

# **APPENDIX: EXTRA INFORMATION ON METHODS AND RESULTS**

Belonging to the study:

**A new modeling approach quantifies the relative importance of different community assembly processes**

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## **A1: Environmental gradients in HiP**

Fieldwork was carried out in Hluhluwe-iMfolozi Park (HiP, 28°00'-28°26'S, 31°41'-32°09'E), South Africa. The reserve is a ~90.000 ha sized area, characterized by a high habitat heterogeneity (Whateley and Porter 1983), with as main vegetation types upland forest, savanna grassland and thickets, woodlands and riverine forests. Rainfall data came from 17 weather stations where rainfall was measured with gauges on a daily basis from 2001 till 2007. These data were used to create a rainfall map for HiP: spatial coordinates of weather station location were used to extract interpolated estimates of rainfall. Mean annual rainfall ranges from 500 to 1000 mm, generally increasing with altitude (Balfour and Howison 2002, van der Plas et al. 2012). At smaller scales, heterogeneity is partially explained by variation in fire frequency, with fire return intervals ranging from 2 to 6 years, and partially by soil variation. Fires are usually ignited by park managers as managed burns, with the HiP reserve authorities monitoring the location and time of fires. Fire return intervals were mostly between 2 and 6 years, depending on landscape position (higher frequencies on more upland, high rainfall sites). The average annual amount of rainfall in HiP during the period 2001-2007 ranged from less than 500 mm in the south to more than 800 mm in the north (Fig. A1A). Plots were partially spread out over this gradient, with the driest plot receiving 548 mm per year, the wettest plot receiving 837 mm per year and an average amount of annual rainfall across all plots being 674 mm per year.

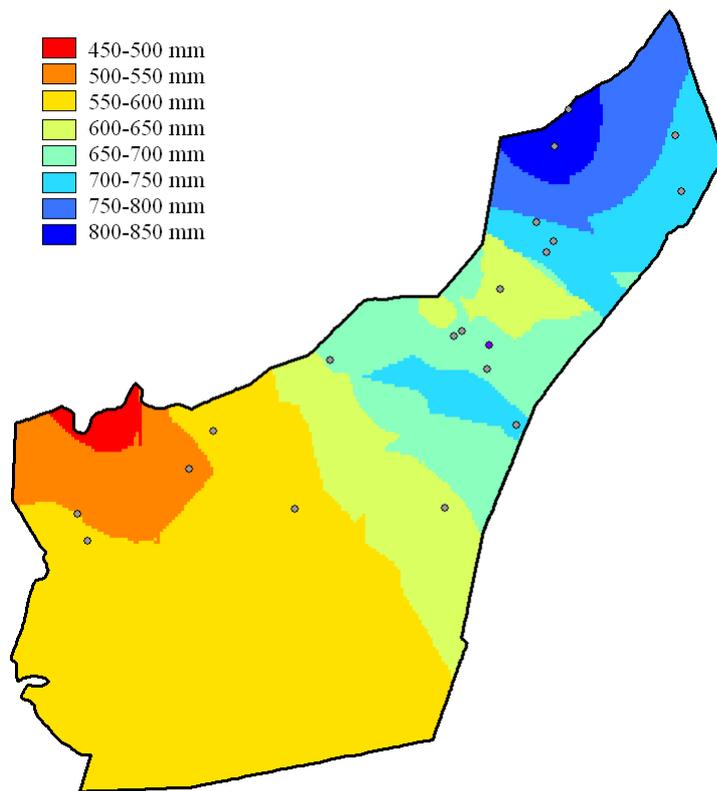


Fig A1A. An average amount of annual rainfall (in mm) map of HiP. The dots represent the plots visited for this study, with the purple dot representing plot nr. 17, used for sensitivity analyses in this study, because it was considered the most ‘representative’ plot. This map was also described in van der Plas et al. (2012).

Another important environmental factor in HiP is the gradient in fire frequency (Fig A1B). Fires in HiP are mostly ignited by park managers. Fire frequency, as measured over the period 1956-2004, ranges from less than 5 to over 25 in HiP. The plots investigated in this study covered most of this range, with the plot with lowest fire frequency experiencing 8 fires over this period, the plot with highest fire frequency experiencing 24 fires over the period and an average fire frequency across plots of 14.8 (Fig A1B). This map is a digitized 200 x 200 meter resolution map with fire annually recorded between 1956 and 2004 by the park management authorities (Fig A1B).

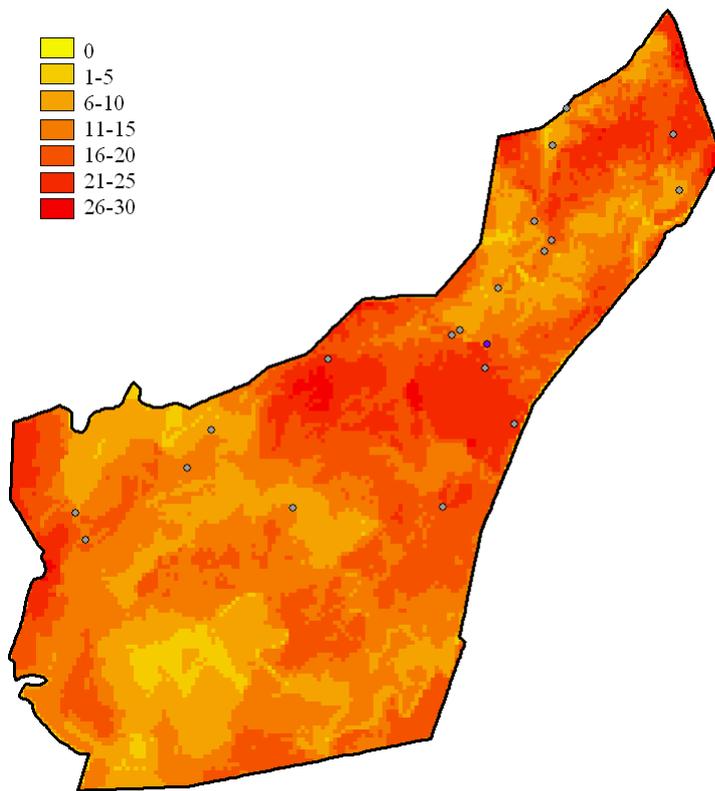


Fig A1B. A fire frequency map of HiP, showing the number of times different locations in the park were burnt in the period of 1956-2004. The dots represent the plots visited for this study, with the purple dot representing plot nr. 17, used for sensitivity analyses in this study, because it was considered the most ‘representative’ plot.

### **A2: Tree community data**

From November till December 2009, we characterized tree communities in 20 plots, stratified at different locations in HiP, covering both the rainfall and fire gradients (Fig A1A & Fig. A1B). For safety reasons plots were established within 500 meter from roads and at least 500 meters from larger rivers. The plots measured 20 x 20 meter and were at least 550 meters away from each other, with an average nearest neighbor distance of 3.0 km. Within these plots, we identified all individual trees taller than 0.5 meter following Pooley (1997).

### **A3: Trait data**

We measured eight different functional traits: Leaf Area (LA), Specific Leaf Area (SLA), wood density (WD) and concentrations of leaf carbon (C), nitrogen (N), phosphorous (P), sulfur (S) and potassium (K). These traits are related to growth – longevity trade-offs, drought tolerance, nutritional status and attractiveness to herbivores (e.g. Brown & Lawton 1991; Marschner 1995; Weiher et al. 1999; Hacke et al. 2011; Westoby et al. 2002). LA, SLA, WD, leaf C and N content were measured for each species in each plot, while the other chemical traits (leaf P, S and K content) were measured for each species in up to 7 plots. For LA measurements, for each species in each plot we collected between 5 and 30 leaves (depending on the size and weight) from multiple individuals. Collected leaves were photographed in the field with a reference scale on the background. We used the software SigmaScanPro v 5.0 (Systat Software Inc., San José, CA) to measure LA (in cm<sup>2</sup>) of fresh leaves. The leaves were dried (48h at 50°C) and weighted to 0.001 g precision. SLA (in cm<sup>2</sup>g<sup>-1</sup>) was calculated by dividing LA by dry weight. For WD measurements, at each site we collected three (20 cm long, diameter 2-13 mm) branches of each species. These were oven dried (48h at 50°C), dry mass was measured and WD was calculated as:  $WD = \frac{\pi r^2 L}{M}$ , with WD in m<sup>2</sup>kg<sup>-1</sup>, where  $r$  is the radius of the branch in m,  $L$  the length of the branch in m and  $M$  the dry weight of the branch in kg. For chemical analyses, we collected bulk samples of healthy, intact leaves for each species at each site. We dried (48h at 50°C) and ground these samples ground using a ball mill. We measured leaf C and N content in duplicate using a Carlo-Erba NA 1500 element analyzer (Carlo-Erba, Milan, Italy). Leaf P, S and K contents were measured at the laboratory of BLGG AgroXpertus in Wageningen via ICP atomic emission spectrometry, conforming to NEN6966.

**A4: Stepwise Community Assembly Models (STEPCAMs): how do Functional Diversity values respond to relative contributions of different community assembly processes?**

In our main analyses, we ran STEPCAMs with different community assembly processes in the following order: (1) dispersal assembly, (2) filtering or (3) limiting similarity. As such, we assumed a certain order in community assembly, which is most in line with other literature on this topic (e.g. Cornwell & Ackerly 2009). However, one might argue that *a priori* assumptions about the order of community assembly processes are risky, because such assumptions could potentially bias model outcomes. To test this, here, we ran several STEPCAMs applied to plot 17, differing in two ways from each other: (1) in the relative contribution of different community assembly steps, and (2) in the order of these community assembly processes. The results of this plus the interpretations can be found in the main document (Fig. 2) of the MS.

**A5: Stepwise Community Assembly Models (STEPCAMs): how do Functional Diversity values respond to a different order of community assembly processes?**

Secondly, we investigated for each of these parameter combinations how the order of community assembly processes changed the FR, FE and FDiv values of resulting communities. This was done by running models with each of the 231 different parameter combinations described above (A4), but with different orders of processes: (1) dispersal assembly steps first, filtering second and finally limiting similarity (as done in the main analyses), (2) dispersal assembly, filtering and limiting similarity steps in separate blocks, but the order of these blocks randomized over replicates (3) the order of dispersal assembly, filtering and limiting similarity steps completely randomized. As such, we thus ran a total of  $231 \times 3 = 693$  different STEPCAMs, applied to plot 17, with 1000 replicates for each model, and we investigated (i) whether the order of different community assembly processes had large absolute effects on functional diversity values of resulting communities and (ii) whether responses of functional diversity values to different relative contributions of different

community assembly steps in models depended on the order of these community assembly steps.

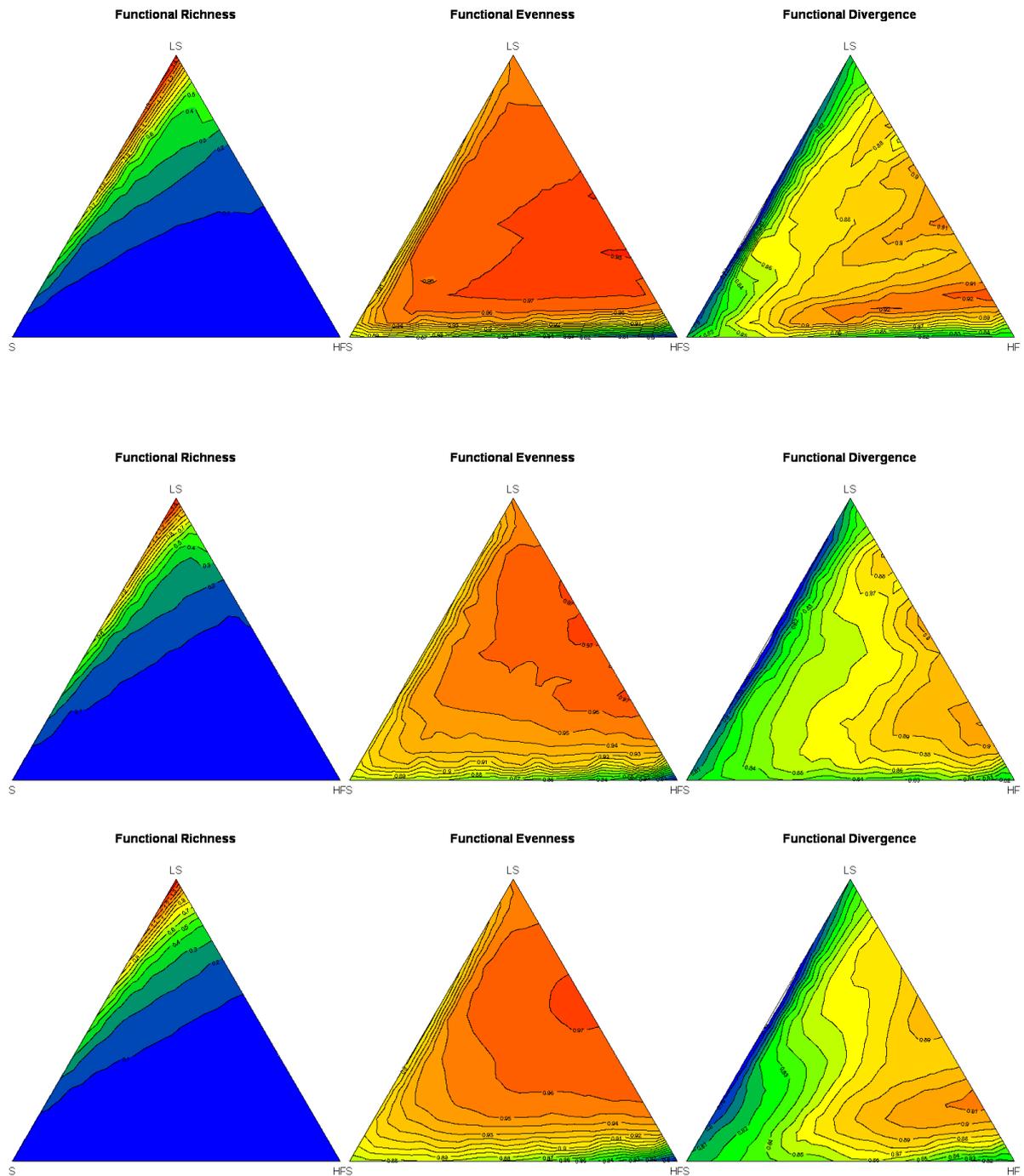


Fig A5A. Ternary plots with the responses of FR (left), FE (middle) and FDiv (right) to changes in the relative contribution of dispersal assembly, filtering and limiting similarity steps in STEPCAMs applied to plot 17. The upper row shows results for STEPCAMs in

which dispersal assembly steps were run first, then filtering steps, then limiting similarity steps. The middle row shows results for STEPCAMs with dispersal assembly, filtering and limiting similarity steps in separate blocks, but the order of these blocks randomized over replicates. The bottom row shows results for STEPCAMs with the order of dispersal assembly, filtering and limiting similarity steps completely randomized.

As can be seen in Fig A5A, changing the order in which different community assembly processes take place does not lead to very large changes in Functional Diversity values. In all scenarios, FR values are highest when limiting similarity processes dominate and lowest when filtering processes dominate in community assembly. FE and FDiv values are highest when dispersal assembly is close to zero, and community assembly is regulated by a combination of filtering and limiting similarity processes. FR, FE and FDiv values of communities created by ‘normal’ STEPCAMs (first dispersal assembly, then filtering and lastly limiting similarity steps) correlated highly with FR, FE and FDiv values from the same parameter combinations but with different orders of processes:  $R^2$  values were 0.973; 0.950 and 0.918 for FR, FE and FDiv values of ‘randomized block order’ STEPCAMs and 0.955; 0.930 and 0.894 for FR, FE and FDiv values of ‘totally random order’ STEPCAMs.

**A6: More details about how the ABC-SMC approach was used to infer the relative contributions of different processes in community assembly.**

Model selection was performed through the method of Approximate Bayesian Computation (ABC) within a Sequential Monte Carlo (SMC) framework (Toni et al. 2009; Beaumont 2010; Hartig et al. 2011). With ABC, model selection is performed through the comparison of one or more summary statistics of observed data (or data created by ‘generator models’ to investigate whether different models create distinguishable summary statistics) with those

generated by candidate models. Parameter combinations ( $\theta$ ) that generate data that is sufficiently similar (approximately identical) to the observed data are accepted, parameter combinations that yield too dissimilar data are rejected. In contrast to standard MCMC approaches where the chain is propelled by the likelihood, in ABC the chain is propelled through the difference in summary statistics (where acceptance is regulated by a threshold maximum difference). For our STEPCAMs no likelihood could be calculated and therefore we relied on the use of four summary statistics: FR, FE, FDiv and CTM values. Before running STEPCAM models, we standardized all summary statistics to a mean of zero and a standard deviation of one, so that each different summary statistic had the same impact on the fitting procedure. The fit of STEPCAMs was calculated as:

$$Fit_{total} = Fit_{FR} + Fit_{FE} + Fit_{FDiv} + Fit_{CTM} ,$$

in which  $Fit_{FR}$ ,  $Fit_{FE}$  and  $Fit_{FDiv}$  are the absolute difference between respectively FR, FE and FDiv values from the observed community and those generated by the STEPCAM, while  $Fit_{CTM}$  is the (multidimensional) Euclidian distance between the 8 CTM values of the observed community and those generated by the STEPCAM. High  $Fit_{total}$  values thus indicated poor fit, while low values indicated good fit. Using the fit of the models, we performed a Sequential Monte Carlo (SMC) resampling scheme. Generally the algorithm first generates  $N$  particles from the prior, and after that resamples  $N$  particles from the obtained distribution, depending on a weighting function. Acceptance of the new particles is dependent on the fit of the data ( $Fit_{total}$ ). As the algorithm proceeds over multiple iterations, the distribution of the  $N$  particles approaches the approximate posterior distribution, which for small thresholds is equivalent to the true posterior distribution. Our ABC-SCM algorithm largely followed Toni (2009), consisting of the following steps:

S1 Initialize vector of acceptance thresholds  $\varepsilon_1 \dots \varepsilon_T$ , set population indicator  $t = 0$

S2.0 Set the particle indicator  $i = 1$

S2.1 If  $t = 0$ , sample  $\theta$  independently from the prior.

Else, sample  $\theta^*$  from the previous population with weights  $w_{t-1}$  and perturb the particle using a normally distributed perturbation kernel  $K$  (mean 0, standard deviation of  $\sigma$ ) to obtain  $\theta^{**}$

S2.2 If  $\pi(\theta) = 0$ , return to S 2.1.

S2.3 Simulate a candidate dataset  $x^*$  using our STEPCAM with parameters  $\theta^{**}$ .

S2.4 If  $Fit_{total} \geq \varepsilon_t$ , return to S2.1

S2.5 Set  $\theta_t^{(i)} = \theta$  and calculate the weight for particle  $\theta_t^{(i)}$ :

If  $t = 0$ ,  $w_t^{(i)} = 1$ .

$$\text{If } t > 0, w_t^{(i)} = \frac{1}{\sum_{j=1}^N w_{t-1}^{(j)} K_t(\theta_{t-1}^{(j)}, \theta_t^{(i)})}$$

If  $i < N$ , set  $i = i + 1$ , go to S2.1

S3 Normalize the weights.

If  $t < T$ , set  $t = t + 1$ , go to S2.0.

We chose our acceptance threshold as an exponentially decreasing series, such that initially samples are easily accepted, but as  $t$  increases, the acceptance rate quickly decreases. Number of particles used ( $N$ ) was chosen to be 1,000; early test runs with higher numbers of particles did not seem to affect outcomes. For each plot, we ran the algorithm ten times, to investigate whether the ABC model selection generated repeatable parameter values. The average parameter values of these ten models are reported in the ‘results’ section of the main manuscript.

Our prior consisted of the full  $[0, s]$  interval for the three parameters under investigation here: dispersal assembly, filtering and competition, in which  $s$  is the number of STEPCAM steps

(= richness of species pool – richness of local community). Perturbation in step 2.1 was performed by randomly picking one of the three parameters and adding a value obtained from a normal distribution with mean 0 and standard deviation of 1. Because the three parameters together have to add up to the full community size, the difference obtained by the perturbation was corrected by subtracting or adding the same amount from the other two parameters. Whereas in Toni et al. (2009) weights are multiplied by the prior probability of the found parameter combination, in our case, this probability is always 1, due to step 2.2. The algorithm was repeated until the acceptance rate (S2.4) had diminished to 1 in a million particles.

**A7: Stepwise Community Assembly Models (STEPCAM): how well can our ABC-SMC model selection procedure distinguish between competing models?**

In order to investigate how well our ABC-SMC approach can distinguish between competing STEPCAMs, we investigated three criteria: (1) how much variation is there in the parameter values from the posterior distribution? (2) does the ABC-SMC approach lead to repeatable patterns, that is: when the algorithm is run several times, are average parameter values of posterior distributions relatively constant across different runs for the same plot? And (3) does the fitting of summary statistics generated by a ‘generator’ STEPCAM lead to the selection of a ‘candidate STEPCAM’ with similar parameter settings?

*1. How much variation is there in the parameter values from the posterior distributions?*

We applied the ABC-SMC model selection approach 10 times to each of the 20 plots we investigated in this study. Each time, the ABC-SMC model selection procedure generated a posterior distribution of parameter values from ‘accepted models’, i.e. STEPCAMs that generated summary statistics that were similar enough to observed summary statistics to be

considered ‘adequate’. In the rest of our study, we reported and analyzed the average parameter values of these posterior distributions, but an interesting question is how much variation there is within this posterior distribution. Ideally, this variation would be as low as possible, which would indicate that models with a small range of parameter values clearly fit the summary statistics better than competing models.

We used the coefficient of variation ( $CV = \frac{sd_{parameter\ value}}{mean_{parameter\ value}}$ ) as a standardized measure for the variation of parameter values in the posterior distribution, with CV values below 1 indicating relatively low variation and CV values above 1 indicating relatively high variation. CV values for dispersal assembly steps ranged from 0.014 to 1.215, with an average of 0.190. CV values for filtering steps ranged from 0.174 to 14.824, with an average of 1.548. CV values for limiting similarity steps ranged from 0.119 to 5.431, with an average of 21.774. A closer look at CV values showed that they were only high when the mean value of the posterior (the denominator of the CV) was very low (< 1%). When such denominators were very low, absolute standard deviations of posterior distributions were also very low (<0.82%), so that even in those cases, in absolute terms, posteriors showed very small variation in parameter values. When ignoring CV values with denominators below 1 %, CV values for dispersal assembly steps still ranged from 0.014 to 1.215, with an average of 0.190, CV values for filtering steps ranged from 0.174 to 1.971, with an average of 0.674 and CV values for limiting similarity steps ranged from 0.119 to 5.431, with an average of 0.730. In general, variation in parameter values from the posterior distribution of ABC-SMC algorithms was therefore reasonably low.

Mean and sd values of posteriors of parameter values for each plot can also be seen in A7A, B and C.

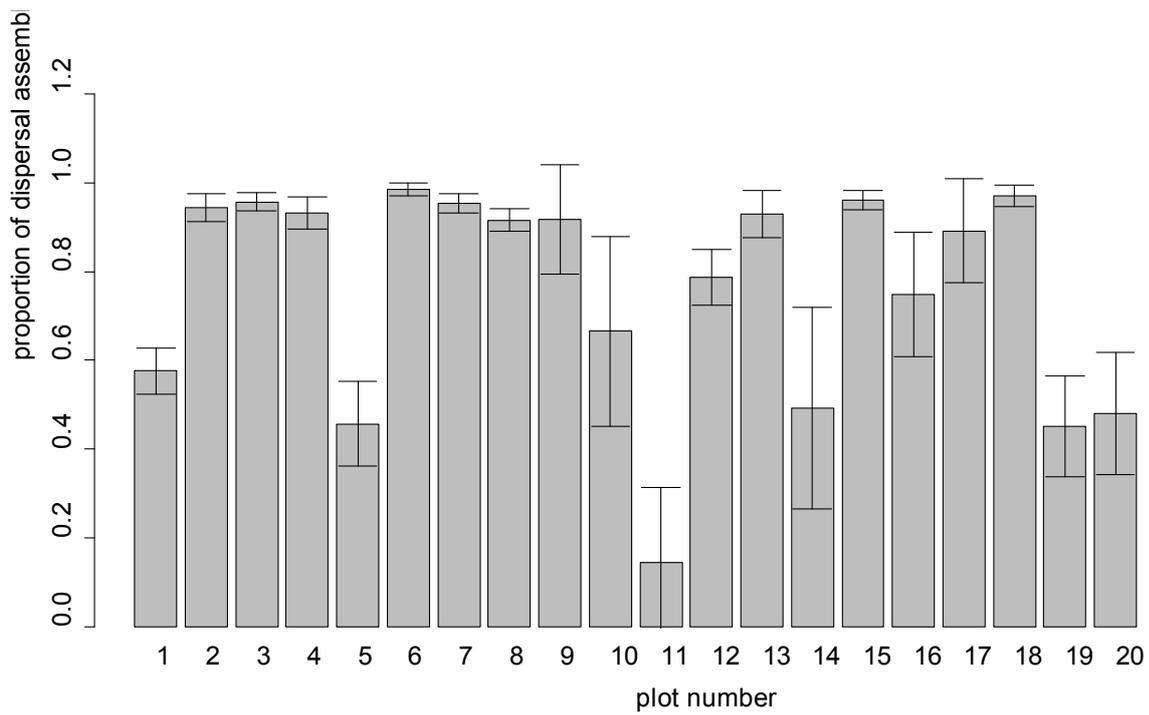


Fig. A7A. Mean and sd values of the posterior distributions of the proportion of dispersal assembly steps for each plot. As each plot was fitted 10 times, the mean and sd values of the posteriors are averages across replicate model fits.

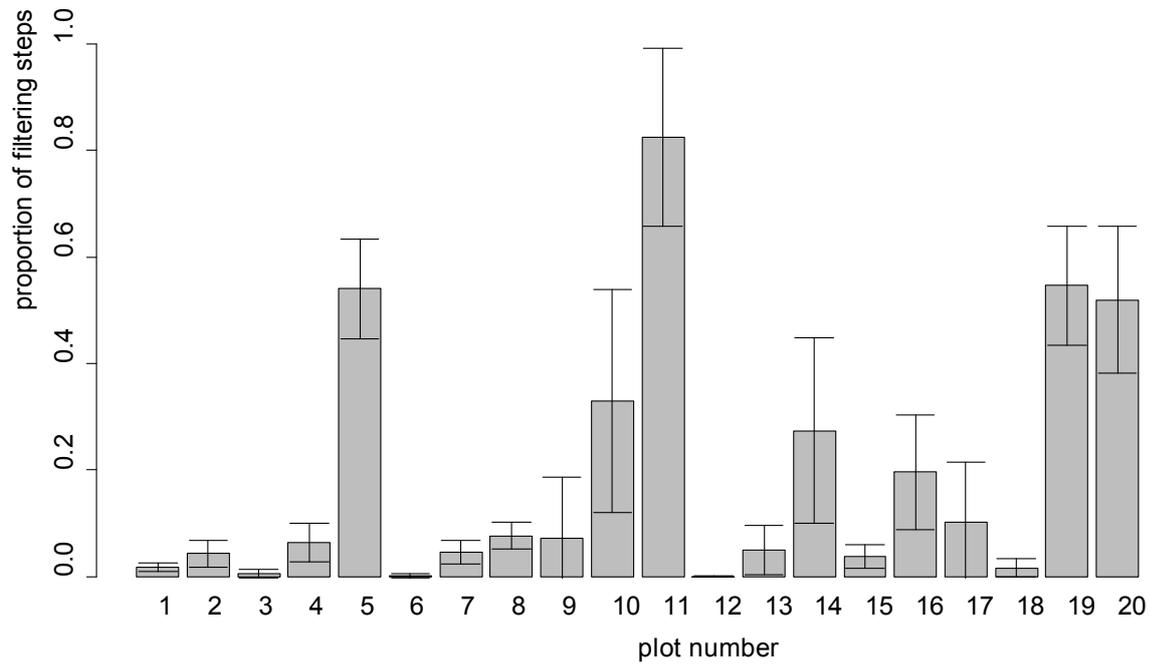


Fig. A7B. Mean and sd values of the posterior distributions of the proportion of filtering assembly steps for each plot. As each plot was fitted 10 times, the mean and sd values of the posteriors are averages across replicate model fits.

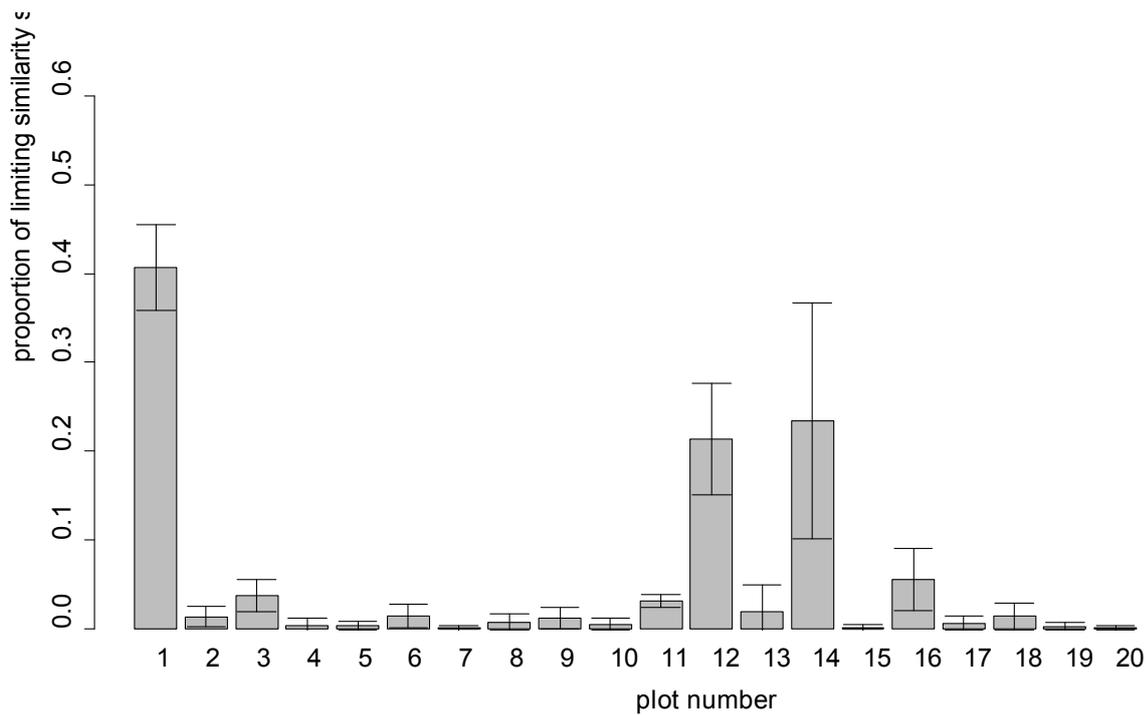


Fig. A7C. Mean and sd values of the posterior distributions of the proportion of limiting similarity assembly steps for each plot. As each plot was fitted 10 times, the mean and sd values of the posteriors are averages across replicate model fits.

## 2. Does the ABC-SMC approach lead to repeatable patterns?

We applied the ABC-SMC model selection approach 10 times to each of the 20 plots we investigated in this study. So not only within posterior distributions there could be variation in parameter values, but also across replicate runs within the same plot, the average parameter value of posterior distributions could differ. Also in this case, ideally, this variation should be as low as possible, which would indicate that the ABC-SMC approach leads to repeatable patterns.

We used the coefficient of variation ( $CV = \frac{sd_{parameter\ value}}{mean_{parameter\ value}}$ ) as a standardized measure

for the variation of average parameter values across replicate model selection runs, with CV

values below 1 indicating relatively low variation and CV values above 1 indicating relatively high variation. CV values for dispersal assembly steps ranged from 0.001 to 0.321, with an average of 0.066. CV values for filtering steps ranged from 0.021 to 1.176, with an average of 0.317. CV values for limiting similarity steps ranged from 0.024 to 0.779, with an average of 0.245. In general, replicate model selection runs thus resulted in very similar average parameter values of posterior distributions. Therefore, we conclude that the ABC-SMC approach leads to repeatable patterns.

3. *Does the fitting (with ABC-SMC) of summary statistics generated by a ‘generator STEPCAM’ lead to the selection of a ‘candidate STEPCAM’ with similar parameter settings?*

We performed the ‘generator STEPCAM fitting procedure’ on plot 17. We used ‘generator models’ with certain parameter settings to generate summary statistics (FR, FE, FDiv and CTM values). With the ABC-SMC approach described in the main document, these summary statistics were used to identify a ‘best fitting candidate model’. We then compared each of the three parameter values of the ‘generator models’ with parameter values of the associated ‘best fitting candidate models’: ideally, if our ABC-SMC approach works perfectly, parameter values of ‘generator models’ and ‘best fitting candidate models’ would be exactly equal. In case our ABC model selection procedure would be totally uninformative, leading to the selection of STEPCAMS with random parameter settings, the average expected parameter deviation would be:

$$DEV_{exp} = \left( \frac{1}{3} - x + 2x^2 - \frac{2}{3}x^3 \right) \cdot 100$$

in which x is the given parameter setting from the ‘generator model’ (e.g. the percentage of dispersal assembly steps in the ‘generator model’). In total, we fitted 10 x 231 ‘generator

models': we ran 'generator models' with each of the 231 parameter settings described above, with ten replicates for each parameter combination.

On average, the deviation in parameter value of 'best fitting candidate models' from the associated 'generator models' was 3.7 % for the relative proportion of dispersal assembly steps, 2.2 % for the relative proportion of filtering steps and 2.0 % for the relative proportion of limiting similarity steps. These deviations shifted slightly over parameter space (Fig A7D, above). Average expected deviations were 27.7 % for each parameter value, and thus much higher than observed. This made us confident that generally, the ABC-SMC approach was adequate in distinguishing STEPCAMs with different parameter combinations. Although expected parameter deviations shifted over parameter space (Fig A7D, below), for almost any parameter combination, observed deviations between 'generator models' and associated 'best fitting models' were smaller than deviations when assuming that our ABC-SMC approach would randomly select models (Fig A7E). Only in the small parameter space within the circles in Fig. A7E, observed deviations between 'generator models' and associated 'best fitting models' were larger than expected by chance. Overall, with almost any parameter combination of the 'generator model', the ABC-SMC procedure performed better than random. When 'generator models' had extreme parameter settings (i.e. the relative contribution of a given community assembly process being either close to 0 % or close to 100 %), the ABC model selection procedure performed relatively better than in cases where parameter settings of 'generator models' were less extreme (Fig A7E).

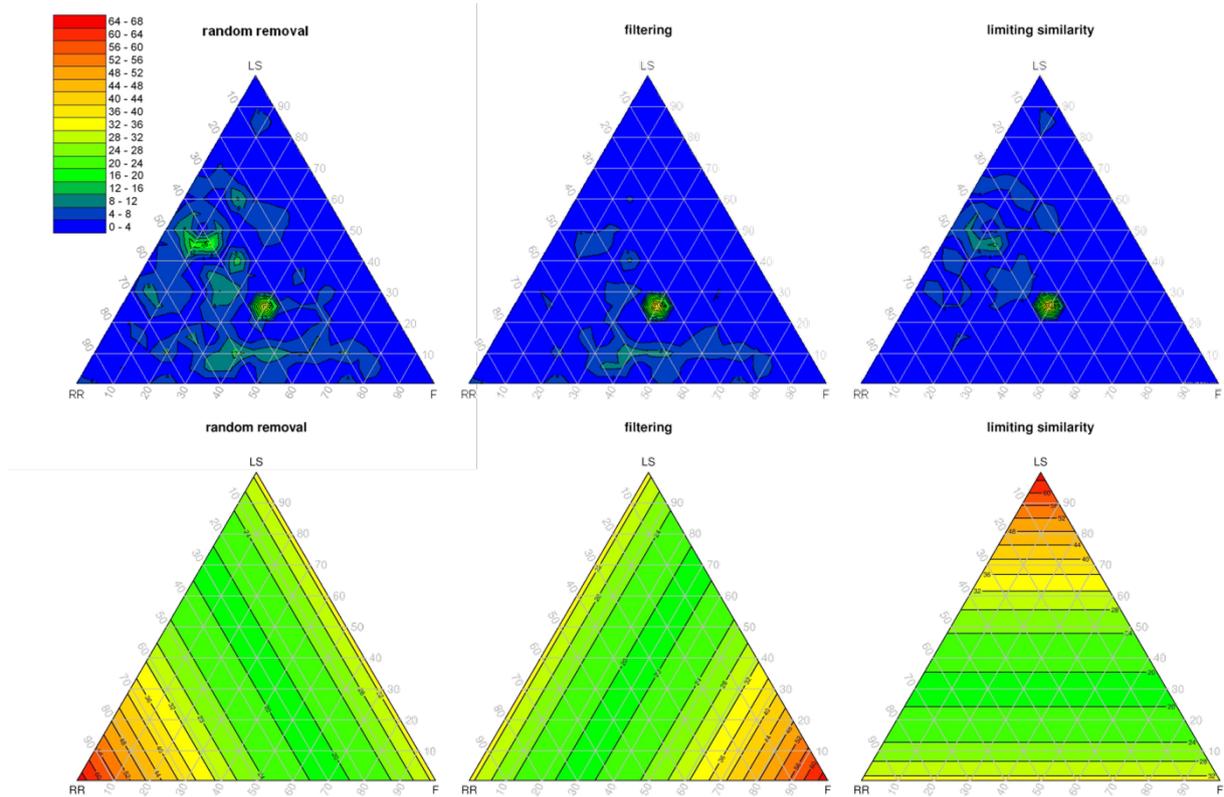


Fig A7D. Ternary plots with on top the absolute deviation between parameter values from ‘generator models’ and their associated ‘best fitting candidate models’, as a response to the parameter values of the ‘generator models’. The three parameter deviations considered are: the relative contribution of (i) dispersal assembly steps (left), (ii) filtering steps (middle) and (iii) limiting similarity steps (right) in community assembly. Below one can see the expected deviation between parameter values from ‘generator models’ and their associated ‘best fitting models’, assuming that the ABC-SMC approach selects ‘best fitting models’ randomly over parameter space. Deviation values for positions in parameter space were estimated using bilinear interpolation. Abbreviations: RR = dispersal assembly, F = filtering and LS = limiting similarity.

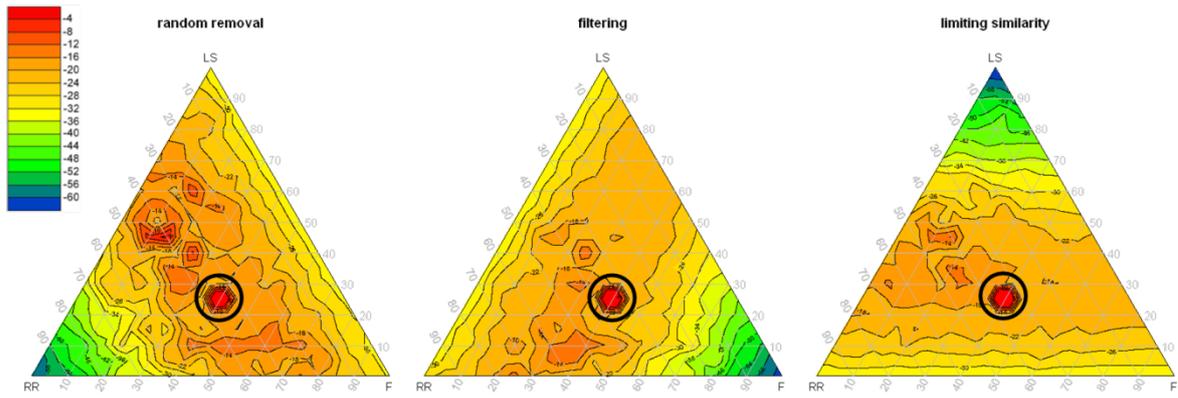


Fig A7E. Ternary plots with the observed – expected deviation between parameter values from ‘generator models’ and their associated ‘best fitting candidate models’, as a response to the parameter values of the ‘generator models’. Note that values are always negative. Deviation values for positions in parameter space were estimated using bilinear interpolation. Abbreviations: RR = dispersal assembly, F = filtering and LS = limiting similarity.

We also investigated whether parameter values of generator models and best fitting models correlated strongly. This was indeed the case for both dispersal assembly, filtering and limiting similarity (Fig. A7F).

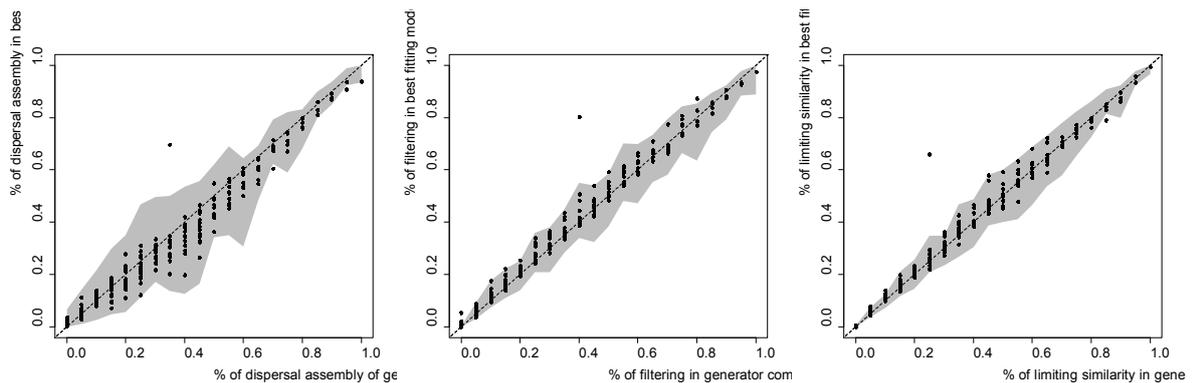


Fig A7F. Parameter values of ‘generator models’ versus those of ‘best fitting models’. If Model fitting works perfectly, points should be on the  $y = x$  lines (dotted line). Points were generally indeed close to this line, and average (across best fitting models applied to the same focal parameter value of the generator community) 95% credible intervals (grey area) always

overlapped with the  $y = x$  line. Adjusted  $R^2$  values are: 0.9619 (dispersal assembly); 0.9791 (filtering) and 0.9786 (limiting similarity).

## **A8: Additional results**

### Drivers of CTM values

To investigate how tree species richness, log abundance of trees and CTM values responded to gradients of rainfall and fire, we created full general linear models (LMs) containing rainfall and fire frequency as predictor variables for species richness, log abundance and CTM values as response variables. We ran a Maximum Likelihood model selection procedure, identifying the model with the lowest AIC value only containing significant predictor variables.

It appeared that tree species richness decreased with an increasing frequency of fires (Table S1), with average richness going down from approximately 19 species in plots with lowest fire frequency to approximately 9 in plots with highest fire frequency. Tree abundances did not respond to fire frequency or annual rainfall (Table A8.1). At areas of high rainfall, trees had largest leaves and highest SLA, but lowest WD. At areas with high fire frequency, trees had on average low SLA, high WD and high leaf C content. Other CTM values did not respond significantly to fire or rainfall. Model comparisons are shown in Table A8.2.

Table A8.1: Relationships between tree communities and environmental gradients (most parsimonious models)

Response variable	Variables in final model with effect sizes	R <sup>2</sup>
<b>Diversity and density</b>		
Species richness	Rainfall (-0.056), fire frequency (-5.220), Rainfall x fire frequency (0.006)	0.267
Log abundance		0.000
<b>CTM values</b>		
Specific Leaf Area	Rainfall (0.152), fire frequency (-1.354)	0.583
Leaf Area	Rainfall (0.030) + fire frequency (-0.259)	0.386
Wood Density	Rainfall (-3.319E-4), fire frequency(2.371E-3)	0.645
C content	Fire frequency (-0.003), fire frequency (0.076)	0.272
N content	Rainfall (0.102E-4), fire frequency 4.751E-3	0.000
P content	Rainfall (0.016)	0.000
S content	Rainfall (0.540), fire frequency (35.166), Rainfall x fire frequency (-0.051)	0.000
K content	Rainfall (0.197), fire frequency (-2.613)	0.000

Table A8.2: Comparisons between different models explaining species richness, log abundance and CTM values. Most parsimonious models are shown in bold.

Response variable	Fire frequency	Rainfall	Fire x rainfall	AIC
<b>Species richness</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>126.93</b>
Species richness	1	1		127.40
Species richness	1			133.54
Species richness		1		128.79
Species richness				133.00
Log abundance	1	1	1	13.03
Log abundance	1	1		11.58
Log abundance	1			10.17
Log abundance		1		9.58
<b>Log abundance</b>				<b>8.17</b>
Specific Leaf Area	1	1	1	164.35
<b>Specific Leaf Area</b>	<b>1</b>	<b>1</b>		<b>162.36</b>
Specific Leaf Area	1			166.27
Specific Leaf Area		1		176.18
Specific Leaf Area				175.88
Leaf Area	1	1	1	104.60
<b>Leaf Area</b>	<b>1</b>	<b>1</b>		<b>102.99</b>
Leaf Area	1			105.37
Leaf Area		1		113.73
Leaf Area				113.13
Wood Density	1	1	1	-88.04
<b>Wood Density</b>	<b>1</b>	<b>1</b>		<b>-89.32</b>
Wood Density	1			-85.95
Wood Density		1		-71.67
Wood Density				-72.59
Leaf Carbon content	1	1	1	39.96

<b>Leaf Carbon content</b>	<b>1</b>	<b>1</b>		<b>39.22</b>
Leaf Carbon content	1			45.48
Leaf Carbon content		1		40.56
Leaf Carbon content				44.90
<b>Leaf N content</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>-8.65</b>
Leaf N content	1	1		-4.84
Leaf N content	1			-6.48
Leaf N content		1		-6.84
Leaf N content				-8.47
Leaf P content	1	1	1	116.41
Leaf P content	1	1		114.44
<b>Leaf P content</b>	<b>1</b>			<b>114.28</b>
Leaf P content		1		114.75
Leaf P content				114.94
Leaf S content	1	1	1	184.01
Leaf S content	1	1		189.57
<b>Leaf S content</b>	<b>1</b>			<b>187.61</b>
Leaf S content		1		189.56
Leaf S content				187.71
Leaf K content	1	1	1	211.83
Leaf K content	1	1		209.86
Leaf K content	1			210.11
Leaf K content		1		211.30
<b>Leaf K content</b>				<b>210.66</b>

### Extra null models

We performed null models ('simple null models') additional to those presented in the main article, in which the chance that a species was included in a local community was purely random and *independent* of its frequency. It appeared that in sic plots, FR was lower than expected based on the simple null model (vs three plots for the null model from the main analysis) and FE and FDiv were lower than expected by chance in two plots (as was also the case in the main analysis).

## **A9: LITERATURE CITED**

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