alteration scenarios

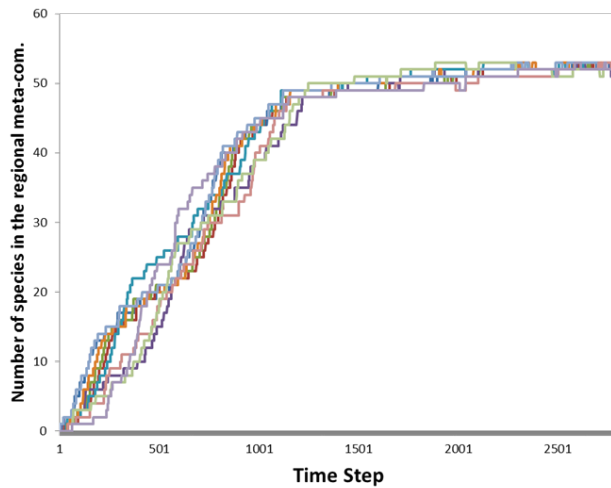
Starting from the same all-forest region, all forest patches were simultaneously cleared of their trees, and transformed into openfield patches. The magnitude of habitat transformation was noted x ($x = 0$ for intact forests and $x = 1$ for forests completely transformed into openfields) and both the carrying capacity of patches and the replacement rates of the different categories of species in these patches were linear functions of x . The replacement rates $r_{sf}(x)$, $r_{so}(x)$ and $r_g(x)$ of the three types of species in a patch with a level of transformation x were computed by affine functions of x satisfying $r_{sf}(0) = r_{sf}(f)$; $r_{sf}(1) = r_{sf}(o)$; $r_{so}(0) = r_{so}(f)$; $r_{so}(1) = r_{so}(o)$; $r_g(0) = r_g(f)$; $r_g(1) = r_g(o)$. Similarly, the carrying capacity $K(x)$ of a patch with level of transformation x was computed by an affine function of x satisfying $K(0) = K_{fmax}$ and $K(1) = K_{omax}$.

2) Protocol used to compute biodiversity metrics at pseudo-equilibrium

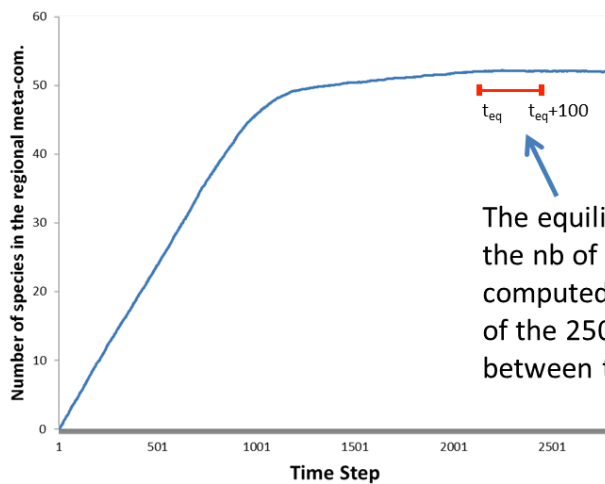
For each set of parameters (i.e. each ecological scenario of habitat configuration), the amount of time (number of time steps) necessary to reach the dynamic equilibrium for a given biodiversity indicator (e.g. the species richness S) was determined through a statistical analysis of the temporal variation of its mean. At the beginning of each scenario, we imposed the initial landscape composition, with initially empty patches, and let colonization by species occur progressively via immigration from the mainland until equilibrium was reached. To do so, in each time step t , indices (i.e. the average abundance $N(t)$, the average regional species richness $S(t)$ and the CSI) were computed as the average of 250 trajectories. In each step t , the values of indices were linearly regressed on time (between t and $t + 100$). Indices were considered to have reached equilibrium at t_{eq} when the slopes of regression were not significant at the 1% level. The amount of time necessary to reach equilibrium was variable across scenarios (typically, 500–5000 time steps depending on parameters). Indices were then computed as the average of the 250 iterations

between t_{eq} and $t_{eq} + 100$. Because the time necessary to reach equilibrium may vary between indices, the value of t_{eq} used to compute equilibrium values of all indices was the longest obtained for abundance, richness and CSI. This protocol is illustrated below for species richness S in the case of the neutral model with maximum amount of habitat reduction (i.e. 'neutral model', open circle on the left of Fig. 2a).

250 trajectories are run (only 10 presented here for clarity)



The 250 trajectories are averaged. Pseudo-equilibrium is assessed through linear regression (t_{eq} is determined)



The equilibrium value of the nb of species (S) is computed as the average of the 250 trajectories between t_{eq} and $t_{eq} + 100$

Figure A1. Relationships between the extent of forest alteration (x parameter, habitat alteration scenario), regional meta-community species richness (S), specialization index (CSI), population growth rates (r) and carrying capacity (K). Both K and S are base 10 log-transformed. Species of the meta-community are issued from a mainland pool of 250 generalist, 125 forest specialist and 125 openfield specialist species (specialization model). In all cases, $P = 30$; $K_f = 200$; $K_o = 67$; $r_{sf(f)} = 1.1$; $r_{so(f)} = 1.01$; $r_{g(f)} = 1.09$; $r_{sf(o)} = 1.01$; $r_{so(o)} = 1.1$; $r_{g(o)} = 1.09$; $c_m = 10^{-4}$; $c_a = 10^{-5}$; $imm = 10$.

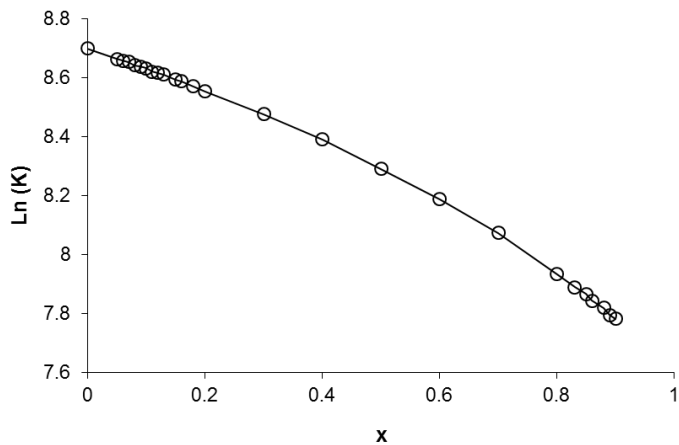
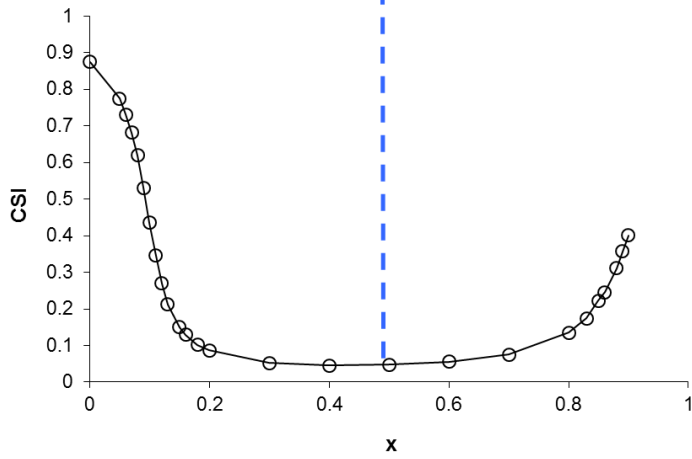
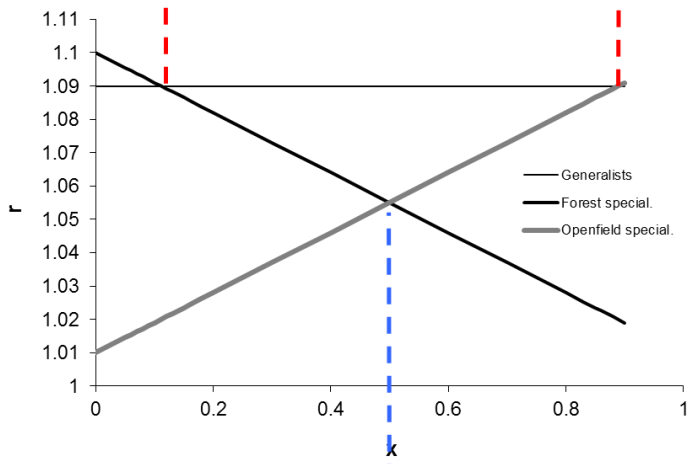
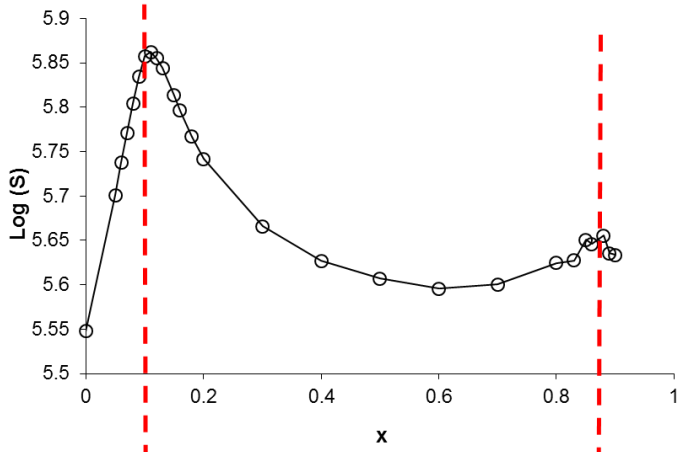


Figure A2. Sensitivity of the relationship between regional meta-community carrying capacity (K) and species richness (S) to various model parameters. Both K and S are base 10 log-transformed. K varies according to a reduction of patch number (Habitat reduction, forest patches only, the number of patches varies from 1 to 30). Species of the regional meta-community are issued from a mainland pool of 250 generalist, 125 forest specialist and 125 openfield specialist species (except for (c)). Unless otherwise noted, parameters used are $P = 30$; $K_f = 200$; $r_{sf(f)} = 1.1$; $r_{so(f)} = 1.01$; $r_{g(f)} = 1.09$; $c_m = 10^{-4}$; $c_a = 10^{-5}$; $imm = 10$.

- (a) sensitivity to the rate of colonization from the mainland c_m
- (b) sensitivity to the regional rate of colonization c_a
- (c) sensitivity to the proportion of specialist species P_s ($Q = 500$ in all cases, and forest and openfield specialists are evenly distributed among immigrants)

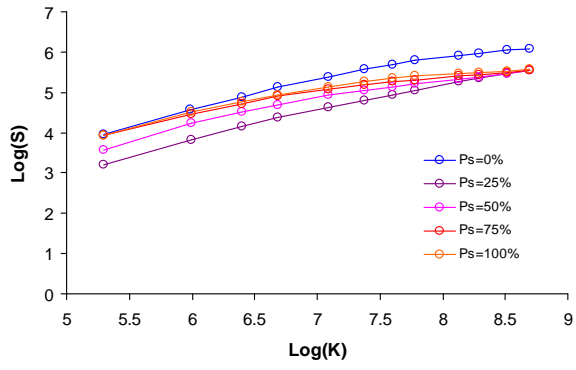
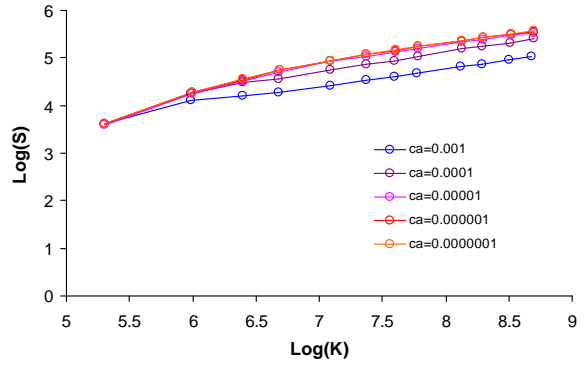
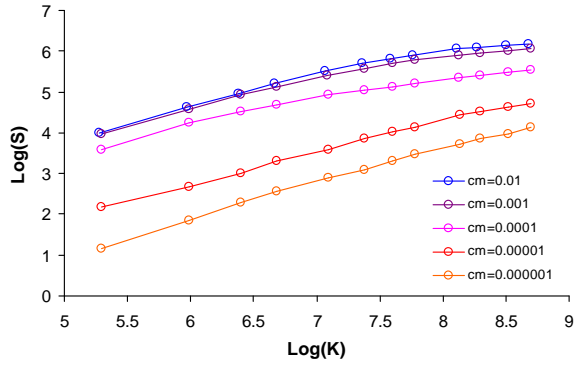


Figure A3. Sensitivity of the relationship between regional meta-community carrying capacity (K) and species richness (S) to various model parameters. Both K and S are base 10 log-transformed. K varies according to a random conversion of forest patches to openfield patches (Patch Conversion, 30 patches of forest or openfield, the proportion of forest varies from 0 to 100%). Species of the meta-community are issued from a mainland pool of 250 generalist, 125 forest specialist and 125 openfield specialist species (except for (c), see below). Unless otherwise noted, parameters used are $P = 30$; $K_f = 200$; $K_o = 67$; $r_{sf(f)} = 1.1$; $r_{so(f)} = 1.01$; $r_{g(f)} = 1.09$; $r_{sf(o)} = 1.01$; $r_{so(o)} = 1.1$; $r_{g(o)} = 1.09$; $c_m = 10^{-4}$; $c_a = 10^{-5}$; $imm = 10$.

- (a) sensitivity to the rate of colonization from the mainland c_m
- (b) sensitivity to the regional rate of colonization c_a
- (c) sensitivity to the proportion of specialist species P_s ($Q = 500$ in all cases, and forest and openfield specialists are evenly distributed among immigrants)
- (d) sensitivity to extent of reduction of carrying capacity in openfields. $K_f = 200$ in all cases; K_o varies from 40 to 200.

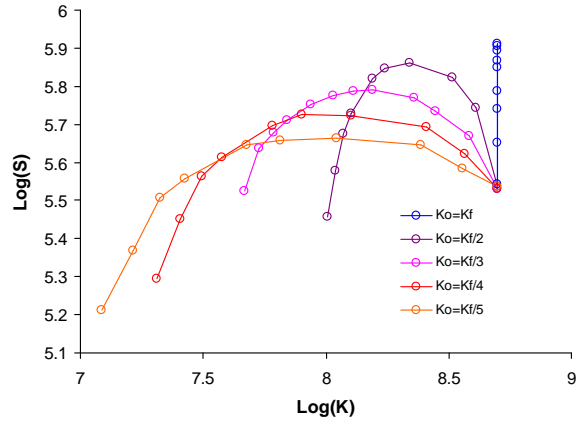
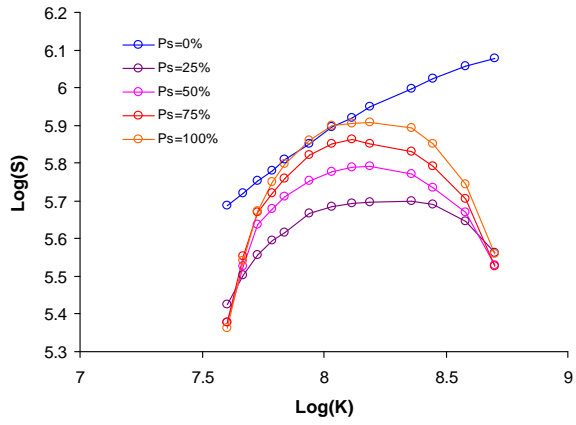
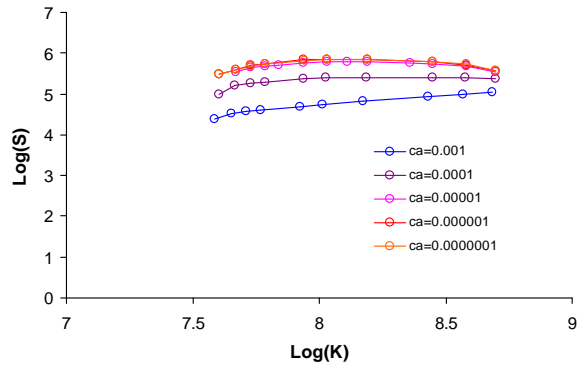
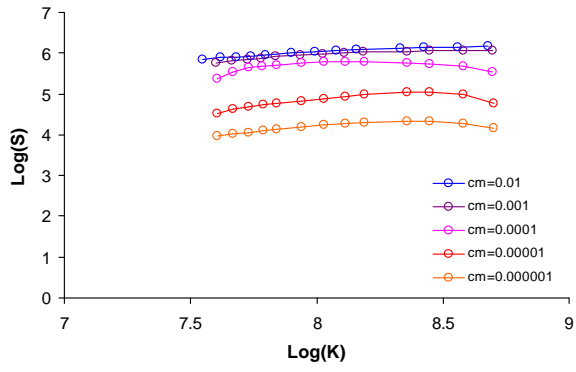
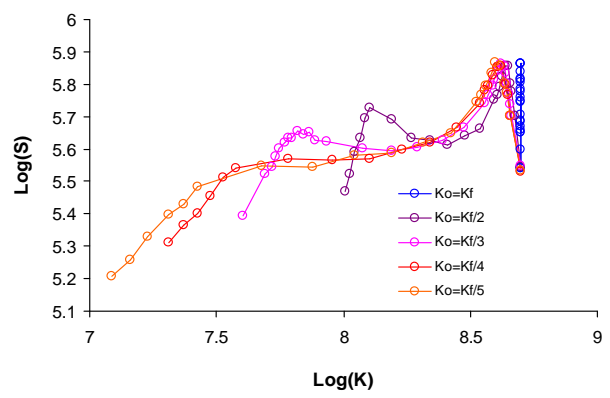
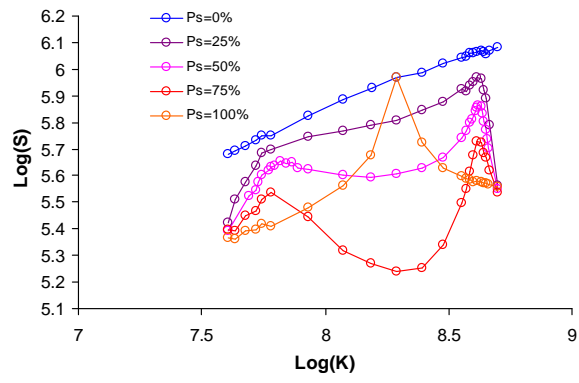
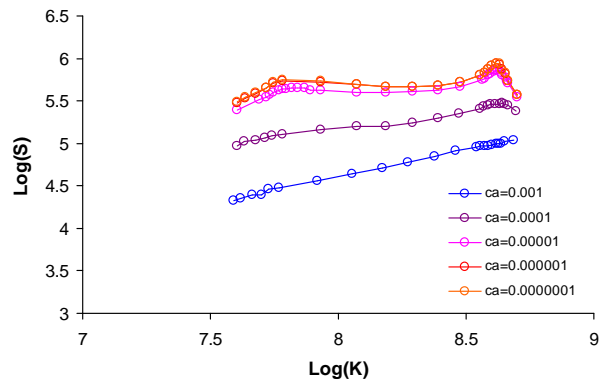
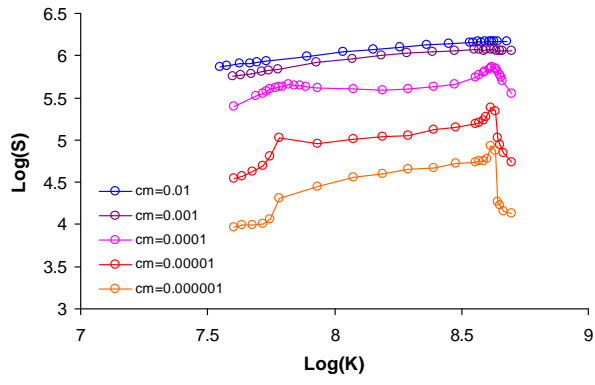


Figure A4. Sensitivity of the relationship between regional meta-community carrying capacity (K) and species richness (S) to various model parameters. Both K and S are base 10 log-transformed. K varies according to a simultaneous alteration of all forest patches to openfields (habitat alteration, 30 patches, the level of alteration varies from 0 to 1). Species of the meta-community are issued from a mainland pool of 250 generalist, 125 forest specialist and 125 openfield specialist species (except for (c)). Unless otherwise noted, parameters used are $P = 30$; $K_f = 200$; $K_o = 67$; $r_{sf(f)} = 1.1$; $r_{so(f)} = 1.01$; $r_{g(f)} = 1.09$; $r_{sf(o)} = 1.01$; $r_{so(o)} = 1.1$; $r_{g(o)} = 1.09$; $c_m = 10^{-4}$; $c_a = 10^{-5}$; $imm = 10$.

- (a) sensitivity to the rate of colonization from the mainland c_m
- (b) sensitivity to the regional rate of colonization c_a
- (c) sensitivity to the proportion of specialist species P_s ($Q = 500$ in all cases, and forest and openfield specialists are evenly distributed among immigrants)
- (d) sensitivity to extent of reduction of carrying capacity in openfields. $K_f = 200$ in all cases; K_o varies from 40 to 200.



Appendix 2

Supplementary results and alternative assumptions

1) Variation in the species abundance distribution of the mainland inflow of species

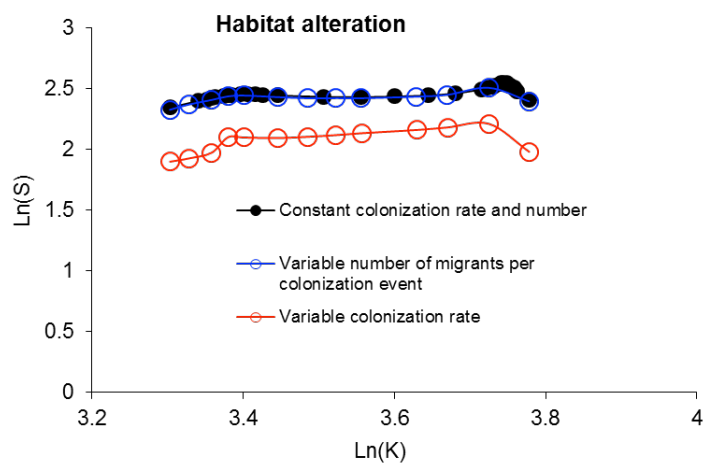
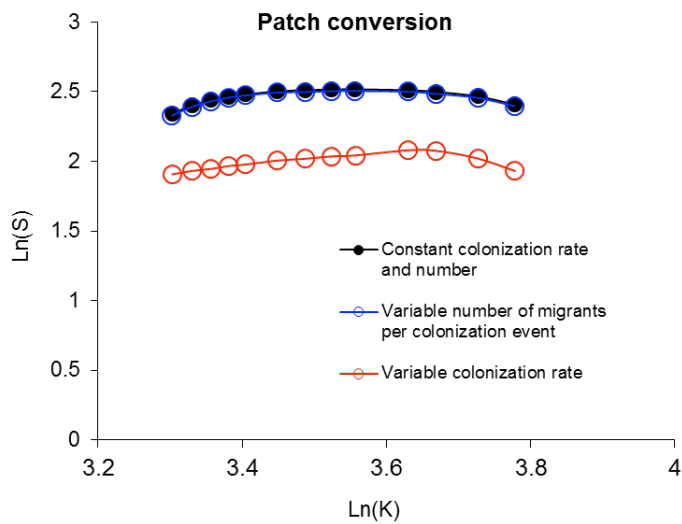
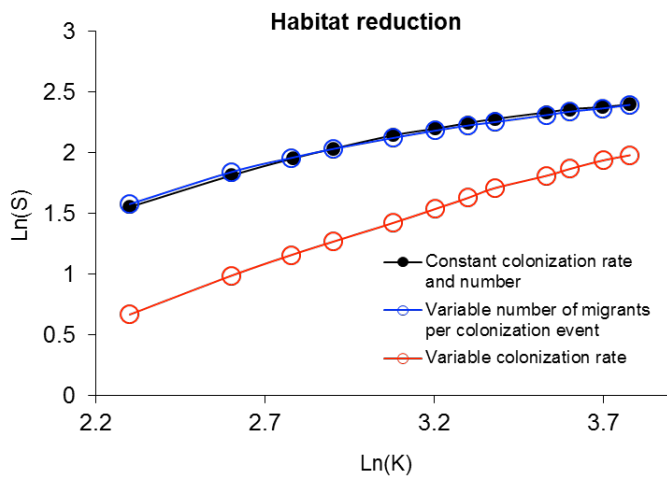
In the main simulations, we assumed that the flow of individuals from the mainland pool was formed of equiprobable species, or more explicitly that 1) the rate c_m of colonization by individuals coming from the mainland was identical for all species; 2) in case of colonization event, the number of immigrants imm was constant and identical for all species.

Here we relax these assumptions and assumed some variation in abundance among species in this flow. This variation was modeled using either a log-normal distribution of species colonization rate or a log-normal distribution of the number of immigrants during colonization events (Dornelas 2010).

Figure A1 below illustrates the effects of habitat reduction, patch conversion and habitat alteration on the relationships between regional meta-community carrying capacity (hence abundance) and richness. The black circles correspond to the scenarios investigated in the main simulations of this work, while red and blue circles correspond to the alternative scenarios assuming variation in the colonization rate from the mainland or in the number of immigrants per colonization event, respectively.

Figure A5. Relationships between regional meta-community carrying capacity (K , x-axes) and richness (S , left panel) at equilibrium. Both K and S are base 10 log-transformed. [Since habitat patches were saturated at equilibrium, these log–log K – S relationships are equivalent to log–log SIRs at equilibrium.] Within each panel, K varies according to either a reduction of patch number (habitat reduction, a), a random conversion of forest patches to openfield patches (patch conversion, b) or a simultaneous alteration of all forest patches to openfields (habitat alteration, c). Species of the meta-community are issued from a mainland pool of 250 generalist, 125 forest specialist and 125 open field specialist species (specialization model). In the case of variable number of migrants, the number of immigrants in each species is drawn from a log-normal distribution yielding approximately an expectation of 10 migrants ($\mu = 2.2$; $\sigma^2 = 0.22$). In the case

of variable colonization rate, the colonization rate c_m in each species is drawn from a Lognormal distribution yielding approximately an expectation of $c_m = 10^{-4}$ ($\mu = -13$; $\sigma^2 = 2.9$).



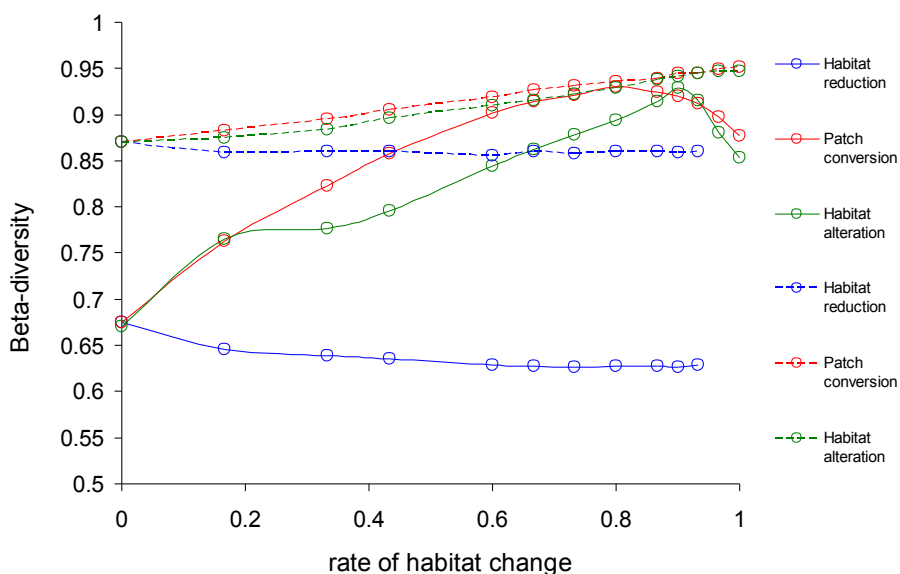
This figure shows that our qualitative results are robust to variation in both parameters. Results however indicate that, for a same simulation, variation among species in the colonization rate from

the mainland consistently leads to reduced species richness for all scenarios of habitat change. This result can be compared to Fig. 3, which shows that a higher colonization rate equal for all species leads to higher regional species richness.

2) *Effects of habitat reduction, patch conversion and habitat alteration on Beta-diversity.*

Below is a figure (Fig. A2) comparing the effects of habitat reduction, patch conversion and habitat alteration on Beta diversity, under the neutral and specialization models. Beta-diversity was computed as the one-complement of the Sørensen similarity index (Condit et al. 2002). All parameters are as in Fig. 2.

Figure A2. Relationships between the extent of habitat change and Beta-diversity at equilibrium (overall regional Beta-diversity). Within each panel, the regional meta-community abundance varies according to either a reduction of patch number (habitat reduction, blue circles), a random conversion of forest patches to open field patches (patch conversion, red circles) or a simultaneous alteration of all forest patches to open fields (habitat alteration, green circles). Species of the meta-community are issued from either a mainland pool of 500 generalist species (neutral model) or 250 generalist, 125 forest specialist and 125 open field specialist species (specialization model). The extent of habitat change relative to a 30 forest patches meta-community is expressed either as the proportion of forest patches replaced by patches of unsuitable habitat or openfield habitat (for reduction and conversion) or the magnitude x of alteration of forest patches into open fields (for habitat alteration). Dashed lines = neutral model; continuous lines = specialization model.



As illustrated in Figure A6, the Beta-diversity curves for the three habitat change scenarios differ between the two models both by their starting value in the all forest configuration and by their shape (except for the reduction scenario).

The higher starting beta-diversity shown under the neutral model reflects the higher number of species (500 equiprobable species) potentially thriving in intact forest patches, compared to the other model (mainly 125 equiprobable forest species).

Under both models, the habitat reduction scenario differs from the two other scenarios by the number of (suitable) patches considered in the computations. For both models, Beta-diversity (between forest patches) slightly decreases with the number of considered patches, until a minimum for two patches. This reflects the decrease in species richness (S) of the regional meta-community, linked to its reduction in number of individuals (K , see Fig.2).

Under the neutral model, the Beta-diversity curves for the conversion and habitat alteration scenarios are similar, approximately linear, and slightly increasing with the rate of habitat change. This is linked to the decreasing mean number of individuals (N_j) in the habitat patches, imposed by the decreasing carrying capacity (K_j) of these patches ($N_j = K_j$): the number of different species combinations of N_j individuals, in a habitat patch, increases when N_j decreases.

Under the specialization model, the beta-diversity curves in response to patch conversion and habitat alteration are convex (with two inflexion points for the habitat alteration scenario), and converge to a same Beta-diversity of higher value, in the final all openfield region, than that of the initial all forest configuration. This last result is again linked to the lower carrying capacity of openfield patches, compared to forest patches: the number of species combinations of $N_j = K_{\text{omax}} = 67$ individuals drawn from a pool of mainly 125 openfield species, in each openfield patch, is much higher than that of $K_f = 200$ individuals in a pool of mainly 125 forest species, in intact forest patches.

Under this model, Beta-diversity is highest for the patch conversion scenario, reflecting the high habitat differences among (intact forest and openfield) patches involved in this scenario.

3) Effects of habitat reduction, patch conversion and alteration on inter-individual diversity at the local and regional scales.

Below is a figure (Fig. A7) illustrating changes in the Shannon-Wiener index of diversity for the habitat reduction, patch conversion and alteration scenarios.

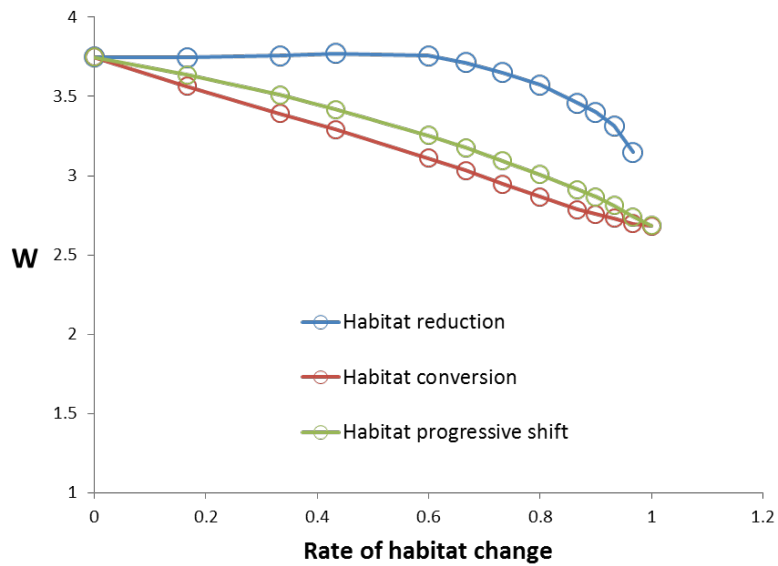
As illustrated in Figure A7, local diversity (upper panel) decreases more rapidly with patch conversion and habitat alteration as compared with habitat reduction, reflecting the reduction of average local carrying capacities in the two first scenarios.

At the regional scale, Shannon diversity remains constant with habitat reduction (lower panel).

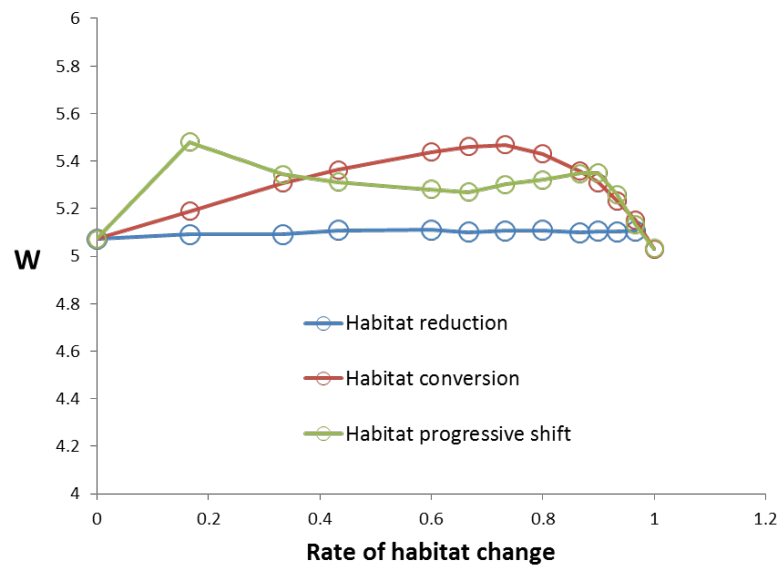
With habitat alteration, the two peaks correspond to situations in which (1) the fitness of generalist species equals that of forest specialists (2) the fitness of generalist species equals that of openfield specialists. With patch conversion, the single peak of diversity corresponds to the unique situation in which the fitness of forest specialists equals that of openfield specialists at the regional scale (which depends on the equality of the number of forest and openfield patches, weighted by the carrying capacities of these patches).

Figure A7. Relationships between the extent of habitat change and Shannon-Wiener index W at equilibrium. W was computed either at a local scale (patch) and averaged (upper panel) or at the regional scale (by pooling individuals of all patches, lower panel). Within each panel, the regional meta-community abundance varies according to either a reduction of patch number (Habitat Reduction, blue circles), a random conversion of forest patches to openfield patches (Patch Conversion, red circles) or a simultaneous shift of all forest patches to openfields (Habitat alteration, green circles). Species of the regional meta-community are issued from a mainland pool of 250 generalist, 125 forest specialist and 125 openfield specialist species (specialization model). The extent of habitat change relative to a 30 forest patches meta-community is expressed either as the proportion of forest patches replaced by patches of unsuitable habitat or openfield habitat (for reduction and patch conversion) or the magnitude x of degradation of forest patches into openfields (for habitat alteration). All parameters as in Fig. 2.

Mean intra-patch Shannon-Wiener index



Regional Shannon-Wiener index



References

- Condit R., Pitman N., Leigh E.G., Chave J., Terborgh J., Foster R.B. et al. 2002. Beta-diversity in tropical forest trees. *Science* **295**: 666–669.
- Dornelas M. 2010. Disturbance and change in biodiversity. *Phil. Trans. Roy. Soc. Lond. B: Biol. Sci.* **365**: 3719–3727.