

Supplementary Information for

The niche is not the range: Dispersal and persistence shape mismatches between ecological niches and geographic distributions of plants

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Supplementary Information Text

In this supplementary information text we provide additional details on Bayesian parameter estimation at different steps in our statistical analyses:

- 1) Demographic response model
- 2) Statistical analyses of relationships between life history traits, demographic rates, niche characteristics and species geographic ranges
- 3) Statistical analysis of the relationships between occupancy and demographic suitability

For each analysis a statistical model was formulated in a Bayesian framework and samples from the parameter posterior distributions were generated with Markov chain Monte Carlo (MCMC) methods in the software JAGS (54). For each model we present the JAGS code together with an overview of all included data variables, parameters and parameter prior distributions.

We furthermore include a description of:

- 4) Additional analyses for alternative calculations of range filling

1) Demographic response model

A comprehensive description of the demographic response model is given in the *Materials and Methods* and a graphical overview of the hierarchical model structure is shown in Fig. S6. Parameters of the demographic response model were estimated separately for each study species. Note that all environmental variables were scaled and centered and the aridity index and soil fertility index were additionally log-transformed before the analyses.

Data variables for the demographic response model

	Variable name [dimensions]	Description	Text symbol
Fecundity data	n.Fec	number of populations with fecundity data	
	Fec.FEC[n.Fec]	total size of the canopy seedbank the of sampled individuals	
	No_Plants.FEC[n.Fec]	number of sampled individuals	
	log_AI.FEC[n.Fec]	log-transformed January aridity index	$\log(AI)$
	min_temp_jul.FEC[n.Fec]	July minimum daily temperature	T_{\min}
	max_temp_jan.FEC[n.Fec]	January maximum daily temperature	T_{\max}
	log_soil_fert.FEC[n.Fec]	log-transformed soil fertility index	$\log(\text{soil fertility})$
	Age.FEC[n.Fec]	stand age	Age
	SP.dens.FEC[n.Fec]	population density	D
Recruitment data	n.SPR	number of populations with recruitment data	
	Seedlings.SPR[n.SPR]	number of recruits	$\#Recruits$
	Parents.SPR[n.SPR]	number of pre-fire parents	$\#Parents$
	Alive.SPR[n.SPR]	number of post-fire (fire-surviving) adults	$\#Adults$
	area.SPR[n.SPR]	sampled area	$Area$
	log_AI.SPR[n.SPR]	log-transformed January aridity index	$\log(AI)$
	min_temp_jul.SPR[n.SPR]	July minimum daily temperature	T_{\min}
	max_temp_jan.SPR[n.SPR]	January maximum daily temperature	T_{\max}
	log_soil_fert.SPR[n.SPR]	log-transformed soil fertility index	$\log(\text{soil fertility})$
	log_PF_Age.SPR[n.SPR]	log-transformed, normalized post-fire stand age	$\min[\log(pf.Age/3), 0]$
	Age.SPR[n.SPR]	length of the previous fire interval, i.e. pre-fire stand age	Age
	SP.dens.SPR[n.SPR]	pre-fire population density	D
Survival data	n.Surv	number of populations with survival data	
	Alive.SURV[n.Surv]	number of fire-surviving adults	$\#Survivors$
	All_Adults.SURV[n.Surv]	total number of pre-fire adults	$\#All.Adults$
	log_AI.SURV[n.Surv]	log-transformed January aridity index	$\log(AI)$
	min_temp_jul.SURV[n.Surv]	July minimum daily temperature	T_{\min}
	max_temp_jan.SURV[n.Surv]	January maximum daily temperature	T_{\max}
	log_soil_fert.SURV[n.Surv]	log-transformed soil fertility index	$\log(\text{soil fertility})$
	Age.SURV[n.Surv]	length of the previous fire interval, i.e. pre-fire stand age	Age
	SP.dens.SURV[n.Surv]	pre-fire population density	D

In this table 'Variable name' refers to a variable in the JAGS code (see below) and 'Text symbol' refers to the corresponding notation in the Methods section, if applicable. Note that in the fecundity submodel the measurements of individual-level sizes canopy seed banks ($Seed.count_{ij}$) were aggregated to the sum ($Fec.FEC$) over all sampled individuals per population ($No_Plants.FEC$) for numerical efficiency. Environmental covariates are organized as separate variables for each submodel, although different demographic data types were often collected for the same population. For the sample sizes ($n.Fec$, $n.SPR$, $n.Surv$) for each species see Tab. S1.

An overview of parameter prior distributions is given in the table below. In three independent MCMC chains, posteriors were sampled from 100,000 iterations after a burn-in period of 500,000 iterations. Convergence of the MCMC sampler was checked by the multivariate scale reduction factor being smaller than 1.1 (55). For all further analyses, the posterior samples were regularly thinned to a sample size of 1,000 for each chain, respectively 3,000 samples in total.

Parameters and prior distributions for the demographic response model

Parameter name	Variable name	Description	Prior distribution	Prior parameters	
$\log(max.fec)$	fec.Intercept	maximum fecundity (log)	Normal	$\mu = 0, \sigma^2 = 10^4$	
$opt.fec_k$	fec.opt.log_AI fec.opt.min_temp_jul fec.opt.max_temp_jan fec.opt.log_soil_fert	environmental optima	Normal	$\mu = 0, \sigma^2 = 10^4$	
	$1/sig.fec_k^2$				fec.sc.log_AI fec.sc.min_temp_jul fec.sc.max_temp_jan fec.sc.log_soil_fert
$\beta.fec$	fec.Age fec.Age_2	age effects	Double-Exponential	$\mu = 0, \lambda = 1$	
	$sh.mat$				zi.sh
$sc.mat$	zi.sc		Gamma	$\alpha = 0.01, \beta = 0.01$	
$\gamma.fec$	fec.SP.dens	strength of density effects	Exponential	$\lambda = 1$	
$k.fec$	size.fec	overdispersion parameter	Gamma	$\alpha = 0.01, \beta = 0.01$	
$max.est$	recr.Intercept	maximum establishment rate	Beta	$a = 1, b = 1$	
	$opt.est_k$	recr.opt.log_AI recr.opt.min_temp_jul recr.opt.max_temp_jan recr.opt.log_soil_fert	environmental optima	Normal	$\mu = 0, \sigma^2 = 10^4$
		$1/sig.est_k^2$			
	$\beta.est$	recr.log_PF_Age	effect of time since fire	Exponential	$\lambda = 1$
	$\gamma.est.SD$	recr.seed.dens	strength of density effects from seeds	Exponential	$\lambda = 1$
	$\gamma.est.AD$	recr.adult.dens	strength of density effects from adults	Exponential	$\lambda = 1$
$max.surv$	surv.Intercept	maximum survival rate	Beta	$a = 1, b = 1$	
	$opt.surv_k$	surv.opt.log_AI surv.opt.min_temp_jul surv.opt.max_temp_jan surv.opt.log_soil_fert	environmental optima	Normal	$\mu = 0, \sigma^2 = 10^4$
		$1/sig.surv_k^2$			
	$opt.surv_{Age}$	surv.opt.Age	age optimum	Normal	$\mu = 0, \sigma^2 = 10^4$
	$1/sig.surv_{Age}$	surv.sc.Age	age response strengths	Exponential	$\lambda = 1$
	$\gamma.surv$	surv.SP.dens	strength of density effects	Exponential	$\lambda = 1$

This is an adjusted version of Tab. S6. In this table 'Parameter name' refers to the notation in the Methods and 'Variable name' to the corresponding variable in the JAGS code (see below).

JAGS code for the demographic response model

```
model {
### Fecundity submodel
for (i in 1:n.Fec){
# Negative-binomial model for the population-level seed count
Fec.FEC[i] ~ dnegbin(prob.FEC[i], size.fec)
prob.FEC[i] <- size.fec/(size.fec + mu.Fec[i] * No_Plants.FEC[i] * I.fec.FEC[i])
I.fec.FEC[i] ~ dbern(zi.fec.FEC[i])

# Age-dependent probability of maturity according to a Weibull model
I.fec.FEC[i] ~ dbern(zi.fec.FEC[i])
zi.fec.FEC[i] <- 1 - exp(-(Age.mat.FEC[i]/zi.sc)^zi.sh)

# Calculation of effects of environment (Gaussian response curves), age and population density
log(mu.Fec[i]) <- fec.Intercept - fec.sc.log_AI * pow(fec.opt.log_AI - log_AI.FEC[i], 2)
- fec.sc.min_temp_jul * pow(fec.opt.min_temp_jul - min_temp_jul.FEC[i], 2)
- fec.sc.max_temp_jan * pow(fec.opt.max_temp_jan - max_temp_jan.FEC[i], 2)
- fec.sc.log_soil_fert * pow(fec.opt.log_soil_fert - log_soil_fert.FEC[i], 2)
+ fec.Age * Age.FEC[i] + fec.Age_2 * pow(Age.FEC[i],2)
- fec.SP.dens * SP.dens.FEC[i]
}

### Establishment submodel
for (j in 1:n.SPR){
# Negative-binomial model for number of observed recruits
Seedlings.SPR[j] ~ dnegbin(prob.SPR[j], size.fec)
prob.SPR[j] <- size.fec/(size.fec + Seeds[j] * p.recrr[j])
p.recrr[j] <- recr.Intercept * mu.recrr[j] * dens.fac[j]

# Age-dependent density effects
dens.fac[j] <- 1/(1 + c[j]) * (recr.seed.dens * Seeds[j]/area.SPR[j] + recr.adult.dens *
Alive.SPR[j]/area.SPR[j])
log(c[j]) <- recr.log_PF_Age * log_PF_Age.SPR[j]

# Calculation of environmental effects (Gaussian response curves)
log(mu.recrr[j]) <- - recr.sc.log_AI * pow(recr.opt.log_AI - log_AI.SPR[j], 2)
- recr.sc.min_temp_jul * pow(recr.opt.min_temp_jul - min_temp_jul.SPR[j], 2)
- recr.sc.max_temp_jan * pow(recr.opt.max_temp_jan - max_temp_jan.SPR[j], 2)
- recr.sc.log_soil_fert * pow(recr.opt.log_soil_fert - log_soil_fert.SPR[j], 2)

# The expected number of seeds is predicted from the fecundity submodel (see above):
Seeds[j] <- mu.Fec.SPR[j] * Parents.SPR[j] * I.fec.SPR[j]
I.fec.SPR[j] ~ dbern(zi.fec.SPR[j])
zi.fec.SPR[j] <- (1 -exp(-(Age.mat.SPR[j]/zi.sc)^zi.sh))
log(mu.Fec.SPR[j]) <- fec.Intercept - fec.sc.log_AI * pow(fec.opt.log_AI - log_AI.SPR[j], 2)
- fec.sc.min_temp_jul * pow(fec.opt.min_temp_jul - min_temp_jul.SPR[j], 2)
- fec.sc.max_temp_jan * pow(fec.opt.max_temp_jan - max_temp_jan.SPR[j], 2)
- fec.sc.log_soil_fert * pow(fec.opt.log_soil_fert - log_soil_fert.SPR[j], 2)
+ fec.Age * Age.SPR[j] + fec.Age_2 * pow(Age.SPR[j], 2)
- fec.SP.dens * SP.dens.SPR[j]
}

### Survival submodel
for (k in 1:n.Surv){
# Binomial model for number of surviving adults
Alive.SURV[k] ~ dbin(p.surv[k], All_Adults.SURV[k])
p.surv[k] <- mu.surv[k] * surv.Intercept
# Calculation of environmental effects from Gaussian response curves
log(mu.surv[k]) <- - surv.sc.log_AI * pow(surv.opt.log_AI - log_AI.SURV[k], 2)
- surv.sc.min_temp_jul * pow(surv.opt.min_temp_jul - min_temp_jul.SURV[k], 2)
- surv.sc.max_temp_jan * pow(surv.opt.max_temp_jan - max_temp_jan.SURV[k], 2)
- surv.sc.log_soil_fert * pow(surv.opt.log_soil_fert - log_soil_fert.SURV[k], 2)
- surv.sc.Age * pow(surv.opt.Age - Age.SURV[k], 2)
- surv.SP.dens * SP.dens.SURV[j]
}

### Prior distributions
fec.opt.log_AI ~ dnorm(0, 0.0001)
fec.opt.min_temp_jul ~ dnorm(0, 0.0001)
fec.opt.max_temp_jan ~ dnorm(0, 0.0001)
fec.opt.log_soil_fert ~ dnorm(0, 0.0001)
recr.opt.log_AI ~ dnorm(0, 0.0001)
recr.opt.min_temp_jul ~ dnorm(0, 0.0001)
recr.opt.max_temp_jan ~ dnorm(0, 0.0001)
recr.opt.log_soil_fert ~ dnorm(0, 0.0001)
surv.opt.log_AI ~ dnorm(0, 0.0001)
surv.opt.min_temp_jul ~ dnorm(0, 0.0001)
surv.opt.max temp_jan ~ dnorm(0, 0.0001)
}
```

```

surv.opt.log_soil_fert ~ dnorm(0, 0.0001)
surv.opt.Age ~ dnorm(0, 0.0001)
fec.sc.log_AI ~ dexp(1)
fec.sc.min_temp_jul ~ dexp(1)
fec.sc.max_temp_jan ~ dexp(1)
fec.sc.log_soil_fert ~ dexp(1)
recr.sc.log_AI ~ dexp(1)
recr.sc.min_temp_jul ~ dexp(1)
recr.sc.max_temp_jan ~ dexp(1)
recr.sc.log_soil_fert ~ dexp(1)
surv.sc.log_AI ~ dexp(1)
surv.sc.min_temp_jul ~ dexp(1)
surv.sc.max_temp_jan ~ dexp(1)
surv.sc.log_soil_fert ~ dexp(1)
surv.sc.Age ~ dexp(1)
fec.Age ~ ddexp(0,1)
fec.Age_2 ~ ddexp(0,1) T(,0)
fec.SP.dens ~ dexp(1)
recr.seed.dens ~ dexp(1)
recr.adult.dens ~ dexp(1)
recr.log_PF_Age ~ dexp(1)
surv.SP.dens ~ dexp(1)
zi.sc ~ dgamma(0.01, 0.01)T(0.1,)
zi.sh ~ dgamma(0.01, 0.01)T(0.1,)
surv.Intercept ~ dbeta(1,1)
fec.Intercept ~ dnorm(0, 0.0001)
recr.Intercept ~ dbeta(1,1)
size.fec ~ dgamma(0.01,0.01)
}

```

2) Statistical analyses of relationships between life-history traits, demographic rates, niche characteristics and species geographic ranges.

We used identically structured normal linear regression models for analyzing effects of life-history traits on different response variables (maximum demographic rates, disturbance niche size, environmental niche size, potential range size, range filling, range size, see Tab. S3). In each case, we formulated a full model that included effects of persistence ability, dispersal ability and their interaction as well as all simplified models nested within this full model. Here we only document the full model structure.

In each regression model we accounted for both uncertainty in the response variable and phylogenetic dependence (56). To account for uncertainty in a response variable that was estimated in a previous analysis (demographic rates, sizes of niches, potential ranges and range filling) we do not directly regress point estimates (posterior means) against traits, but treat the true value of the response variable as a latent variable that is known only up to a certain precision (species-specific posterior variance analog to a measurement error). Hence, the likelihood of the previously estimated species-specific posterior means (**Y.mean**) of the response variable depends on the vector of its true (but unknown) values **Y** and the respective posterior variances (**Y.var**):

$$\mathbf{Y.mean} \mid \mathbf{Y}, \mathbf{Y.var} \sim \text{Normal}(\mathbf{Y}, \mathbf{Y.var})$$

For the latent variable **Y** we then formulated a multivariate normal regression model

$$\mathbf{Y} \mid \mathbf{X}, \boldsymbol{\beta}, \sigma, \boldsymbol{\Sigma}, \lambda \sim \text{MVN}(\mathbf{X}\boldsymbol{\beta}, \sigma^2\boldsymbol{\Sigma}_\lambda)$$

where $\mathbf{X}\boldsymbol{\beta}$ is the linear predictor of the regression against traits (persistence ability, dispersal ability and their interaction) and $\boldsymbol{\Sigma}_\lambda$ is an adjusted variance-covariance matrix to account for phylogenetic dependencies. Based on a molecular phylogeny of our study species (Fig. S8), we first calculated the variance-covariance matrix $\boldsymbol{\Sigma}$ under a Brownian motion model using R package *ape* (57). As quantitative measure of the degree of phylogenetic dependence the model

furthermore includes Pagel's λ (ranging from zero to one) (52) and the adjusted Σ_λ is calculated as $\Sigma_\lambda = \lambda\Sigma + (1 - \lambda)\mathbf{I}$, where \mathbf{I} is the identity matrix.

Bayesian parameter estimations were performed in JAGS using largely uninformative prior distributions (see table below). For each model we ran three independent MCMC chains with 200,000 iterations, the first half of which was discarded as burn-in and convergence was checked by the multivariate scale reduction factor being smaller than 1.1 (55).

Data variables for the regression of niche and range characteristics against life history traits

Variable name [dimensions]	Description	Text symbol
n.Spec	number of species (26)	
Y.mean[n.Spec]	response variable (posterior means)	Y.mean
Y.Var[n.Spec, n.Spec]	uncertainty of the response variable (posterior variances as diagonal matrix)	Y.var
Disp[n.Spec]	species' dispersal ability (log-transformed and scaled)	
Pers[n.Spec]	species' persistence ability (0 = nonsprouter, 1 = resprouter)	
A[n.Spec, n.Spec]	unadjusted covariance matrix	Σ
ID[n.Spec, n.Spec]	identity matrix	I

In this table 'Variable name' refers to a variable in the JAGS code (see below) and 'Text symbol' refers to the corresponding notation in the Methods section, if applicable. Note that for the response variable 'range size' we have no quantification of interspecific variation in precision (i.e. posterior variances) and thus Y.Var was set to zero in those analyses.

Parameters for the regression of niche and range characteristics against life history traits

Parameter name	Variable name	Description	Prior distribution	Prior parameters
β_0	alpha	intercept	Normal	$\mu = 0, \sigma^2 = 10^4$
β_{Disp}	beta.D	effect of dispersal ability	Normal	$\mu = 0, \sigma^2 = 10^4$
β_{Pers}	beta.P	effect of persistence ability	Normal	$\mu = 0, \sigma^2 = 10^4$
$\beta_{Disp:Pers}$	beta.DP	interaction effect	Normal	$\mu = 0, \sigma^2 = 10^4$
λ	lambda	Pagel's λ	Beta	a = 2, b = 2
σ^2	sig2	residual variance	Inv.-Gamma	$\alpha = 0.01, \beta = 0.01$

In this table 'Parameter name' refers to the notation in the Methods (and Tab. S3) and 'Variable name' to the corresponding variable in the JAGS code (see below).

JAGS code for the regression of niche and range characteristics against life history traits (full model)

```

model {
# Multivariate normal model
Y.mean[1:n.Spec] ~ dnmnorm(mu[],TAU[,])

# Linear predictor for each species
for (i in 1:n.Spec) {
  mu[i] <- alpha + beta.D*Disp[i] + beta.P*Pers[i] + beta.DP*Disp[i]*Pers[i]
}

# Calculation of the adjusted, combined covariance matrix
Mlam <- sig2*(lambda*A[,] + (1-lambda)*ID) + Y.Var[,]
TAU <- inverse(Mlam)

### Prior distributions
alpha ~ dnorm(0, 1.0E-04)
beta.D ~ dnorm(0, 1.0E-04)
beta.P ~ dnorm(0, 1.0E-04)
beta.DP ~ dnorm(0, 1.0E-04)
lambda ~ dbeta(2,2)
tau ~ dgamma(0.01,0.01)
sig2 <- 1/tau
}

```

3) Statistical analysis of the relationship between occupancy and demographic suitability

We used a binomial non-linear regression model to analyse the relationship between each species' occupancy in the $1' \times 1'$ grid cells within its geographic range and the respective predicted intrinsic population growth rate r_0 . The model describes the number of presence records ($y_{s,i}$) for species s in the grid cell i as

$$y_{s,i} \sim \text{Binomial}(\psi_{s,i}, N_i)$$

$$\psi_{s,i} = a_s / (1 + \exp(-b_s(r_{0s,i} - c_s)))$$

where N_i is the number of Protea Atlas sampling locations within the grid cell. The regression is performed jointly for all species, while estimating species-specific values for the regression parameters (a_s , b_s , c_s). In order to allow predictions of the average relationships between occupancy and demographic suitability for different persistence abilities (Fig. 3b), the model includes separate hyperparameters for the mean of each regression parameter among nonsprouter resp. resprouter species.

Bayesian parameter estimation was performed in JAGS using largely uninformative prior distributions (see table below). We ran three independent MCMC chains with 20,000 iterations, the first half of which was discarded as burn-in and convergence was checked by the multivariate scale reduction factor being smaller than 1.1 (55).

Data variables for the regression of occupancy against demographic suitability

Variable name [dimensions]	Description	Text symbol
n.Dat	number of data points (91288) (species-grid cell combinations)	
vis[n.Dat]	number of presence-absence data (Protea Atlas records) in the grid cell	N
pres[n.Dat]	number of recorded species presences in the grid cell	y
R[n.Dat]	predicted demographic suitability	r_0
SP[n.Dat]	numerical species index	s
n.Spec	number of species (26)	
Pers[n.Spec]	species' persistence ability (0 = nonsprouter, 1 = resprouter)	

In this table 'Variable name' refers to a variable in the JAGS code (see below) and 'Text symbol' refers to the corresponding notation in the Methods section, if applicable.

Parameters for the regression of occupancy against demographic suitability

Parameter name	Variable name	Description	Prior distribution	Prior parameters
<i>a</i>	a[n.Spec]	species-specific regression parameter <i>a</i>		
	MU.a[2]	mean of logit(<i>a</i>) for nonsprouters resp. sprouters	Normal	$\mu = 0, \sigma^2 = 10^4$
	sig2.a	interspecific variation in logit(<i>a</i>)	Inv.-Gamma	$\alpha = 0.01, \beta = 0.01$
<i>b</i>	b[n.Spec]	species-specific regression parameter <i>b</i>		
	MU.b[2]	mean of log(<i>b</i>) for nonsprouters resp. sprouters	Normal	$\mu = 0, \sigma^2 = 10^4$
	sig2.b	interspecific variation in log(<i>b</i>)	Inv.-Gamma	$\alpha = 0.01, \beta = 0.01$
<i>c</i>	c[n.Spec]	species-specific regression parameter <i>c</i>		
	MU.c[2]	mean of <i>c</i> for nonsprouters resp. sprouters	Normal	$\mu = 0, \sigma^2 = 10^4$
	sig2.c	interspecific variation in <i>c</i>	Inv.-Gamma	$\alpha = 0.01, \beta = 0.01$

In this table 'Parameter name' refers to the notation in the Methods and 'Variable name' to the corresponding variable in the JAGS code (see below). Note that prior distributions are not specified for the species-specific regression parameters, but for the hyperparameters that describe interspecific variation in regression parameters.

JAGS code for the regression of occupancy against demographic suitability

```
model {
# Non-linear regression of occupancy against r0 for each species-site combination
for (i in 1: n.Dat) {
  pres[i] ~ dbin(psi[i],vis[i])
  psi[i] <- a[SP[i]]/(1 + exp(-b[SP[i]]*(R[i] - c[SP[i]])))
}

# Interspecific variation in regression parameters a, b, c
for (sp in 1:n.Spec) {
  logit(a[sp]) <- logit.a[sp]
  logit.a[sp] ~ dnorm(mu.a[sp], tau.a)
  mu.a[sp] <- MU.a[Pers[sp] + 1]

  log(b[sp]) <- log.b[sp]
  log.b[sp] ~ dnorm(mu.b[sp], tau.b)
  mu.b[sp] <- MU.b[Pers[sp] + 1]

  c[sp] ~ dnorm(mu.c[sp], tau.c)
  mu.c[sp] <- MU.c[Pers[sp] + 1]
}

### Prior distributions
MU.a[1] ~ dnorm(0,1.0E-04)
MU.a[2] ~ dnorm(0,1.0E-04)
tau.a ~ dgamma(0.01,0.01)
sig2.a <- 1/tau.a
MU.b[1] ~ dnorm(0,1.0E-04)
MU.b[2] ~ dnorm(0,1.0E-04)
tau.b ~ dgamma(0.01,0.01)
sig2.b <- 1/tau.b
MU.c[1] ~ dnorm(0,1.0E-04)
MU.c[2] ~ dnorm(0,1.0E-04)
tau.c ~ dgamma(0.01,0.01)
sig2.c <- 1/tau.c
}
```

4) Additional analyses for alternative calculations of range filling

In addition to our analysis of range filling that identified potentially suitable area as grid cells with a predicted positive intrinsic growth rate of small populations ($r_0 > 0$, see *Species distribution data, geographic ranges and range filling* in the *Materials and Methods*) we also applied two alternative approaches for quantifying species' range filling.

Adjusted r_0 -thresholds

First, we tested whether potential species-specific biases in predicted r_0 could affect the analysis of interspecific variation in range filling. In particular, a spurious positive correlation between dispersal ability and range filling could emerge if our demographic response model systematically over-predicted r_0 for species with low dispersal ability, thus predicting a larger potential range and lower range filling for these species. To test this, we alternatively quantified range-filling based on species-specific adjusted r_0 -thresholds. These thresholds were calibrated to each species' occurrence data. For each posterior prediction of spatial variation in r_0 , we generated binary predictions of potentially suitable area by applying various r_0 -thresholds and then calculated the true-skill-statistic (TSS) (58) to assess the agreement between predicted suitability and the observed presence-absence of the species across the study region ($1' \times 1'$ grid cells). We chose the r_0 -threshold that maximized TSS. These r_0 -thresholds varied across species (-0.18 - 0.23, mean = 0.03, Fig. S3a), but were not correlated with species' dispersal ability (Spearman's $\rho = 0.20$, $p = 0.32$). Range filling that was then estimated based on the chosen r_0 -thresholds and the resulting potentially suitable areas showed interspecific variation very similar to the range filling based on the original r_0 -threshold of zero (Fig. S3b). A regression of the alternative range filling values against species' life-history traits (see *Statistical analyses of relationships between life-history traits, demographic rates, niche characteristics and species geographic ranges*) identified again a DIC-minimal model that includes a significant positive effect of dispersal ability ($p = 0.009$, Fig. S3c) and no effects of persistence ability (Parameter posterior means \pm standard deviations: $\beta_0 = -0.22 \pm 0.36$, $\beta_{\text{Disp}} = 0.64 \pm 0.27$, $\Lambda = 0.24 \pm 0.19$, $\sigma = 1.12 \pm 0.24$; see Tab. S3 for comparison).

Standard species distribution models

Secondly, we quantified range filling based on simple species distribution models (SDMs) that were directly fitted to the presence-absence data (per $1' \times 1'$ grid cell of the study region) of each species. As a standard SDM approach we used generalized linear regression models with a binomial error distribution and a logit-link (59). By including linear and quadratic effects of each of the four climatic-edaphic covariates and of the mean of the site-specific probability distributions of fire return intervals, these models can describe occurrence-environment relationships in a functionally similar way as in the demographic response models. Species-specific regression parameters were estimated using the function *glm* in the statistical software R (60). We translated SDM predictions (occurrence probability per grid cell) into binary predictions of potentially suitable area by again selecting the threshold that maximized the agreement (TSS, see above) with the observed presence-absence of each species. Range filling was then calculated

as the proportion of this potentially suitable area that lies within the geographic range, as before. As expected, predictions of suitable area from the SDMs that were directly fitted to species occurrence data indicated a generally higher degree of range filling across species (Fig. S3b). A regression of the alternative range filling values against species' life-history traits (see *Statistical analyses of relationships between life-history traits, demographic rates, niche characteristics and species geographic ranges*) identified again a DIC-minimal model that includes an effect of dispersal ability and no effects of persistence ability (Parameter posterior means \pm standard deviations: $\beta_0 = 1.21 \pm 0.39$, $\beta_{\text{Disp}} = 0.42 \pm 0.24$, $\Lambda = 0.33 \pm 0.22$, $\sigma = 1.20 \pm 0.21$; see Tab. S3 for comparison), but the weaker effect of species' dispersal ability on range filling was not significant ($p = 0.073$, Fig. S3d).

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Supplementary Tables

Table S1. Overview of study species, samples sizes of demographic data and geographic distribution data

Species	Resprouting ability	No. sampled populations	Sample sizes of demographic data			No. presence records*	Geographic range size (km ²) [†]
			Fecundity	Recruitment	Survival		
<i>Leucadendron album</i>	nonsprouter	48	41	22	15	672	8,720
<i>Leucadendron coniferum</i>	nonsprouter	68	45	23	0	793	3,075
<i>Leucadendron eucalyptifolium</i>	nonsprouter	70	19	51	0	5,248	26,157
<i>Leucadendron lauroleum</i>	nonsprouter	75	68	28	23	3,453	8,658
<i>Leucadendron modestum</i>	nonsprouter	80	76	18	14	647	3,576
<i>Leucadendron muiirii</i>	nonsprouter	80	70	16	6	599	2,956
<i>Leucadendron rubrum</i>	nonsprouter	136	69	77	17	4,634	36,220
<i>Leucadendron salignum</i>	resprouter	141	99	79	77	24,373	60,228
<i>Leucadendron spissifolium</i>	resprouter	90	80	37	36	4,676	35,653
<i>Leucadendron xanthoconus</i>	nonsprouter	85	61	38	16	7,170	5,999
<i>Protea acaulos</i>	resprouter	89	80	51	47	3,802	17,408
<i>Protea amplexicaulis</i>	nonsprouter	77	74	22	26	1,242	8,879
<i>Protea compacta</i>	nonsprouter	85	77	30	22	902	3,226
<i>Protea cynaroides</i>	resprouter	86	83	27	24	8,488	33,533
<i>Protea eximia</i>	nonsprouter	98	53	47	2	2,391	22,995
<i>Protea laurifolia</i>	nonsprouter	100	78	38	20	10,934	25,516
<i>Protea longifolia</i>	nonsprouter	84	78	34	28	1,635	5,234
<i>Protea lorifolia</i>	nonsprouter	142	54	91	4	5,259	24,904
<i>Protea neriifolia</i>	nonsprouter	150	68	95	16	6,382	30,129
<i>Protea nitida</i>	resprouter	83	76	30	30	9,943	42,426
<i>Protea obtusifolia</i>	nonsprouter	83	62	27	7	1,337	5,262
<i>Protea punctata</i>	nonsprouter	85	50	37	2	2,319	21,546
<i>Protea repens</i>	nonsprouter	292	104	224	42	15,291	59,077
<i>Protea scabra</i>	resprouter	92	85	65	65	2,254	5,970
<i>Protea scolopendriifolia</i>	resprouter	76	76	30	30	1,283	21,444
<i>Protea susannae</i>	nonsprouter	83	48	36	1	963	5,112

* Protea Atlas data base (17)

[†] Approximate geographic range size was calculated as overlap between an alpha-convex hull over the presence records of a species and the Fynbos biome (study region).

Table S2. Explained intraspecific variation in demographic rates and occurrence

Species	Demographic rates (R^2_N)			Presence-absence (AUC)	Within-range occupancy (R^2_N)
	Fecundity	Recruitment	Survival*		
<i>Leucadendron album</i>	0.91	0.69	-	0.96	0.55
<i>Leucadendron coniferum</i>	0.38	0.46	-	0.95	0.30
<i>Leucadendron eucalyptifolium</i>	0.38	0.38	-	0.75	0.34
<i>Leucadendron laureolum</i>	0.29	0.45	-	0.87	0.01
<i>Leucadendron modestum</i>	0.43	0.84	-	0.93	0.46
<i>Leucadendron muirii</i>	0.34	0.36	-	0.96	0.22
<i>Leucadendron rubrum</i>	0.48	0.05	-	0.64	0.04
<i>Leucadendron salignum</i>	0.69	0.26	0.52	0.54	0.06
<i>Leucadendron spissifolium</i>	0.80	0.45	0.52	0.59	0.20
<i>Leucadendron xanthoconus</i>	0.56	0.44	-	0.92	0.27
<i>Protea acaulos</i>	0.53	0.32	-	0.69	0.01
<i>Protea amplexicaulis</i>	0.81	0.53	-	0.70	0.15
<i>Protea compacta</i>	0.59	0.66	-	0.93	0.05
<i>Protea cynaroides</i>	0.71	0.61	0.64	0.69	0.11
<i>Protea eximia</i>	0.67	0.48	-	0.70	0.12
<i>Protea laurifolia</i>	0.55	0.12	-	0.55	0.01
<i>Protea longifolia</i>	0.48	0.36	-	0.92	0.27
<i>Protea lorifolia</i>	0.62	0.30	-	0.77	0.07
<i>Protea neriifolia</i>	0.44	0.38	-	0.69	0.20
<i>Protea nitida</i>	0.70	0.23	0.41	0.57	0.17
<i>Protea obtusifolia</i>	0.51	0.50	-	0.95	0.26
<i>Protea punctata</i>	0.53	0.47	-	0.74	0.43
<i>Protea repens</i>	0.73	0.17	-	0.59	0.11
<i>Protea scabra</i>	0.63	0.51	0.81	0.53	0.02
<i>Protea scolopendriifolia</i>	0.69	0.50	0.83	0.73	0.01
<i>Protea susannae</i>	0.60	0.46	-	0.97	0.28

*Note that intraspecific variation in adult fire survival rates was modelled only for resprouter species but not for nonsprouter species (indicated by '-') that have very low fire survival rates with little intraspecific variation (19).

Table S3. Effects of life history traits on maximum demographic rates and the sizes of ecological niches and geographic ranges

Response variable	Model parameters					
	β_0	β_{Disp}	β_{Pers}	$\beta_{Disp:Pers}$	Λ	σ
Maximum fecundity (log)	9.10 ± 0.45	-	-1.03 ± 0.81	-	0.64 ± 0.26	0.77 ± 0.22
Maximum establishment rate (logit)	0.78 ± 0.41	-	-	-	0.59 ± 0.28	0.69 ± 0.19
Maximum survival rate (logit)	-4.70 ± 0.42	-	10.67 ± 0.65	-	0.41 ± 0.23	1.00 ± 0.23
Disturbance niche size (logit)	0.55 ± 0.23	-	1.34 ± 0.41	-	0.82 ± 0.19	0.52 ± 0.11
Environmental niche size (logit)	-1.42 ± 0.60	1.00 ± 0.40	-	-	0.30 ± 0.21	1.78 ± 0.42
Potential range size (log)	8.81 ± 0.35	0.30 ± 0.19	-	-	0.40 ± 0.24	0.97 ± 0.20
Range filling (logit)	0.12 ± 0.49	0.58 ± 0.29	-	-	0.45 ± 0.25	1.33 ± 0.27
Range size (log)	7.78 ± 0.39	0.46 ± 0.24	1.08 ± 0.54	-	0.23 ± 0.18	1.20 ± 0.21

Effects of life history traits on each of the different response variables were estimated by Bayesian normal linear regression analysis with model selection. Each full model included main effects of dispersal ability (*Disp*) and persistence ability (*Pers*; coded as 0 = nonsprouter, 1 = resprouter) as well as their interaction. All simplified models nested in the full model were compared by the deviance information criteria (DIC) and estimated parameters (posterior mean ± standard deviation) are shown for the respective DIC-minimal model ('-' indicates non-included terms). Significant regression coefficients (95% credibility interval does not overlap with zero) are in bold font. All models corrected for phylogenetic relatedness by estimating Pagel's Λ . σ denotes the residual standard deviation.

Table S4. Model evaluation for populations established outside the species' geographic ranges

Species	No. populations	Proportion with $r_0 > 0$
<i>Protea eximia</i>	206	89%
<i>Protea compacta</i>	162	35%
<i>Protea neriifolia</i>	90	100%
<i>Protea laurifolia</i>	48	100%
<i>Protea susannae</i>	36	31%
<i>Leucadendron coniferum</i>	25	20%
<i>Leucadendron laeololum</i>	25	92%
<i>Protea lorifolia</i>	21	81%
<i>Protea obtusifolia</i>	13	62%
<i>Leucadendron eucalyptifolium</i>	8	100%
<i>Protea longifolia</i>	7	100%
<i>Leucadendron xanthoconus</i>	6	67%
<i>Protea punctata</i>	6	83%
<i>Protea cynaroides</i>	4	75%
<i>Leucadendron rubrum</i>	2	100%
<i>Leucadendron muirii</i>	1	100%
<i>Protea amplexicaulis</i>	1	100%
<i>Leucadendron album</i>	0	n.a.
<i>Leucadendron modestum</i>	0	n.a.
<i>Leucadendron salignum</i>	0	n.a.
<i>Leucadendron spissifolium</i>	0	n.a.
<i>Protea acaulos</i>	0	n.a.
<i>Protea nitida</i>	0	n.a.
<i>Protea repens</i>	0	n.a.
<i>Protea scabra</i>	0	n.a.
<i>Protea scolopendriifolia</i>	0	n.a.

The table shows for each species the number of recorded populations that were established outside their respective geographic range (17). We evaluated model predictions of the intrinsic population growth rate r_0 for the locations of these populations and report here for each species the proportion of populations for which a positive growth rate (demographic suitability) was predicted.

Table S5. Correlation (Spearman's rho) between observed population densities and each of the environmental variables for the sampling sites of each study species.

Species	Aridity	Tmin	Tmax	Soil fertility index*	Fire return interval
<i>Leucadendron album</i>	0.08	0.17	-0.14	n.a.	0.26
<i>Leucadendron coniferum</i>	0.23	0.20	0.16	0.21	-0.04
<i>Leucadendron eucalyptifolium</i>	0.14	-0.01	0.08	0.22	-0.28
<i>Leucadendron laureolum</i>	-0.24	-0.26	-0.08	-0.08	-0.01
<i>Leucadendron modestum</i>	-0.01	-0.17	0.10	0.04	-0.11
<i>Leucadendron muirii</i>	-0.29	-0.04	0.17	n.a.	-0.17
<i>Leucadendron rubrum</i>	0.06	0.11	-0.01	-0.03	-0.25
<i>Leucadendron salignum</i>	0.05	0.05	-0.11	-0.21	-0.21
<i>Leucadendron spissifolium</i>	0.13	0.08	0.08	0.23	-0.07
<i>Leucadendron xanthoconus</i>	-0.26	-0.07	0.00	0.01	-0.27
<i>Protea acaulos</i>	-0.20	0.01	0.00	-0.06	-0.09
<i>Protea amplexicaulis</i>	-0.23	0.06	0.33	-0.06	0.12
<i>Protea compacta</i>	-0.19	-0.15	0.08	0.03	-0.39
<i>Protea cynaroides</i>	0.42	-0.11	0.20	0.17	-0.15
<i>Protea eximia</i>	-0.04	0.01	0.04	0.22	-0.30
<i>Protea laurifolia</i>	-0.02	0.11	0.08	-0.06	-0.34
<i>Protea longifolia</i>	0.12	0.00	0.01	0.02	-0.11
<i>Protea lorifolia</i>	0.08	-0.07	0.10	-0.17	-0.06
<i>Protea neriifolia</i>	0.16	0.08	0.07	0.12	-0.15
<i>Protea nitida</i>	0.16	0.24	-0.23	-0.32	-0.39
<i>Protea obtusifolia</i>	0.22	-0.11	-0.15	0.05	-0.31
<i>Protea punctata</i>	0.04	-0.06	-0.11	-0.09	-0.10
<i>Protea repens</i>	0.03	0.05	0.07	0.12	-0.06
<i>Protea scabra</i>	0.01	-0.05	0.30	-0.05	-0.14
<i>Protea scolopendriifolia</i>	-0.43	0.06	-0.16	0.34	-0.19
<i>Protea susannae</i>	-0.13	0.12	0.05	0.15	-0.06

* Note that for two small-ranged study species (*Leucadendron album* and *Leucadendron muirii*) the soil fertility index did not vary across the sampled populations and thus no correlation could be estimated.

Table S6. Prior distributions for parameters of the demographic response model

Model parameter	Description	Prior distribution	Prior parameters
Fecundity	$\log(max.fec)$	maximum fecundity (log)	Normal $\mu = 0, \sigma^2 = 10^4$
	$opt.fec_k$	environmental optima	Normal $\mu = 0, \sigma^2 = 10^4$
	$1/sig.fec_k^2$	environmental response strengths	Exponential $\lambda = 1$
	$\beta.fec$	age effects	Double-Exponential $\mu = 0, \lambda = 1$
	$sh.mat$	Weibull parameters for age of maturity	Gamma $\alpha = 0.01, \beta = 0.01$
	$sc.mat$		Gamma $\alpha = 0.01, \beta = 0.01$
	$\gamma.fec$	strength of density effects	Exponential $\lambda = 1$
	$k.fec$	overdispersion parameter	Gamma $\alpha = 0.01, \beta = 0.01$
Establishment	$max.est$	maximum establishment rate	Beta $a = 1, b = 1$
	$opt.est_k$	environmental optima	Normal $\mu = 0, \sigma^2 = 10^4$
	$1/sig.est_k^2$	environmental response strengths	Exponential $\lambda = 1$
	$\beta.est$	effect of time since fire	Exponential $\lambda = 1$
	$\gamma.est.SD$	strength of density effects from seeds	Exponential $\lambda = 1$
	$\gamma.est.AD$	strength of density effects from adults	Exponential $\lambda = 1$
Survival	$max.surv$	maximum survival rate	Beta $a = 1, b = 1$
	$opt.surv_k$	environmental optima	Normal $\mu = 0, \sigma^2 = 10^4$
	$1/sig.surv_k^2$	environmental response strengths	Exponential $\lambda = 1$
	$opt.surv_{Age}$	age optimum	Normal $\mu = 0, \sigma^2 = 10^4$
	$1/sig.surv_{Age}$	age response strengths	Exponential $\lambda = 1$
	$\gamma.surv$	strength of density effects	Exponential $\lambda = 1$

Supplementary Figures

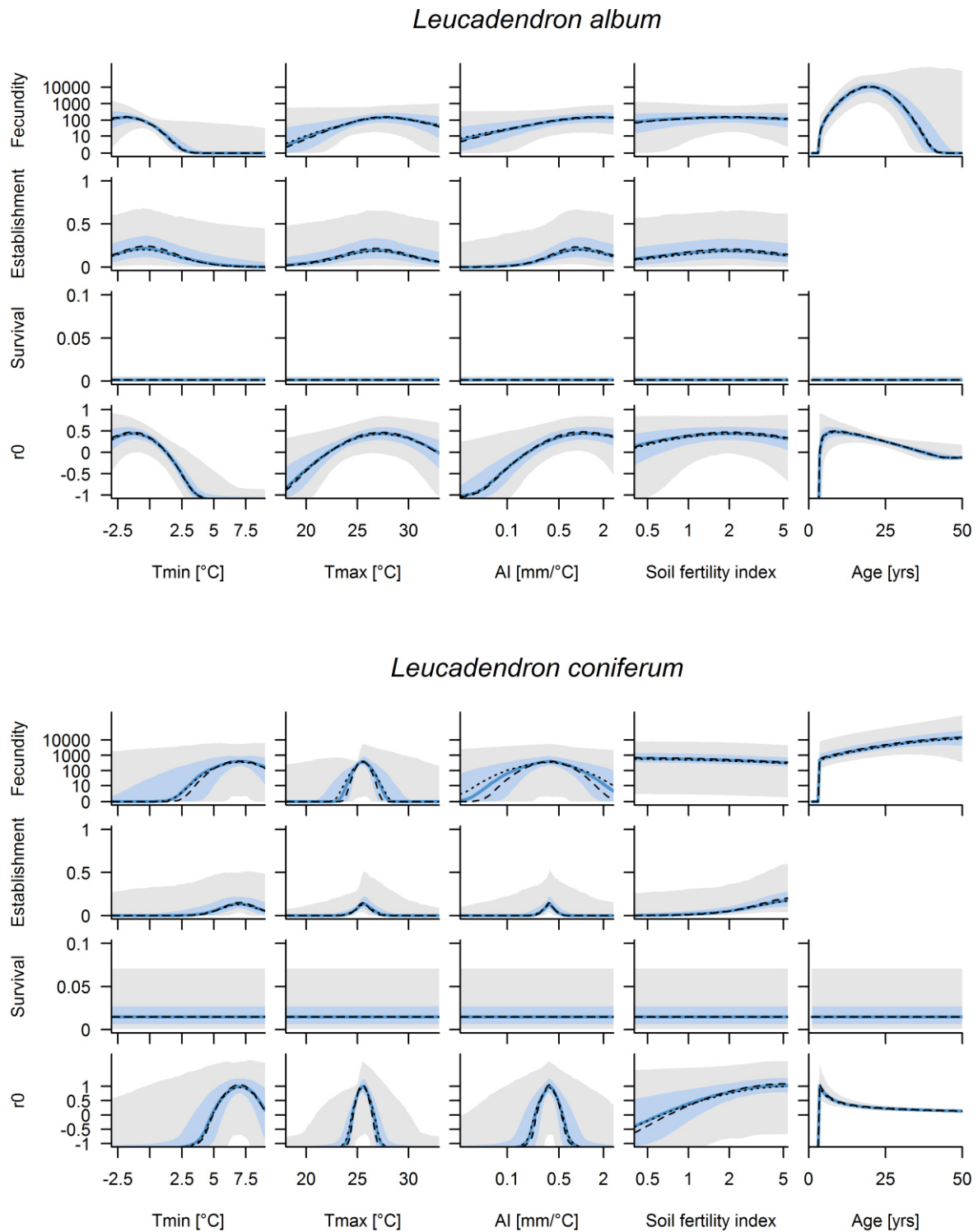
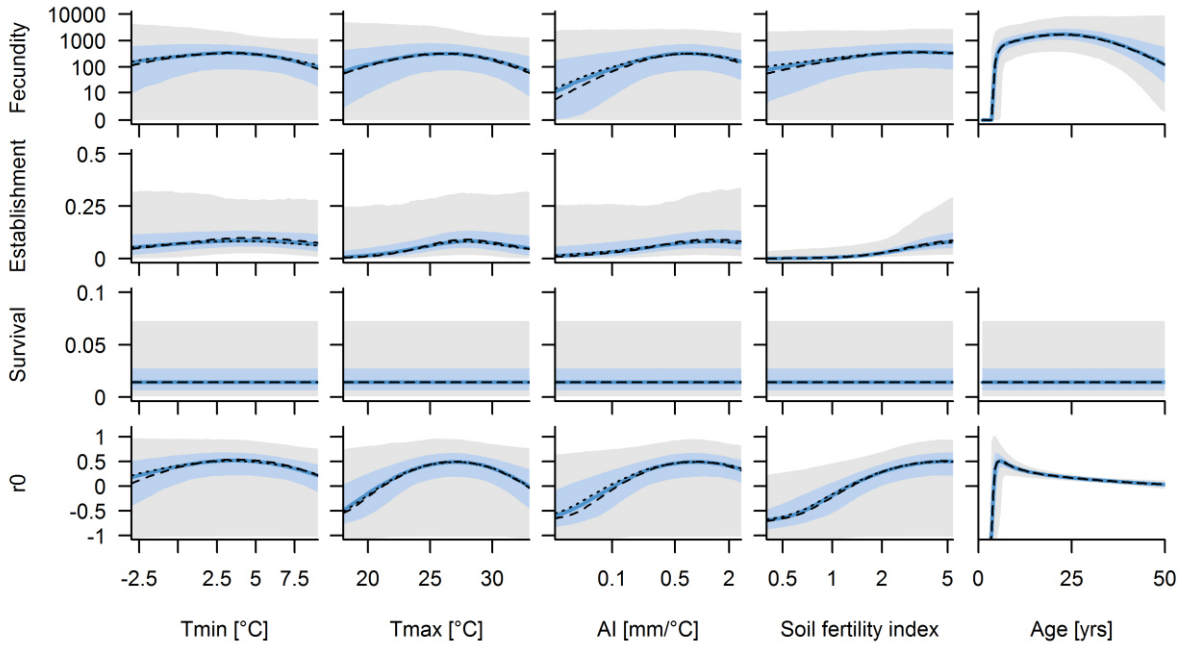


Fig. S1. Responses of demographic rates (μ_{fec} , π_{recr} , π_{surv}) and intrinsic population growth rate r_0 to environmental covariates. Blue lines show the posterior median of predicted rates and the shaded areas the 50% (dark shading) and 95% (light shading) credibility intervals. Response curves were generated by varying each covariate over the range of environmental conditions in the study region while keeping other covariates at the value that optimizes r_0 . The sensitivity of estimated response curves to the chosen parameter prior distribution was investigated by estimating response curves also for alternative variances of the normal prior distributions for the environmental optima (opt_{fec} , opt_{est} , opt_{surv}). Black lines show the posterior median of predicted rates when the original prior variance of 10^4 was changed to either 10^2 (dashed line) or 10^6 (dotted line).

Leucadendron eucalyptifolium



Leucadendron laureolum

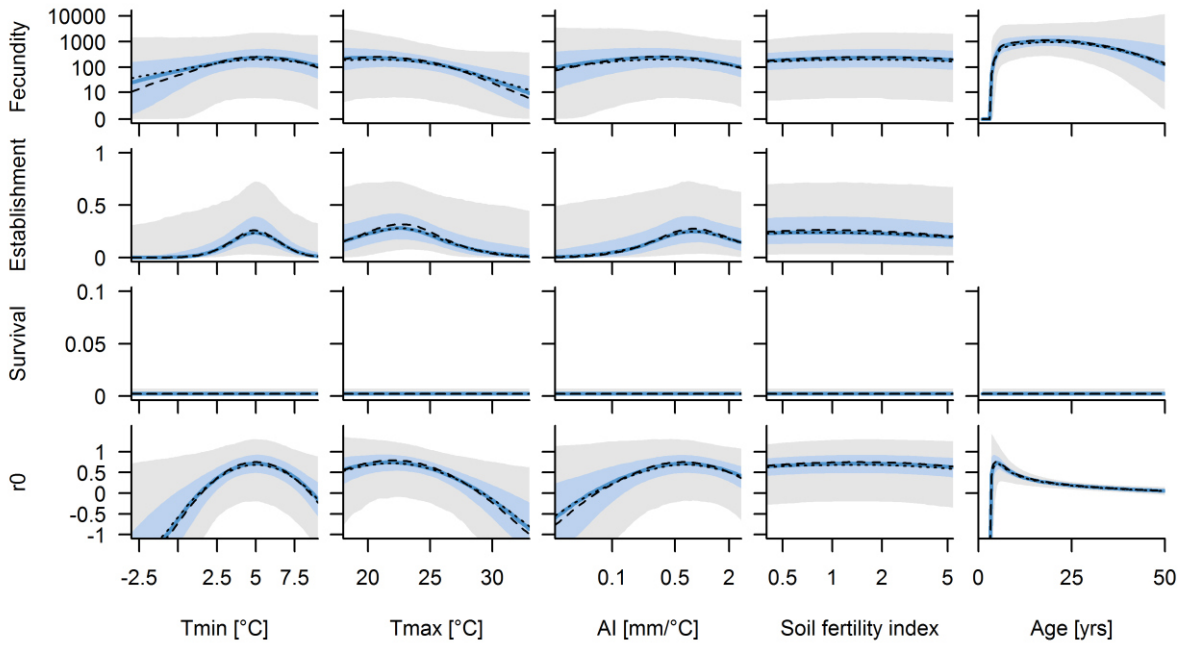
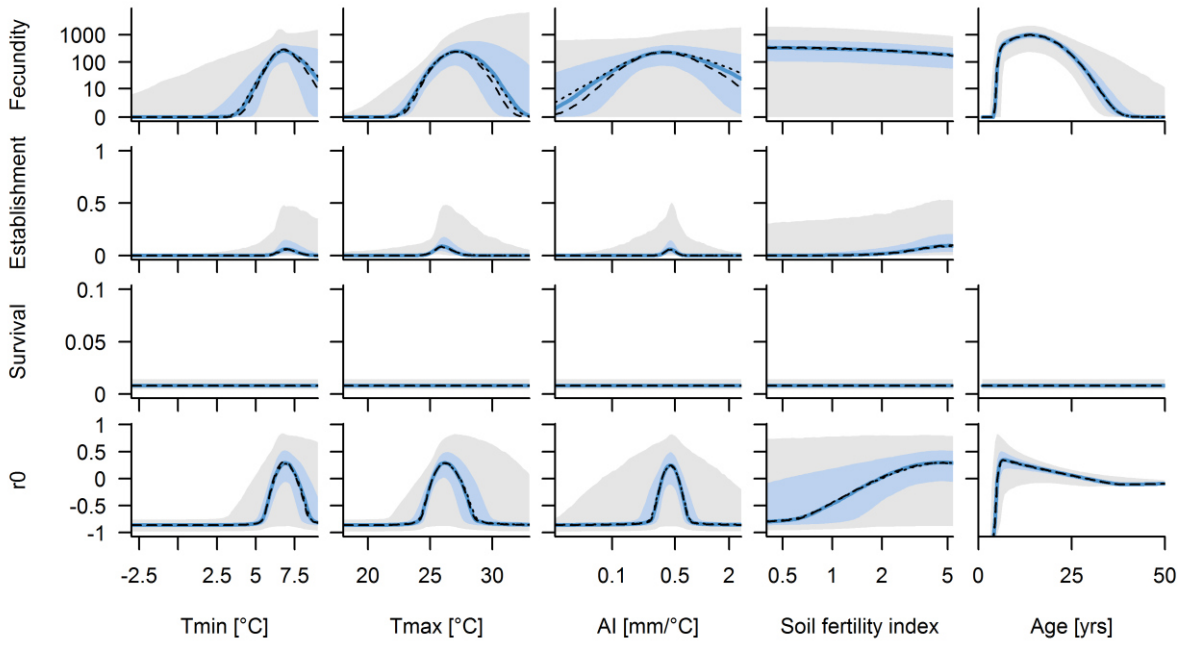


Fig. S1. (continued)

Leucadendron modestum



Leucadendron muiirii

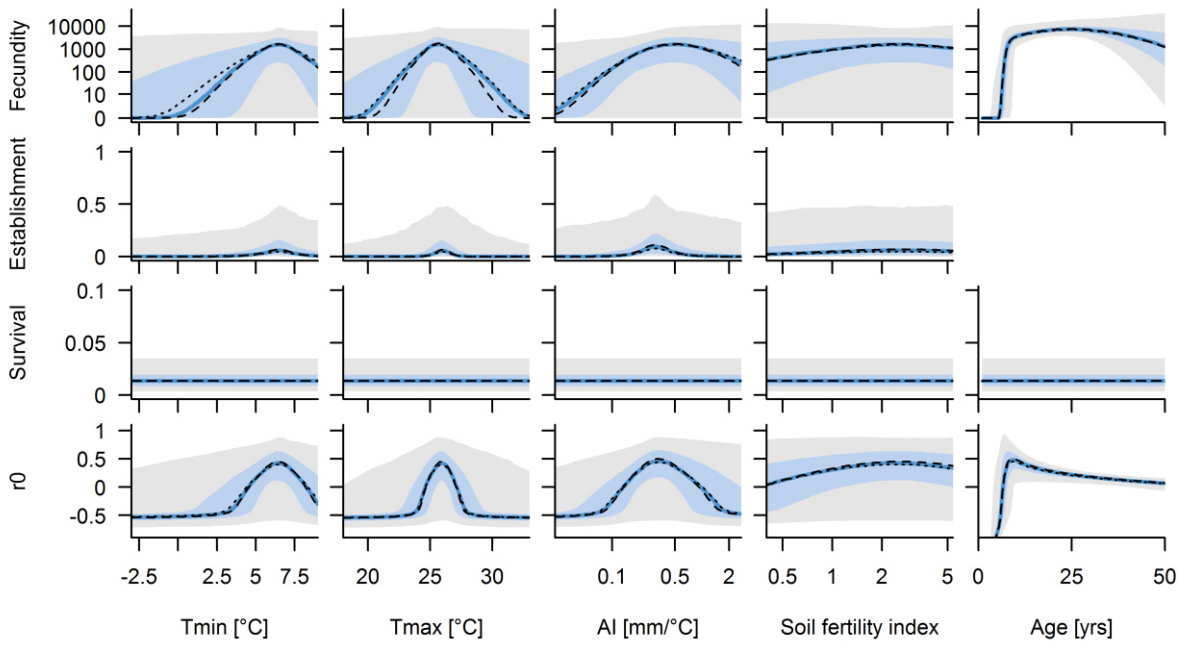
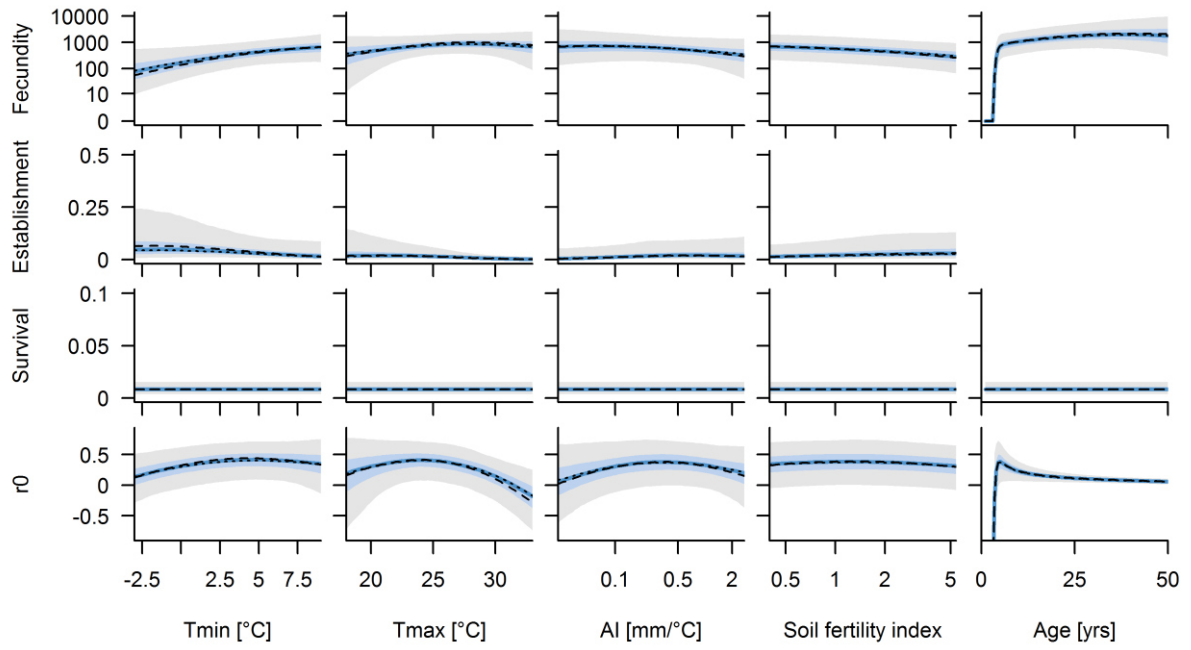


Fig. S1. (continued)

Leucadendron rubrum



Leucadendron salignum

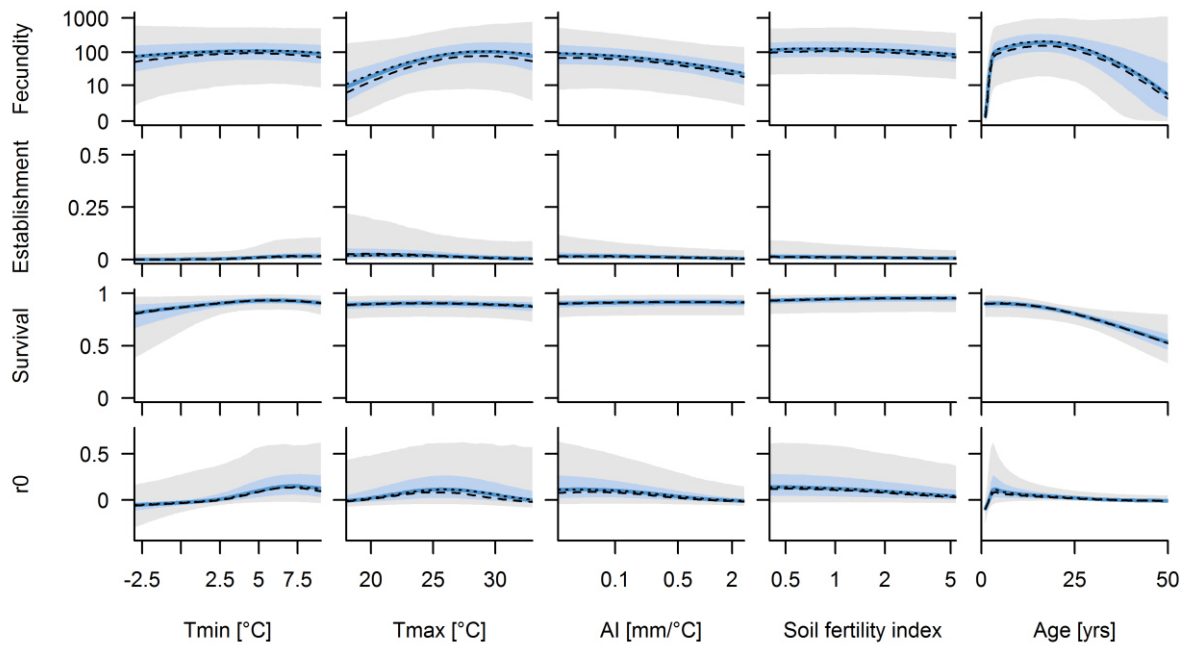
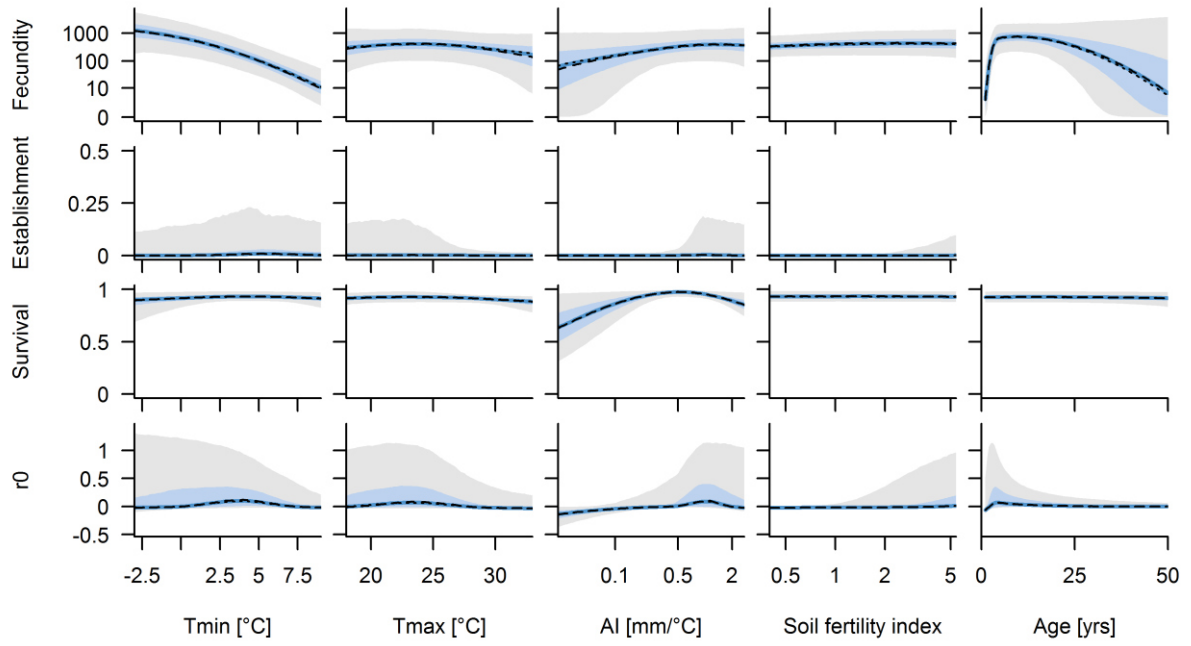


Fig. S1. (continued)

Leucadendron spissifolium



Leucadendron xanthoconus

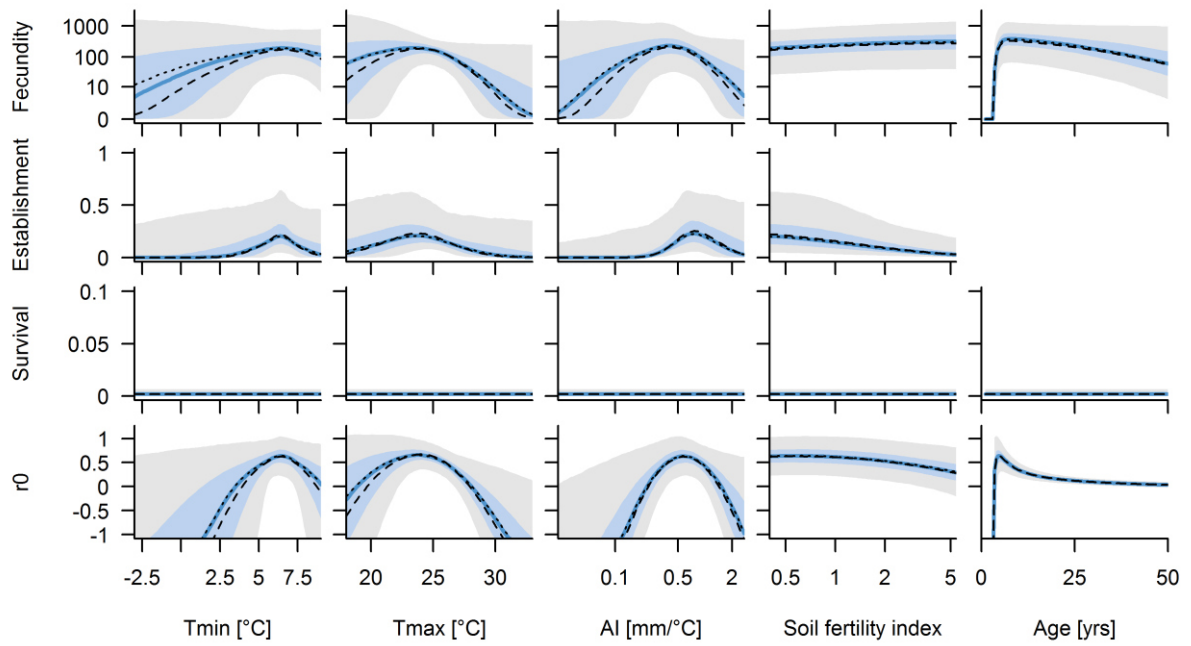


Fig. S1. (continued)

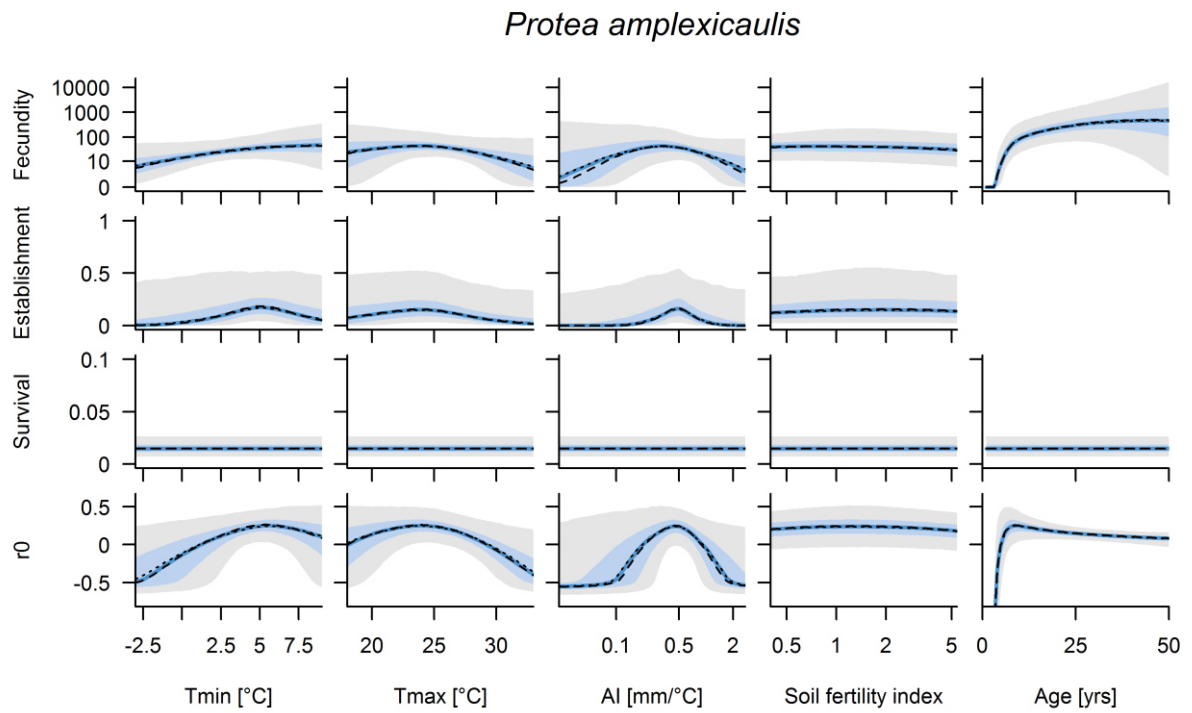
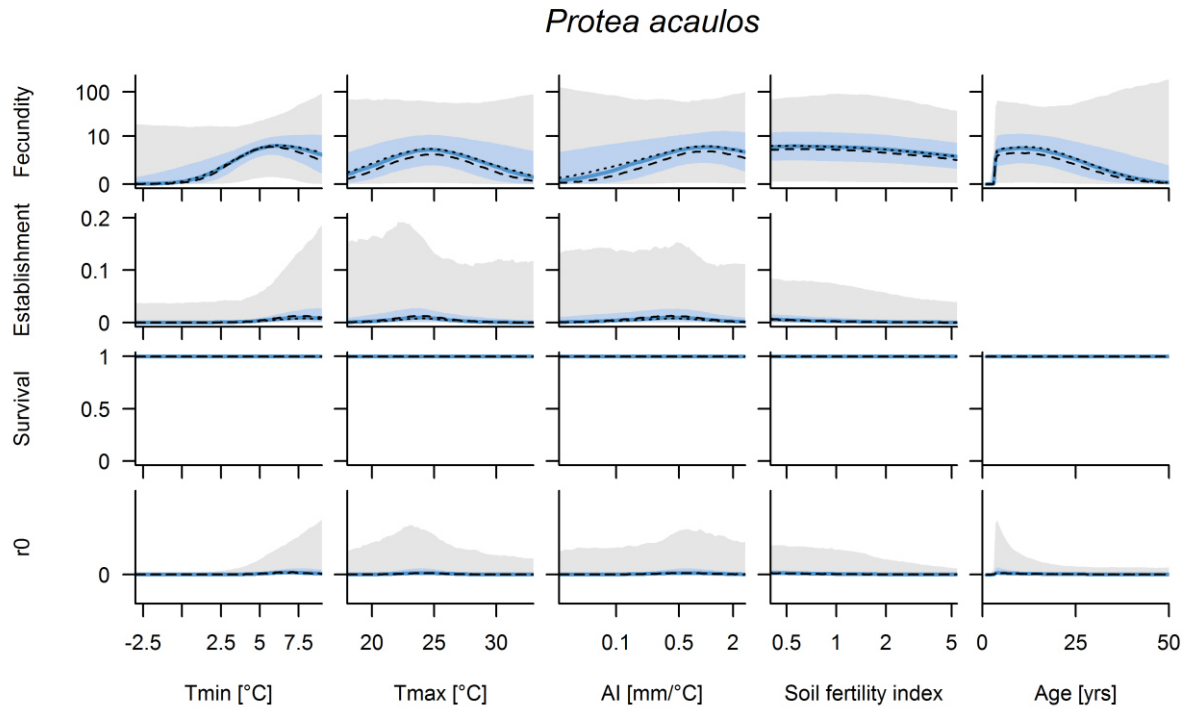
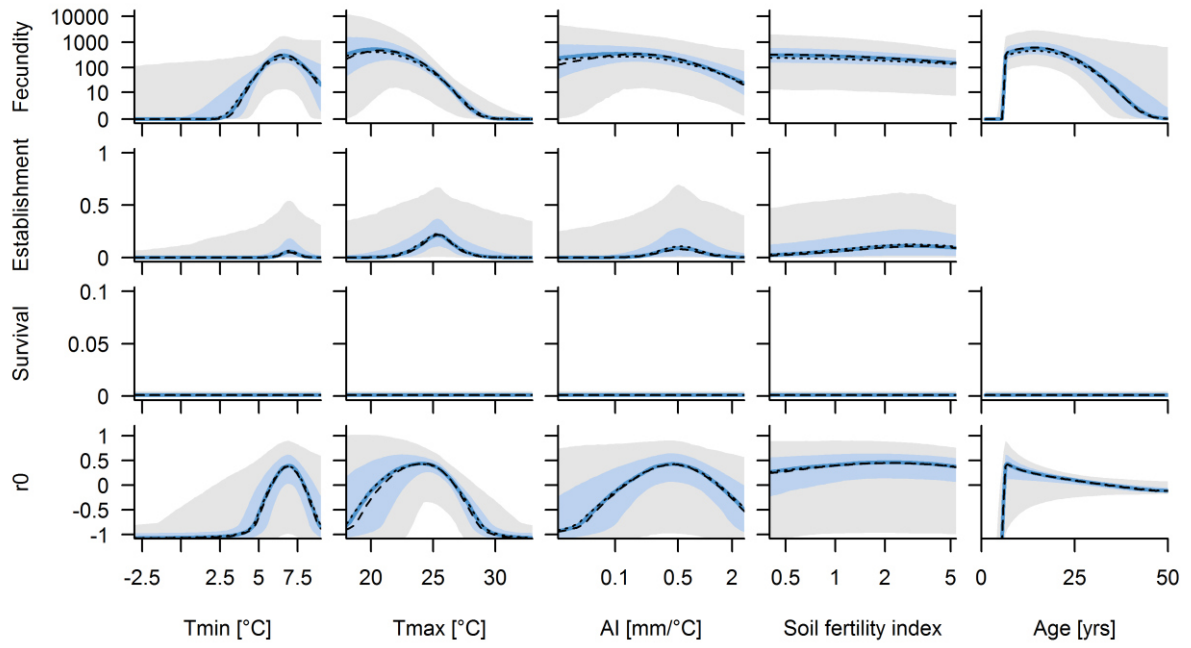


Fig. S1. (continued)

Protea compacta



Protea cynaroides

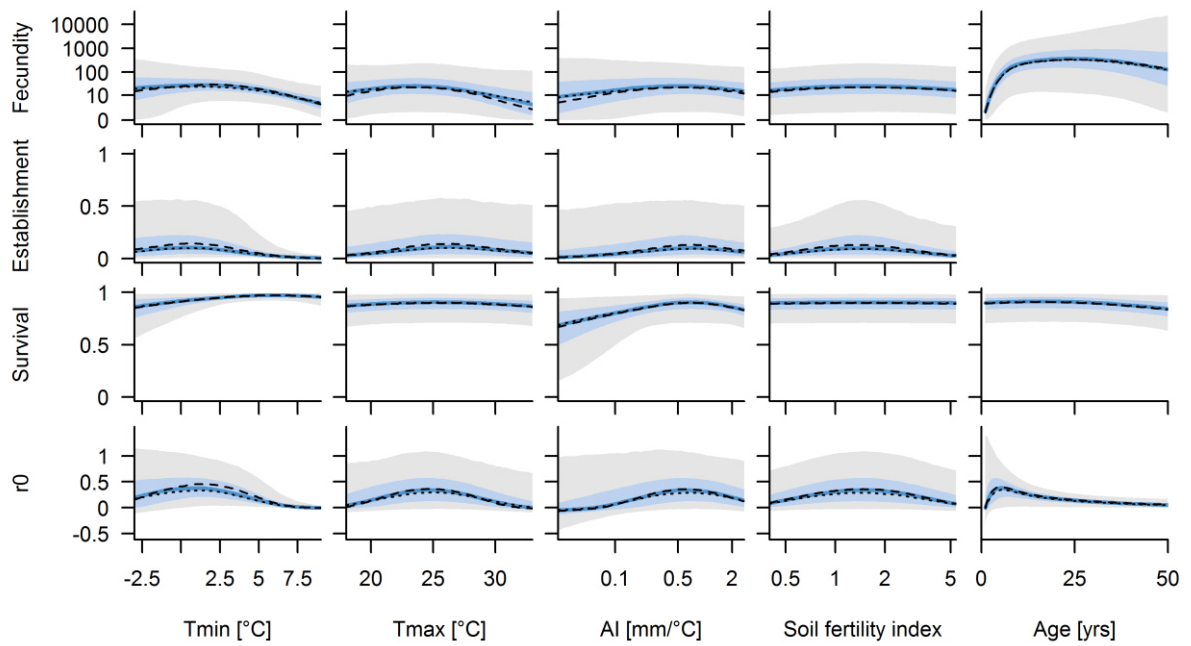


Fig. S1. (continued)

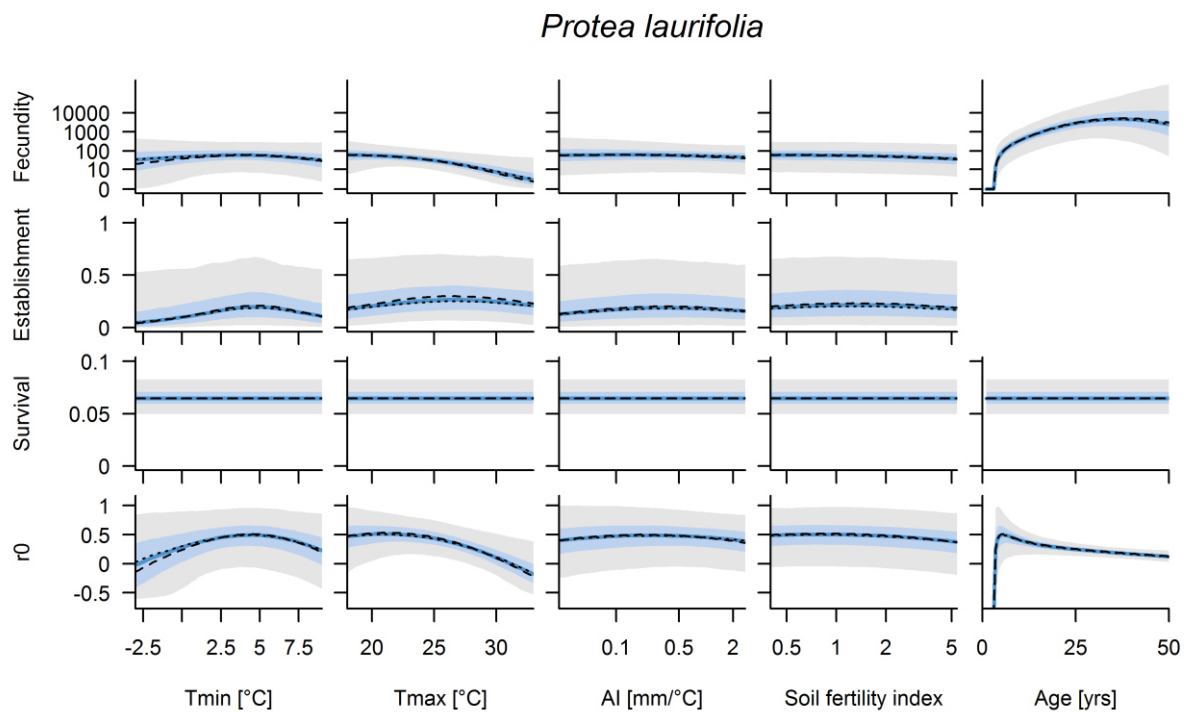
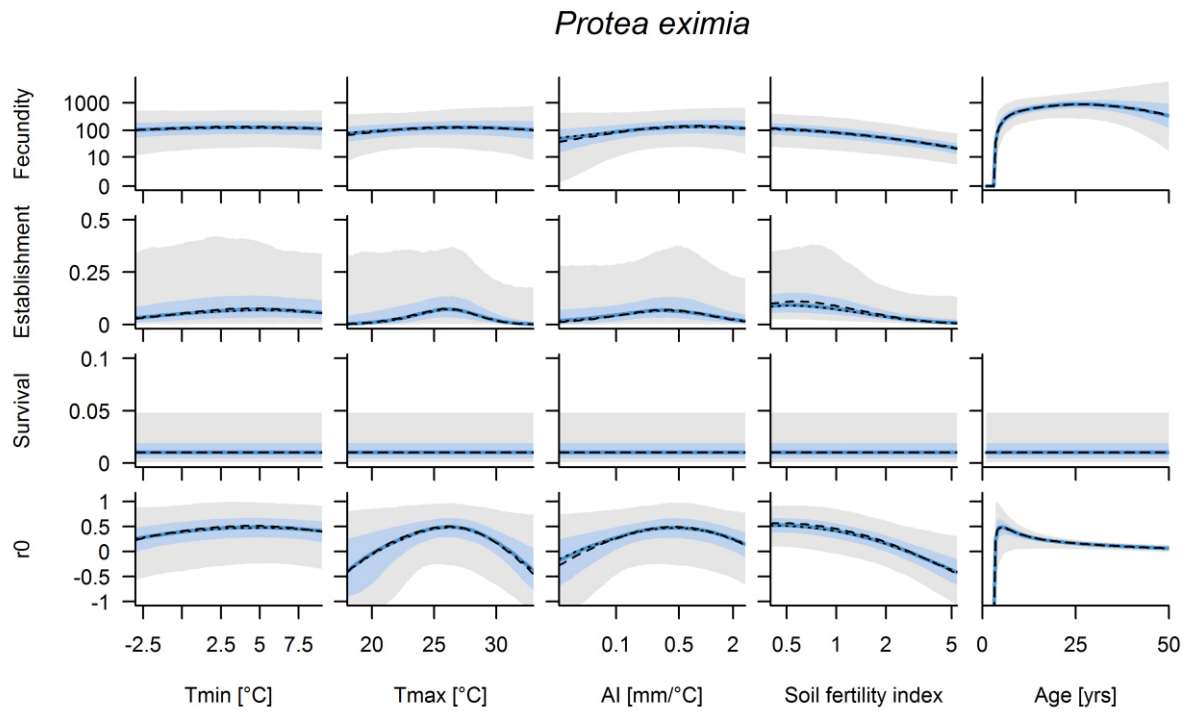
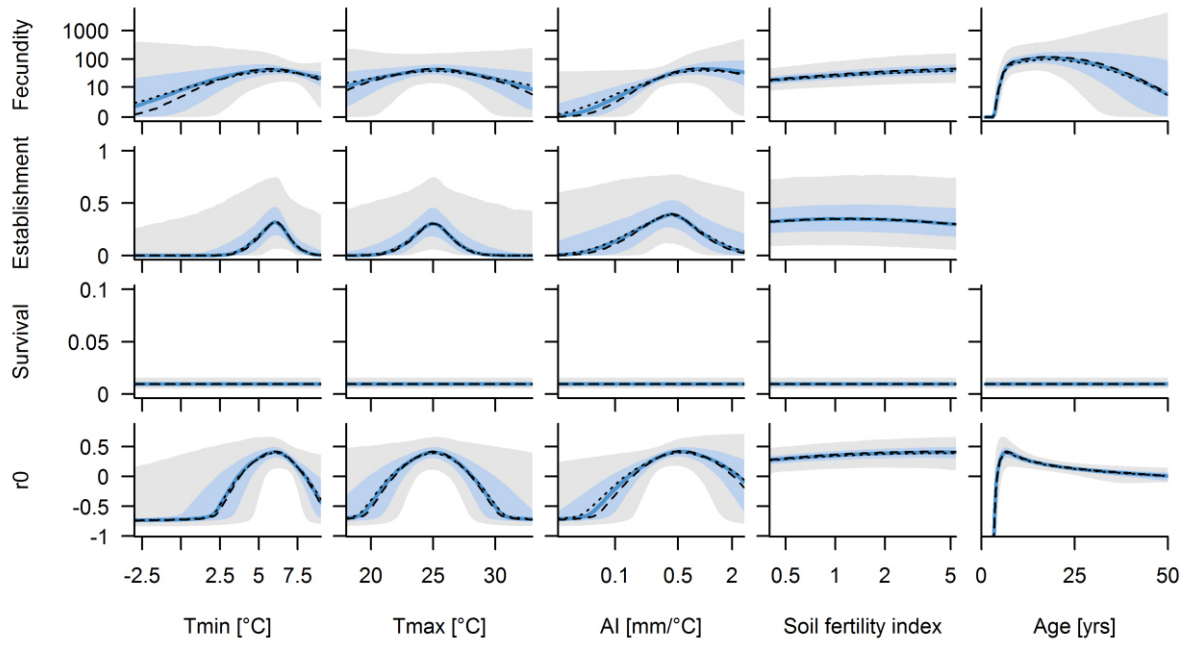


Fig. S1. (continued)

Protea longifolia



Protea lorifolia

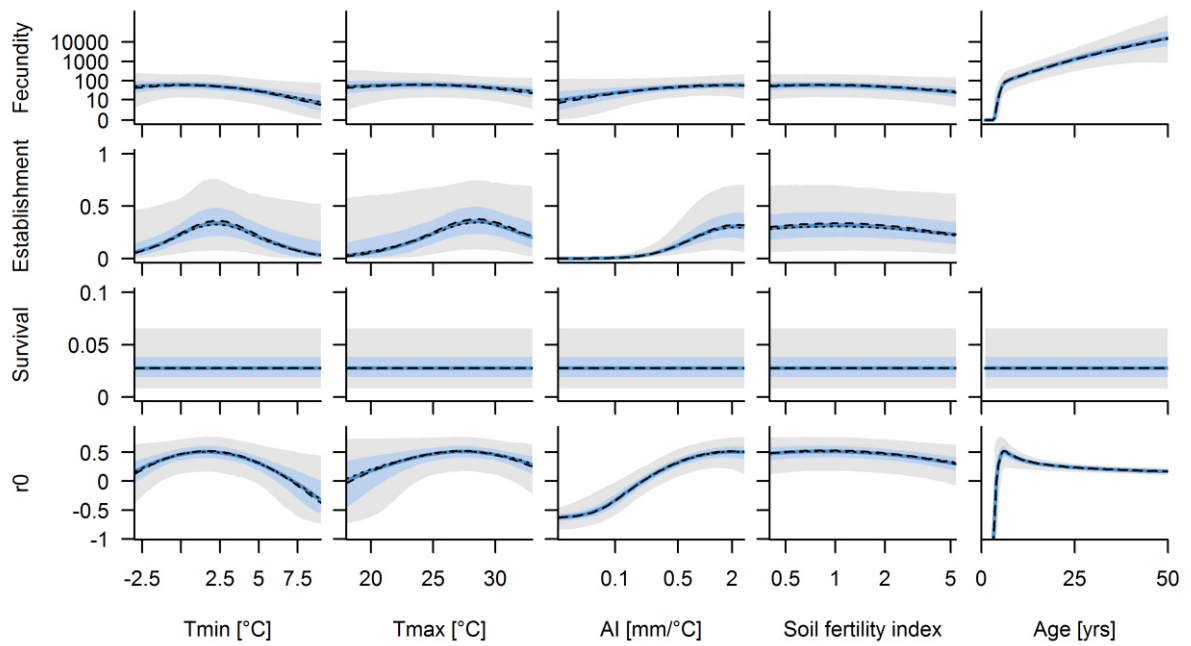
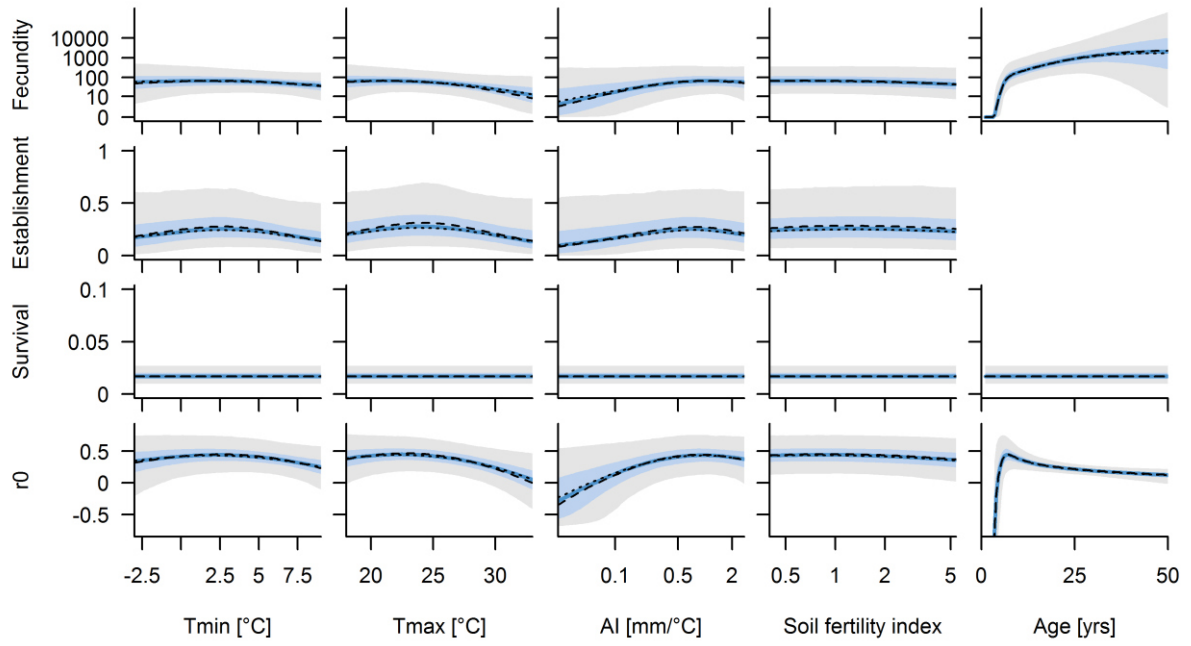


Fig. S1. (continued)

Protea neriifolia



Protea nitida

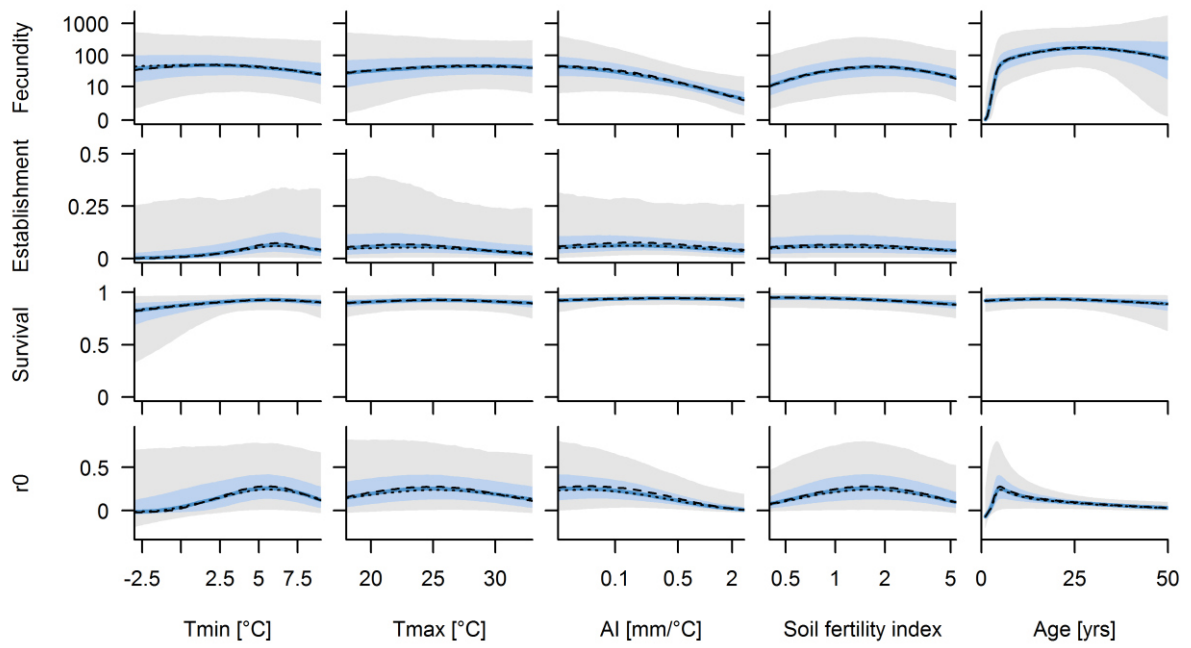
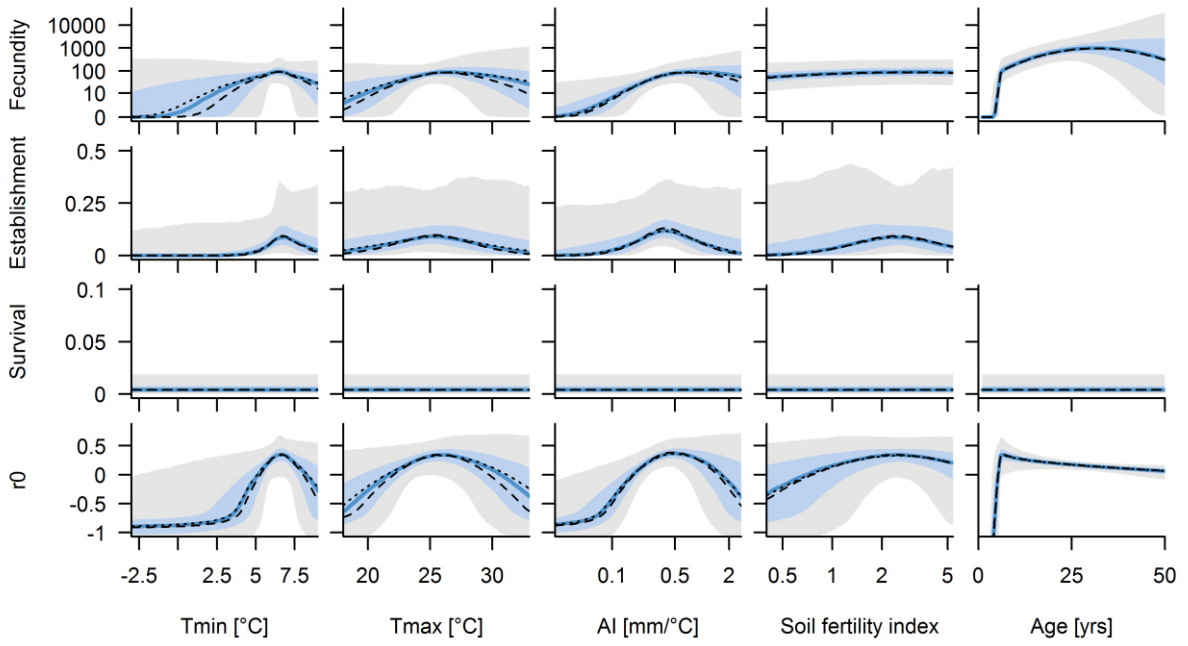


Fig. S1. (continued)

Protea obtusifolia



Protea punctata

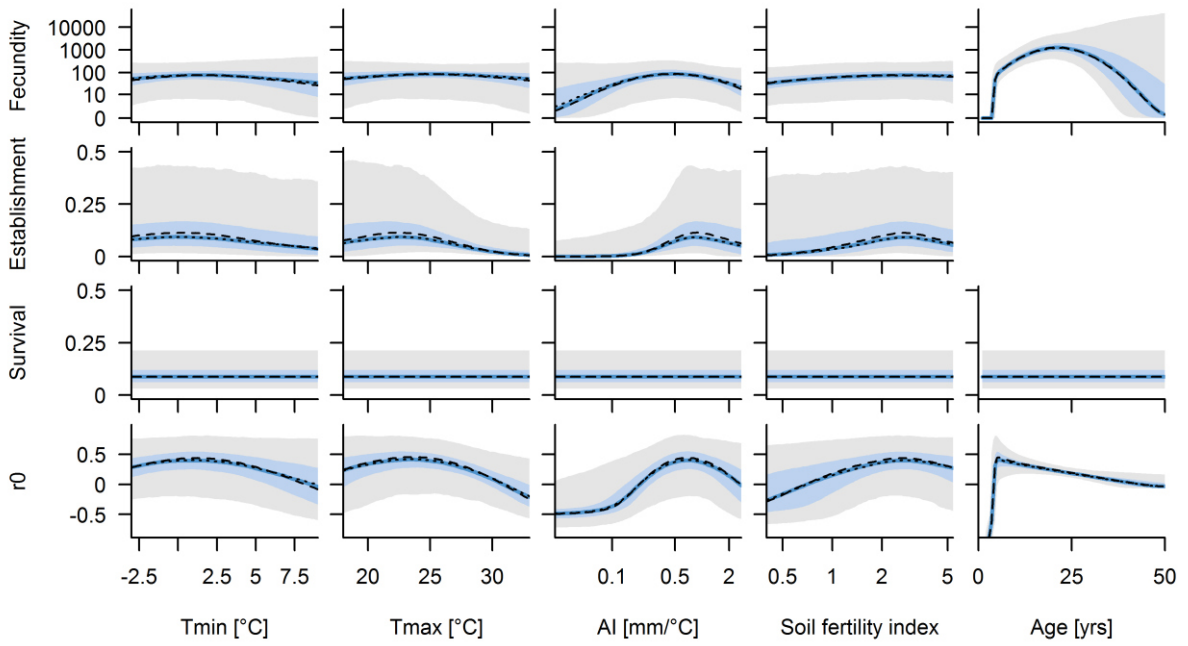
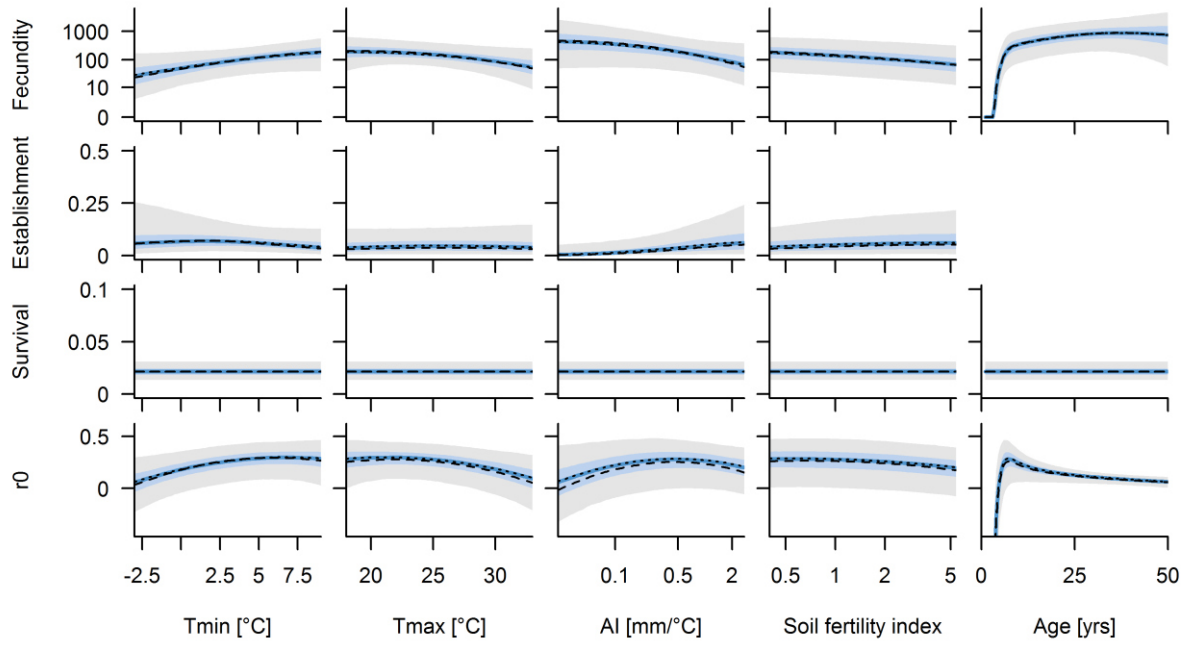


Fig. S1. (continued)

Protea repens



Protea scabra

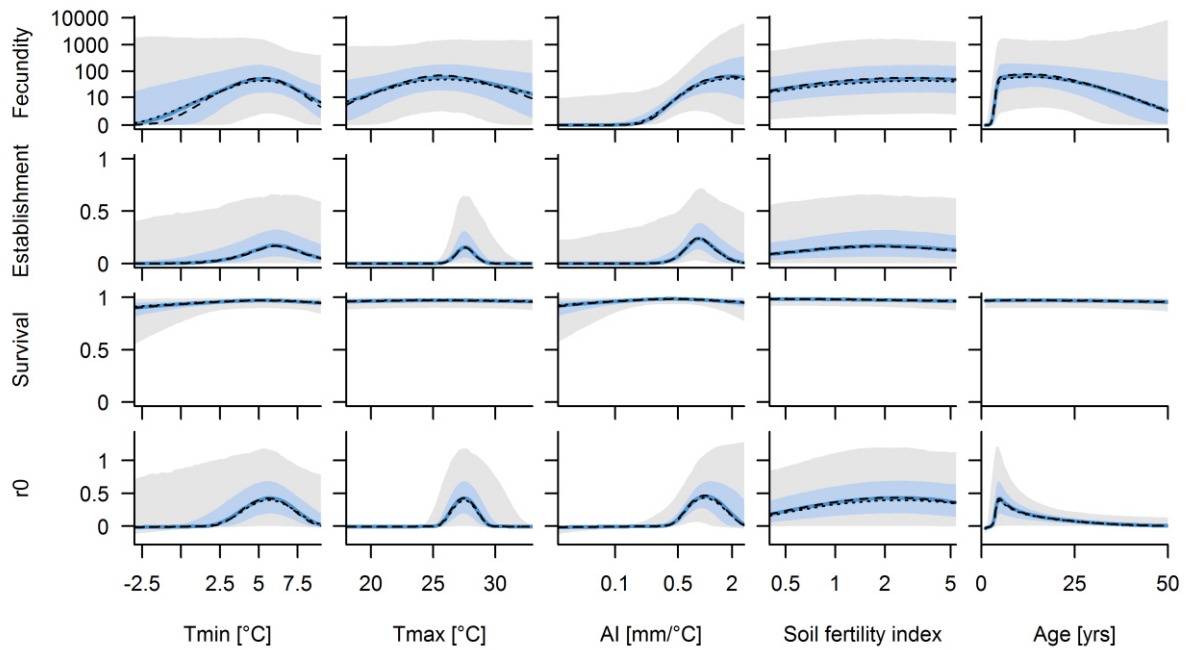
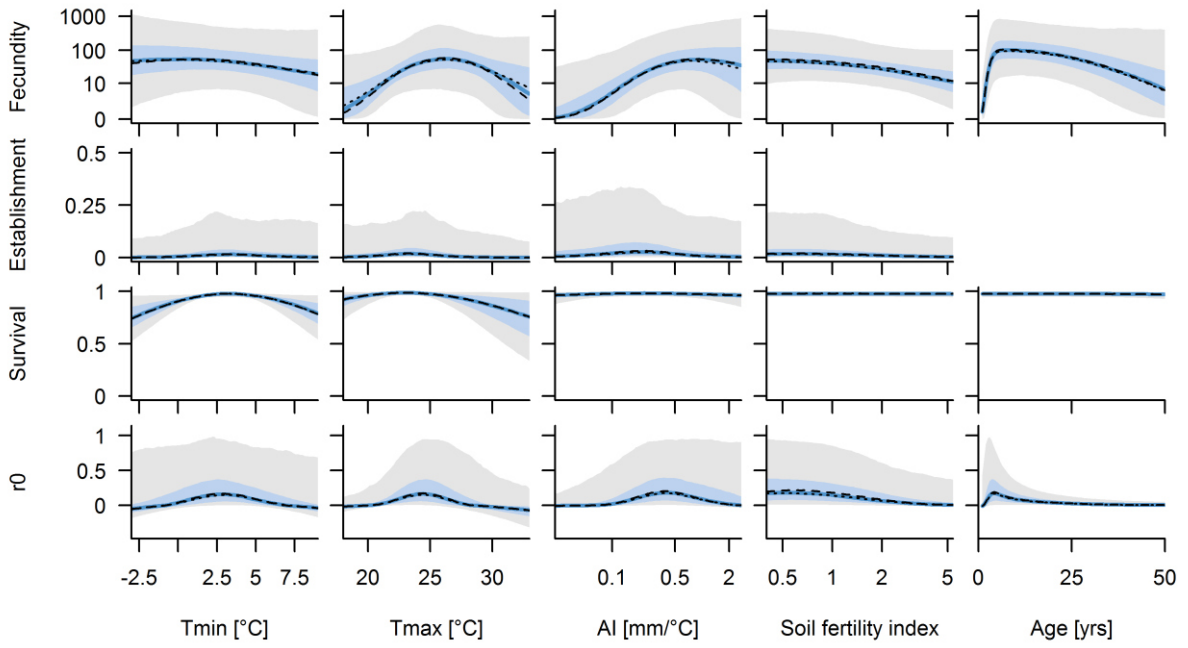


Fig. S1. (continued)

Protea scolopendriifolia



Protea susannae

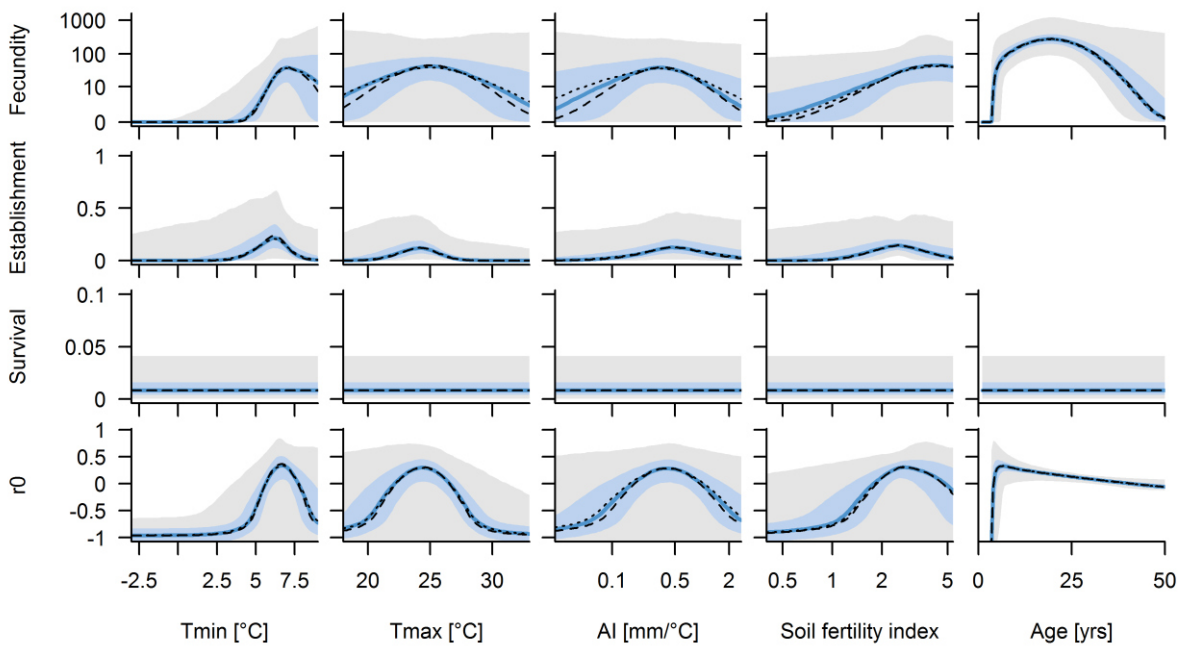


Fig. S1. (continued)

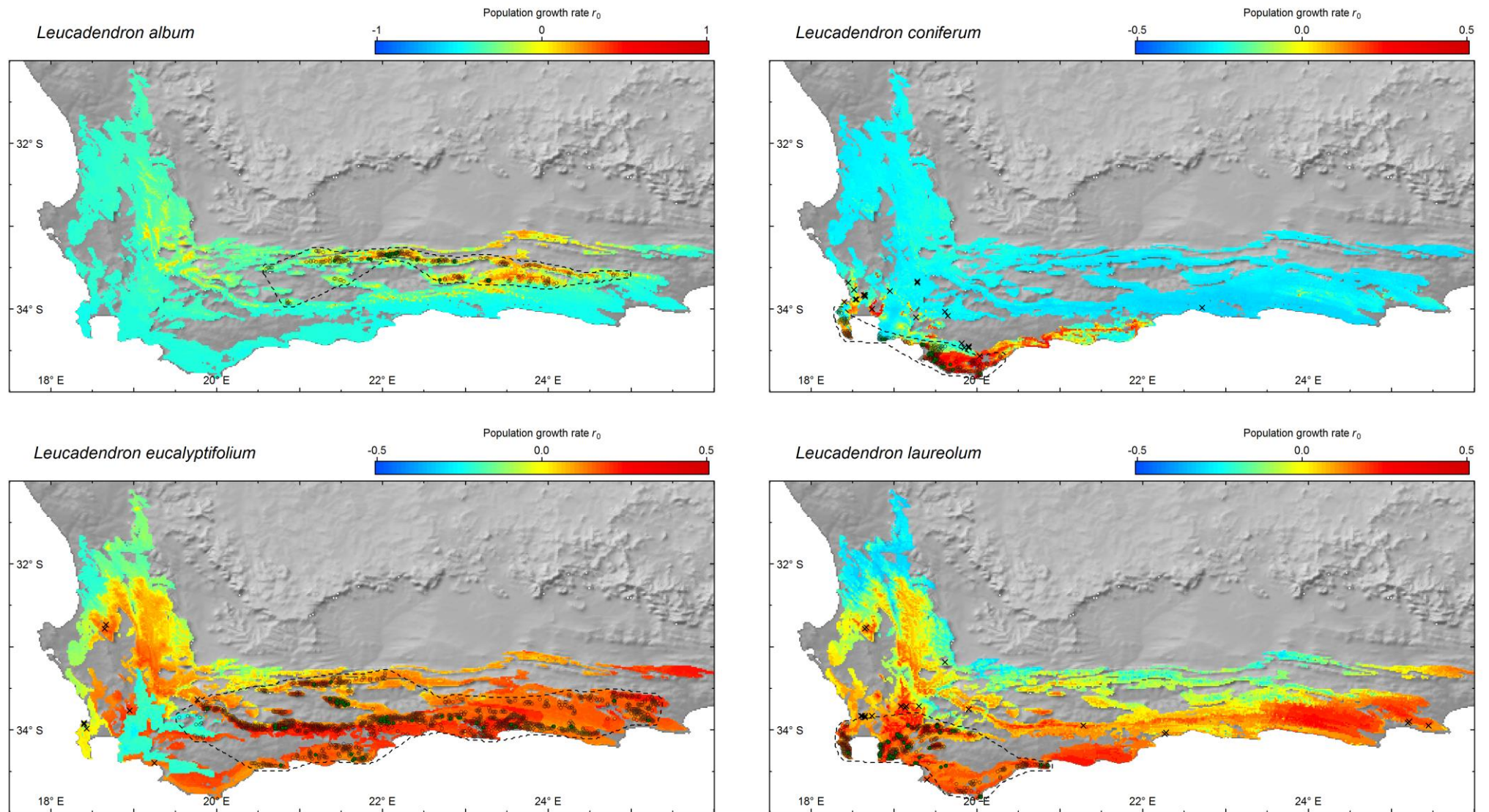


Fig. S2. Geographic projection of predicted intrinsic population growth rate r_0 across the Fynbos biome (coloured areas) in comparison to the natural geographic range (dashed lines) for each study species. Point symbols show the demographic sampling sites (green circles), presence records of natural populations (open circles) and populations established outside the natural range (crosses). Depicted values of r_0 are the medians of the respective Bayesian posterior distributions.

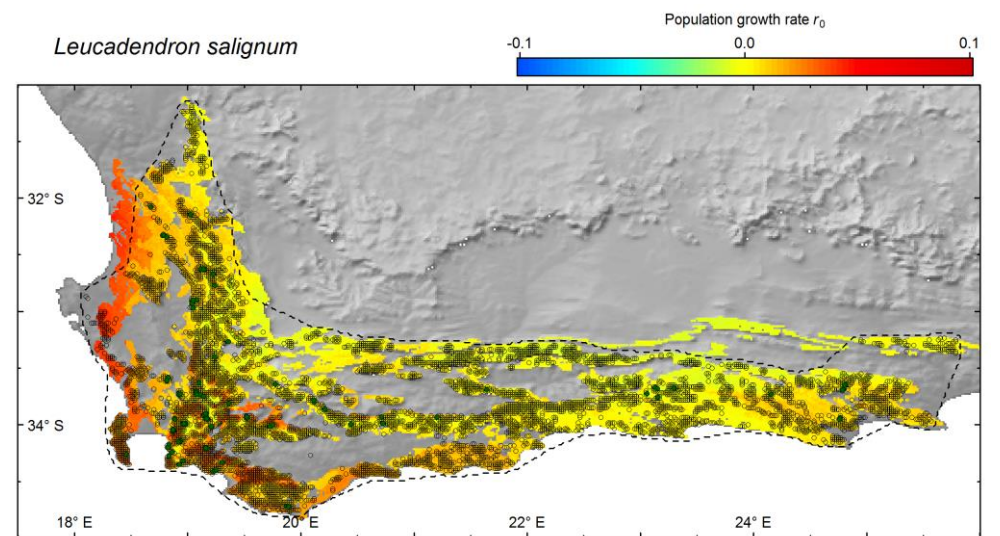
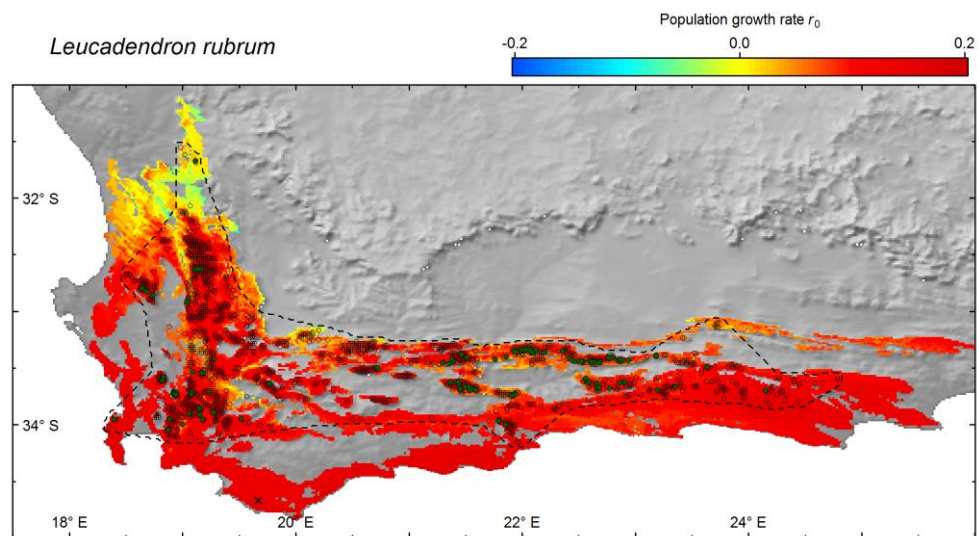
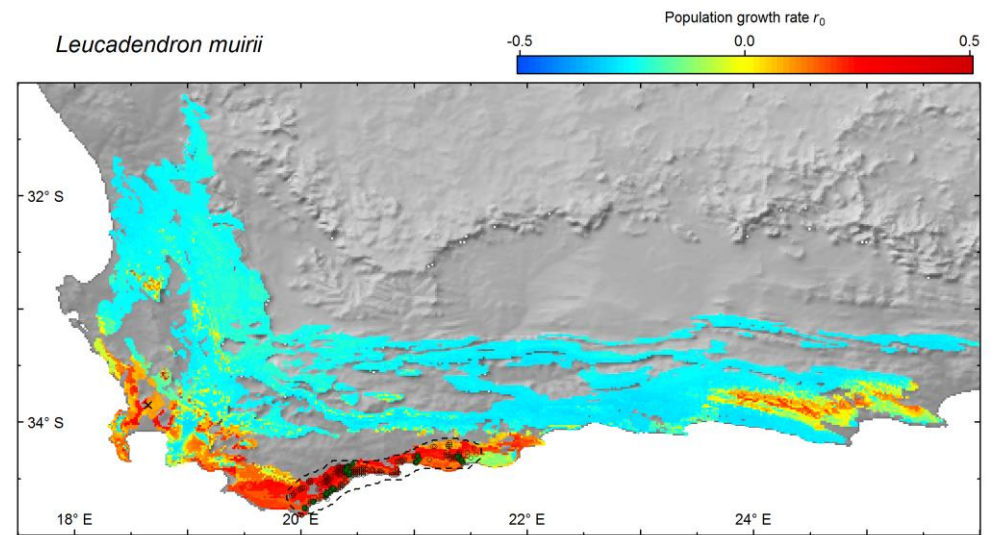
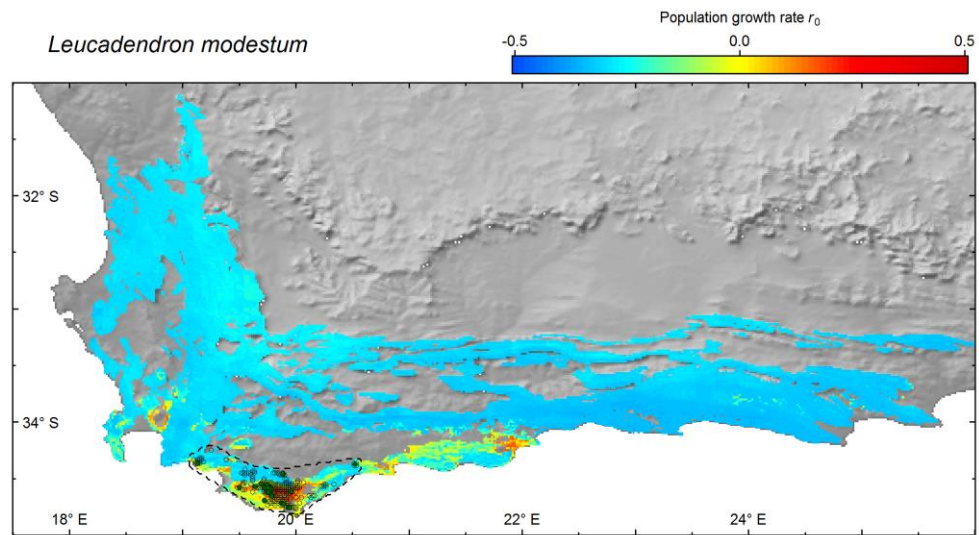


Fig. S2. (continued)

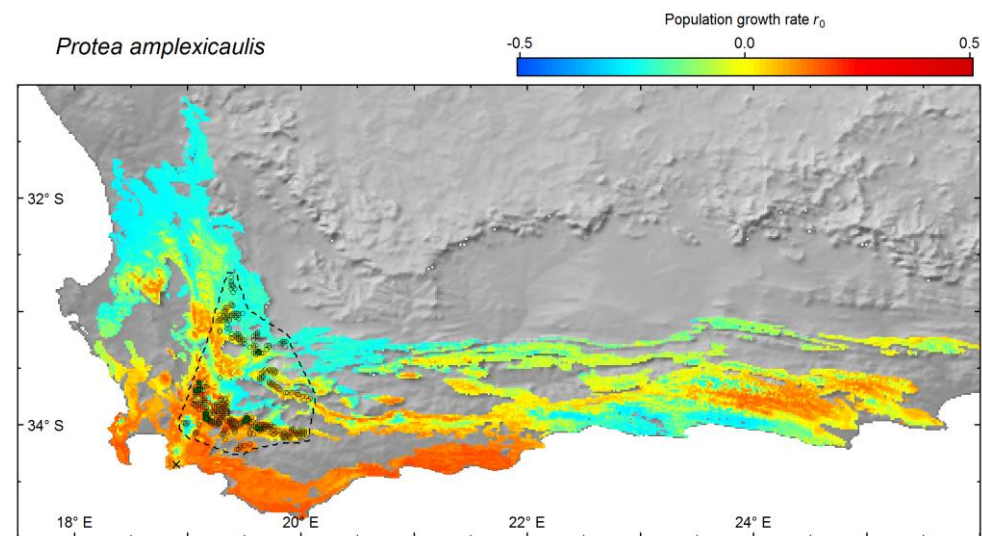
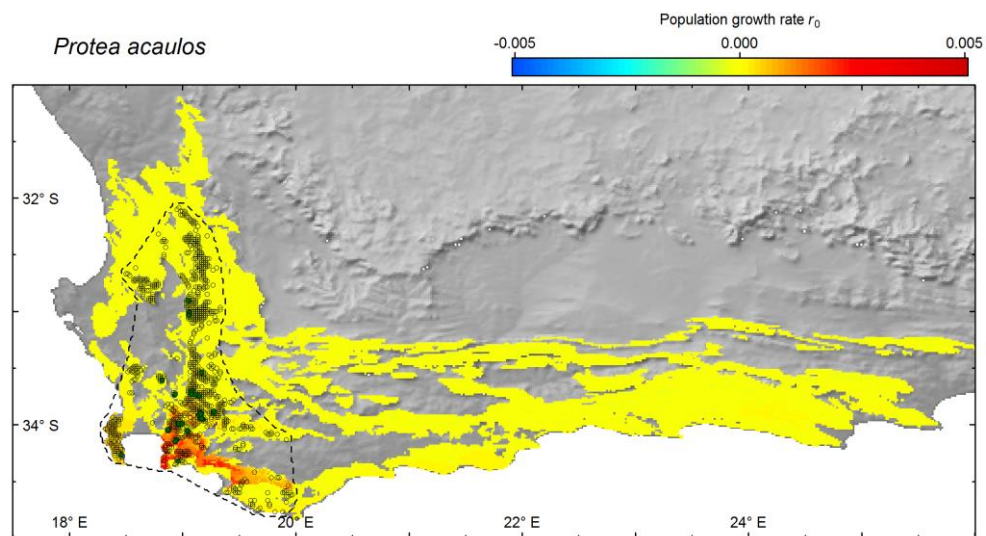
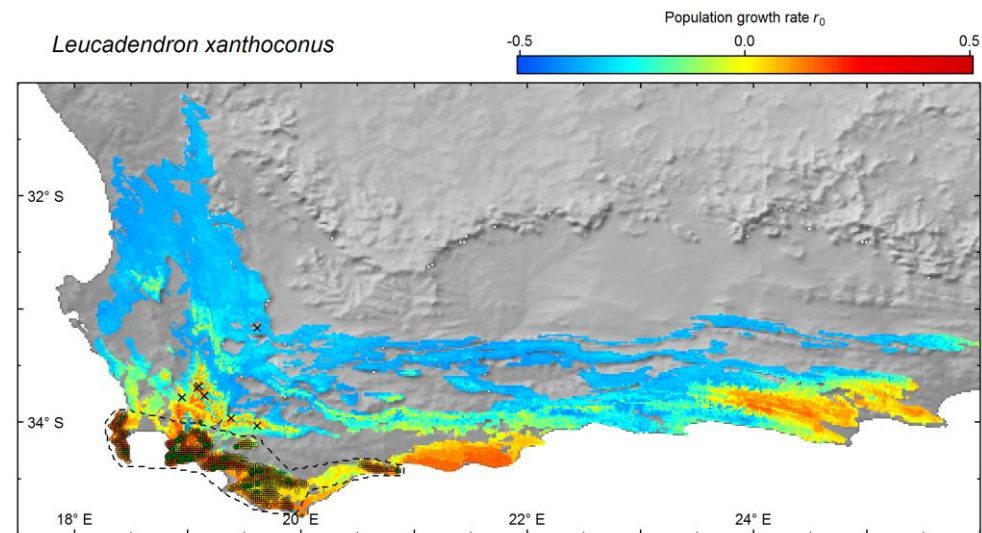
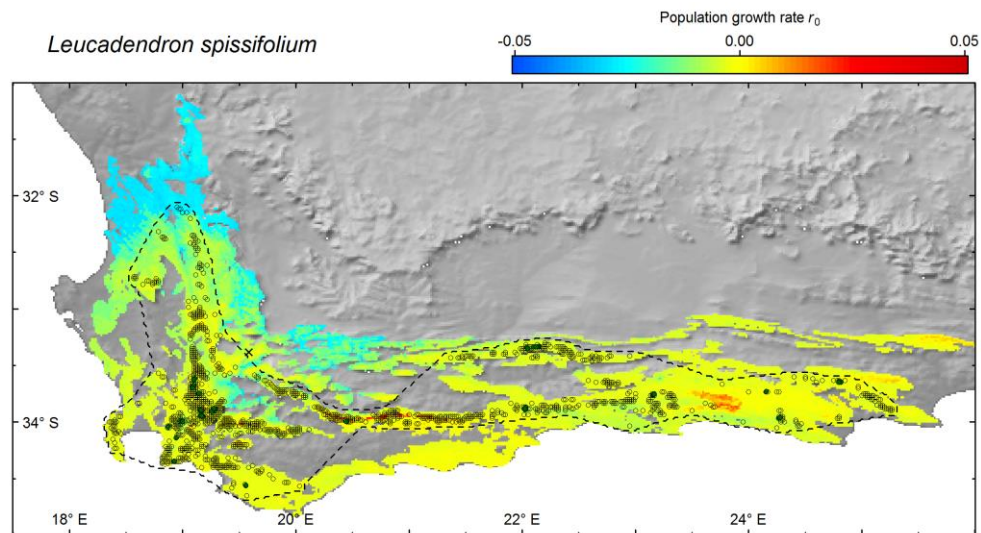


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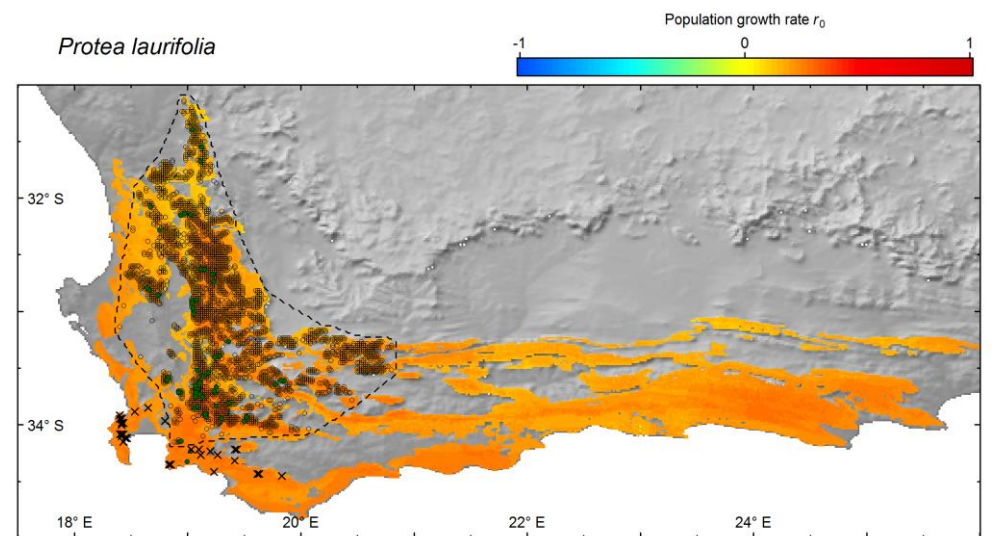
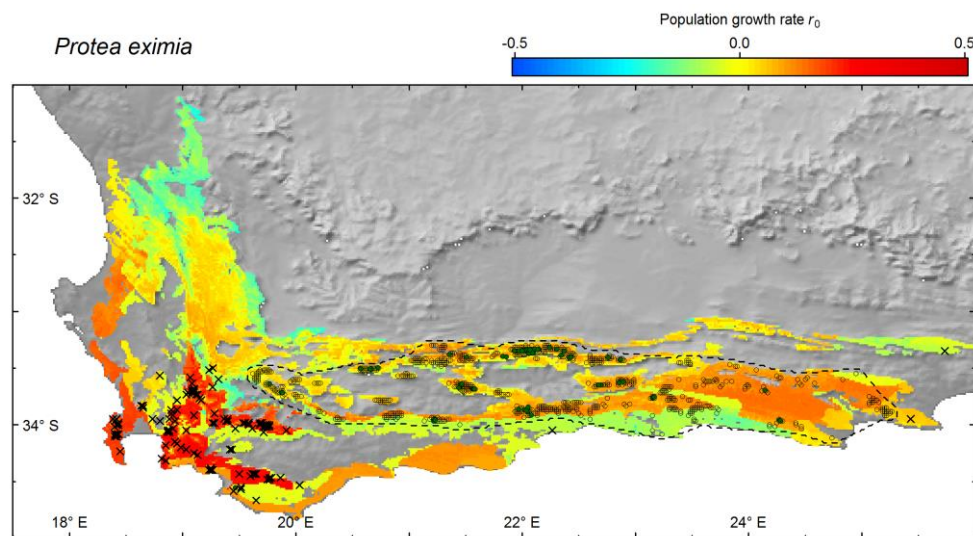
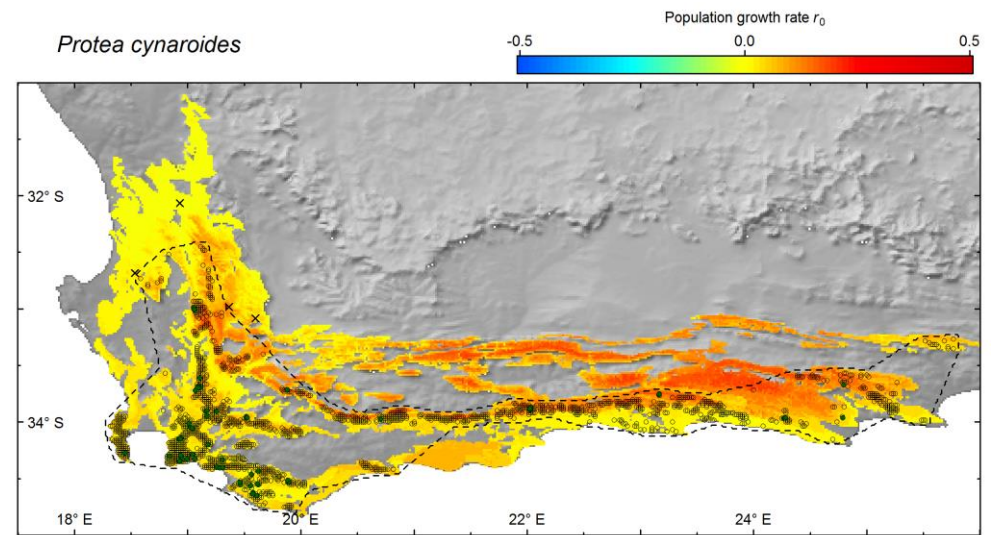
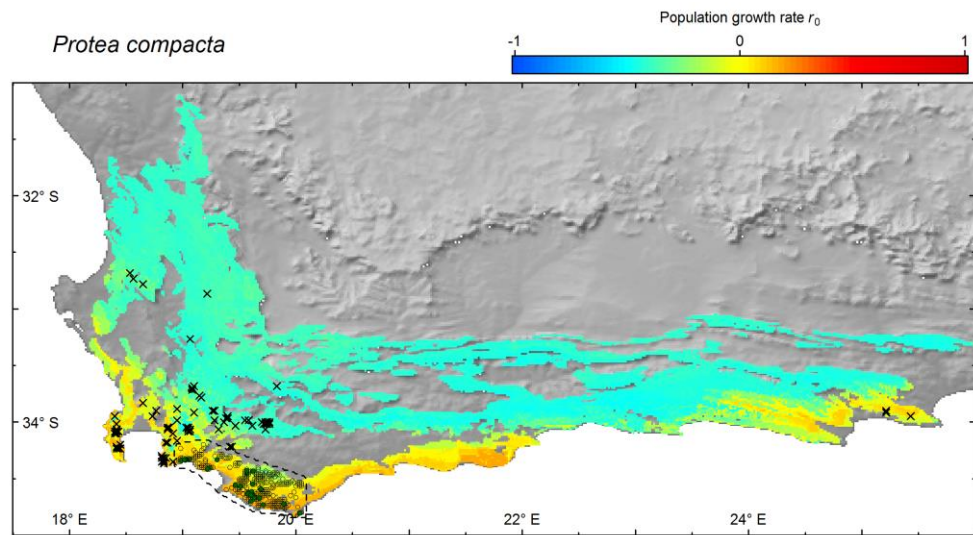


Fig. S2. (continued)

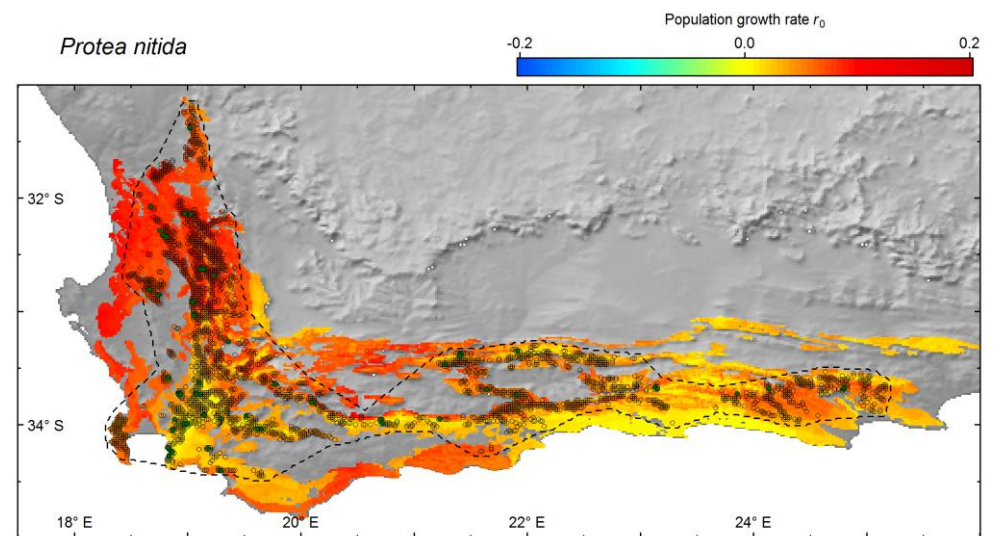
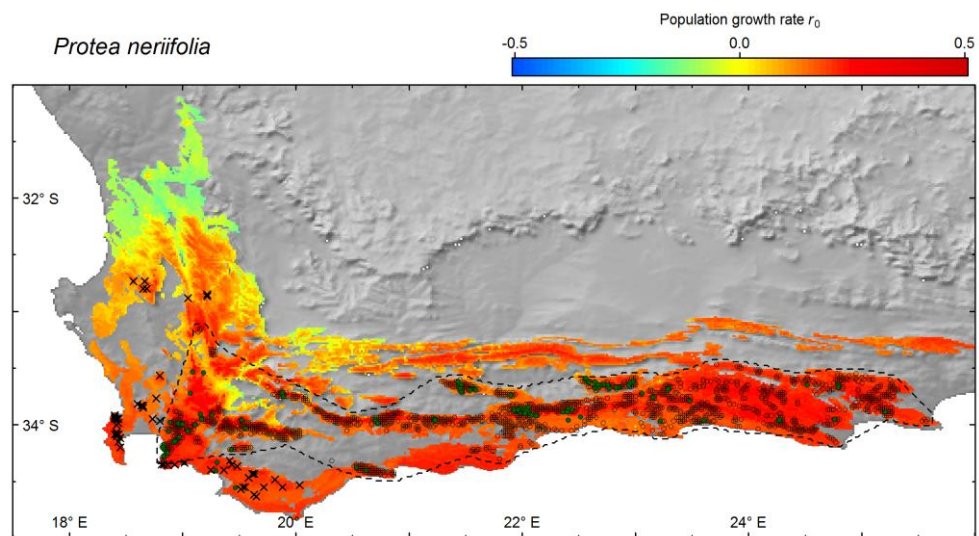
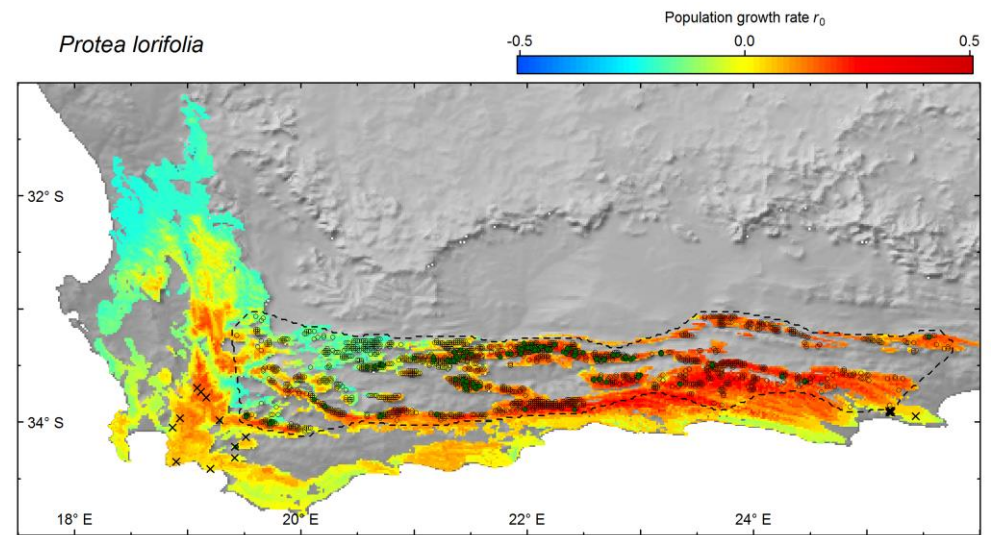
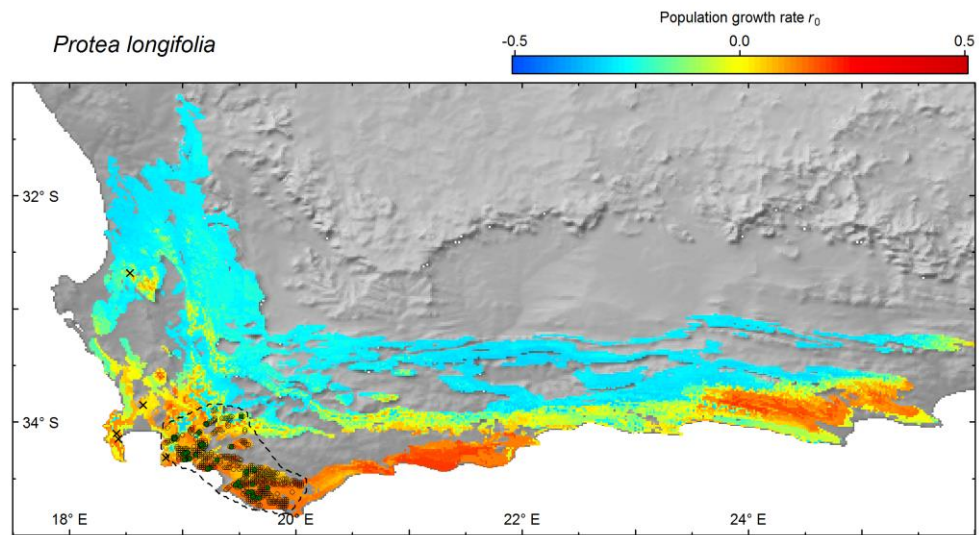


Fig. S2. (continued)

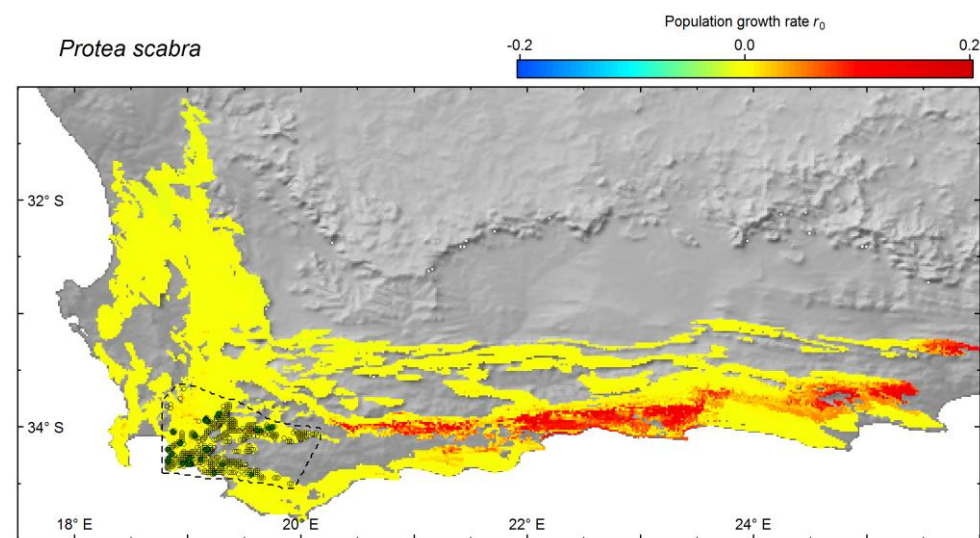
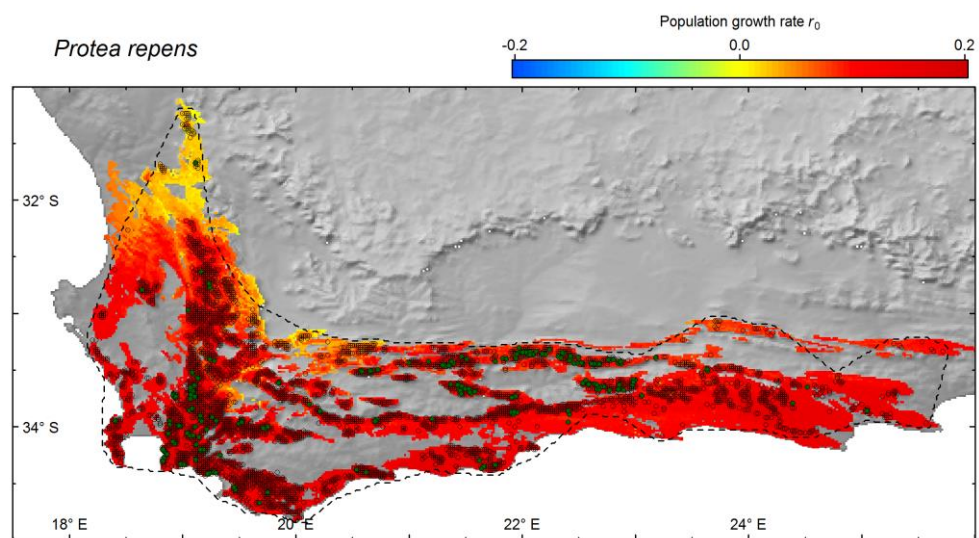
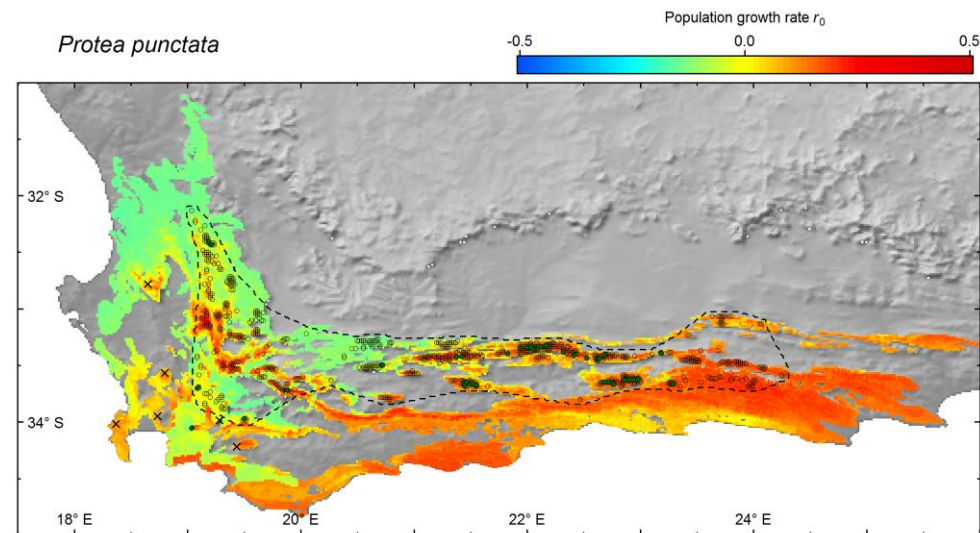
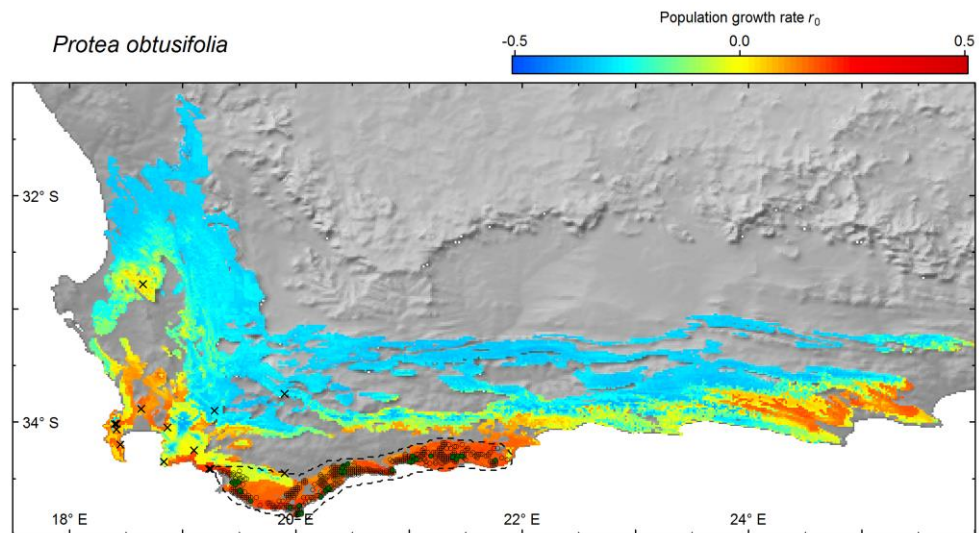


Fig. S2. (continued)

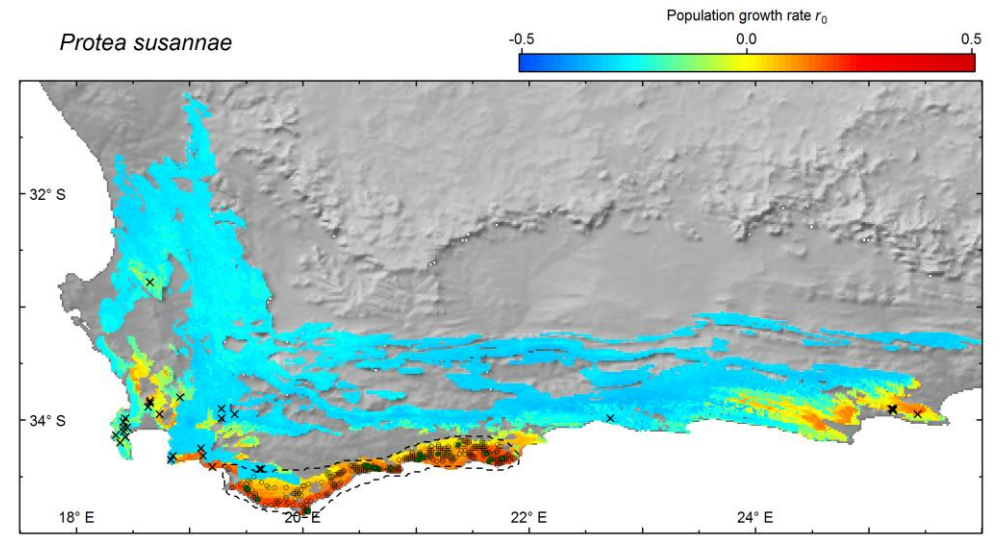
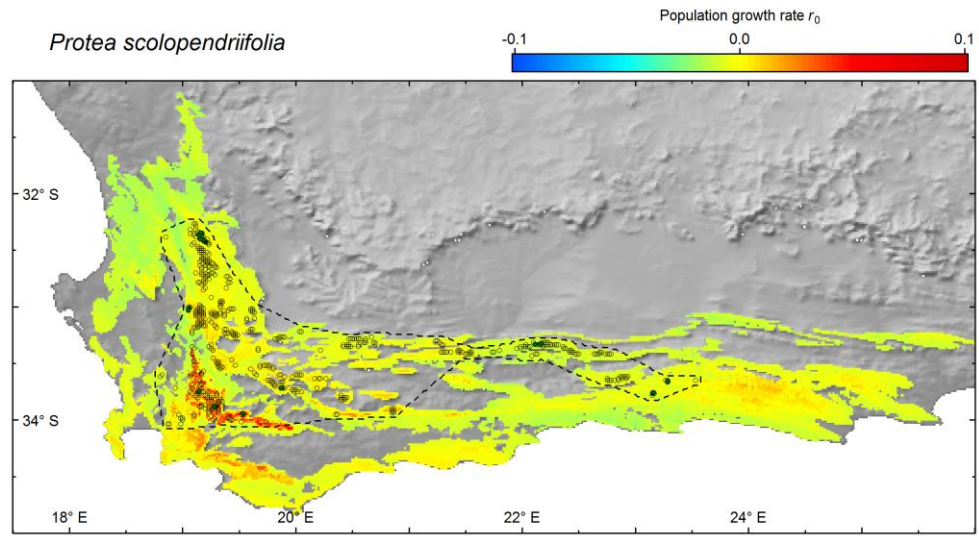


Fig. S2. (continued)

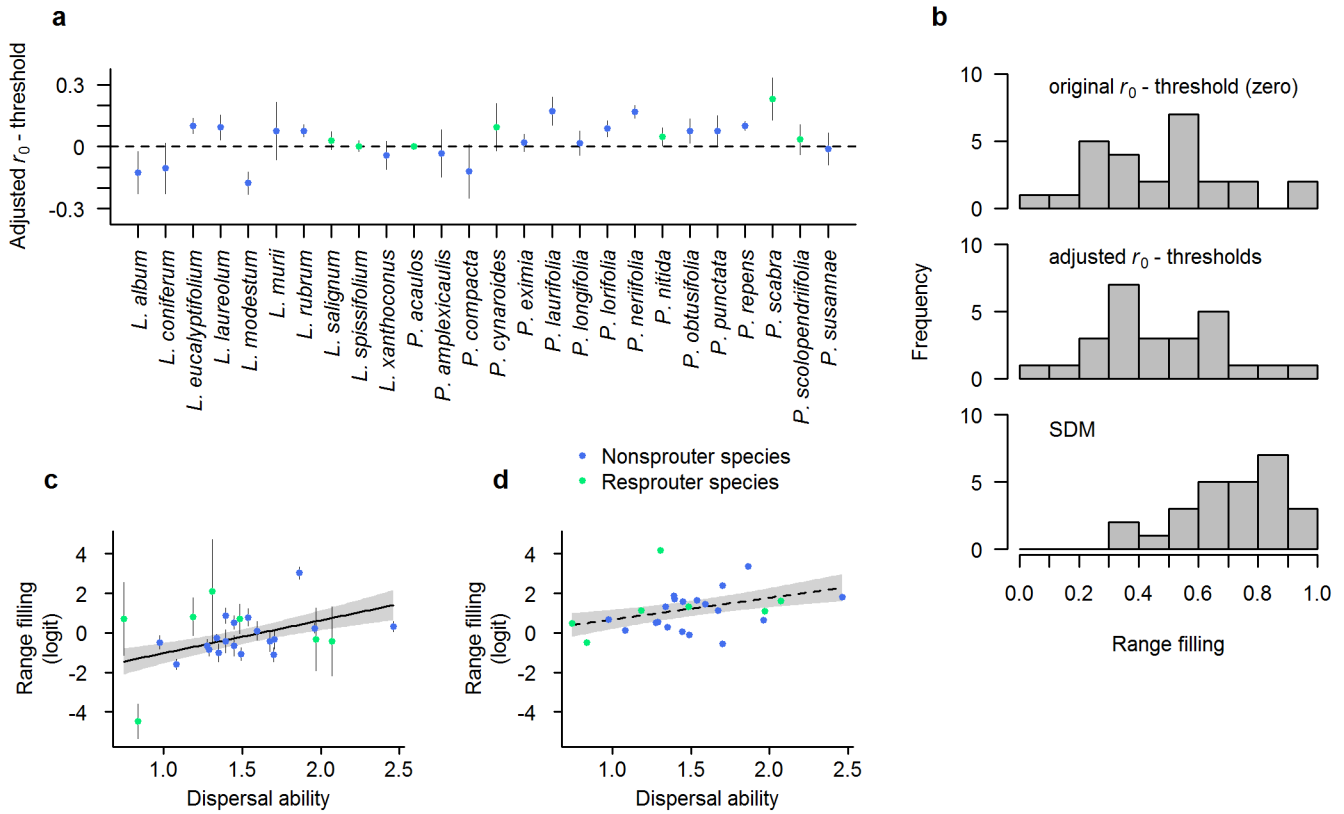


Fig. S3. Results for alternative quantifications of range filling. (a) Species-specific adjusted thresholds (points: posterior means, bars: posterior standard deviations) for determining suitable areas from the predicted spatial variation of the intrinsic population growth rate r_0 . For each posterior prediction of r_0 , the adjusted r_0 -threshold maximizes the agreement (TSS value) between predicted suitability and the observed presence-absence of the species. (b) Frequency distributions of estimated range filling values across the 26 study species for (i) the original analysis (range of values: 0.08 - 0.95, mean = 0.47), (ii) applying the adjusted r_0 -thresholds to predict suitable areas (0.02 - 0.95, mean = 0.48) and (iii) based on predictions of a species distribution model (SDM) fitted to the presence-absence data per species (0.36 - 0.98, mean = 0.72). (c) Estimated effect of dispersal ability on range filling (points: posterior means, bars: posterior standard deviations) quantified by applying the adjusted r_0 -thresholds. The line shows the estimated linear regression (posterior means, 90% credibility interval as shaded areas, slope = 0.64 ± 0.27 , $p = 0.009$). (d) Estimated effect of dispersal ability on range filling (points: posterior means, bars: posterior standard deviations) quantified from SDM predictions. The dashed line shows the estimated linear regression (posterior means, 90% credibility interval as shaded areas, slope = 0.42 ± 0.24 , $p = 0.073$). See Fig. 3a and Table S3 for results of this regression analyses based on the original r_0 -threshold ($r_0 > 0$).

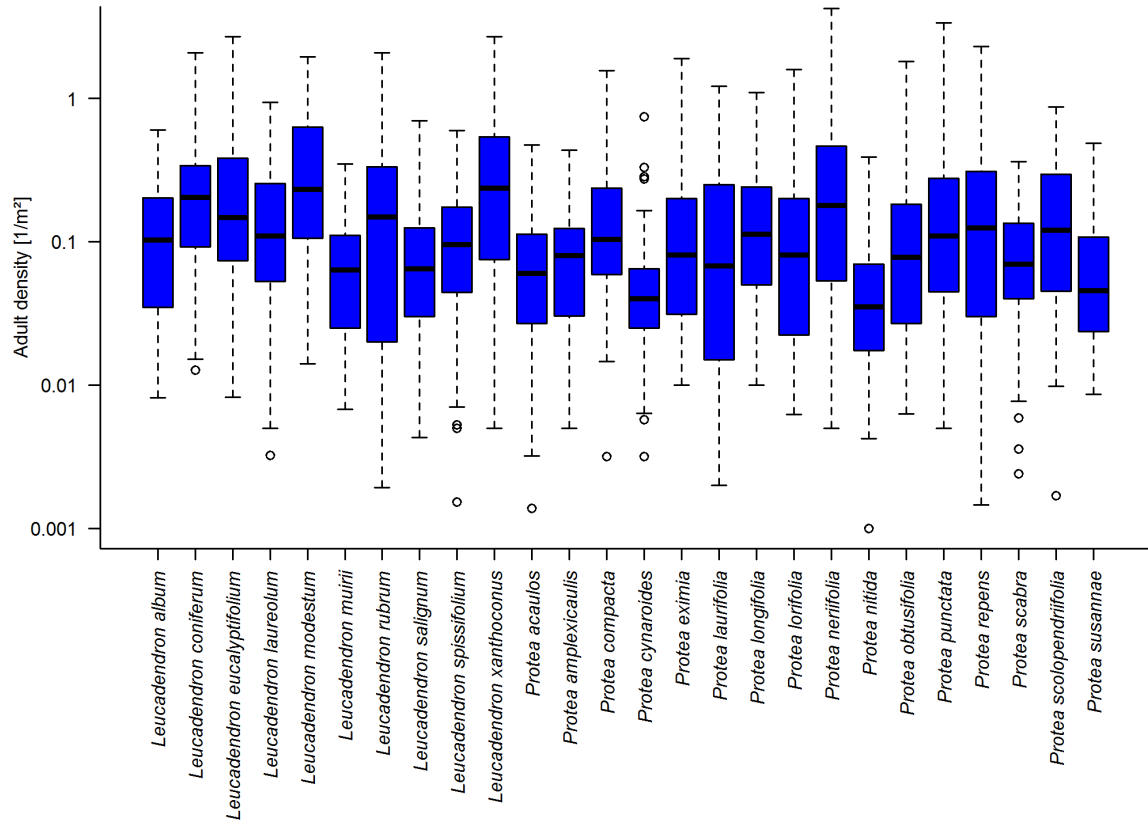


Fig. S4. Variation in observed population densities across the sampling sites for demographic records of each of the 26 study species.

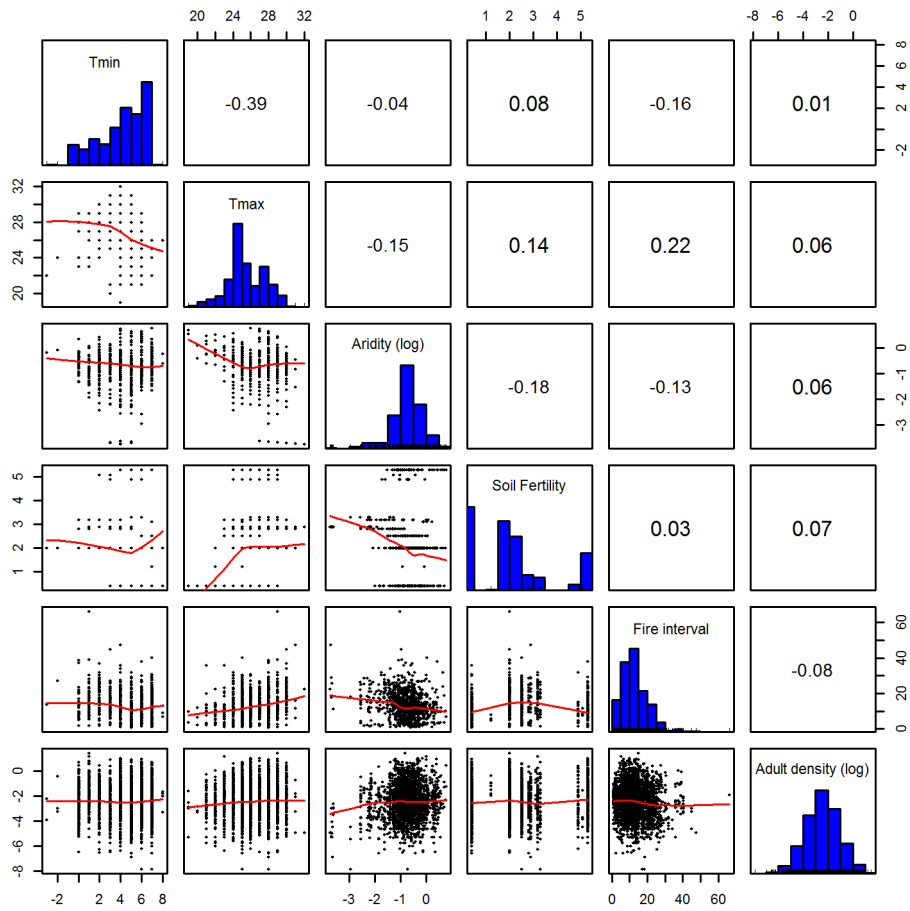


Fig. S5. Covariance of environmental variables and population densities across all sampling sites for demographic records of the 26 study species. Histograms show the distribution of each variable across all sampling sites. Lower-left panels show pair-wise scatterplots with a LOESS (locally estimated scatterplot smoothing) curve. Values in the top-right panels indicate the Spearman correlation coefficients for each pair of variables.

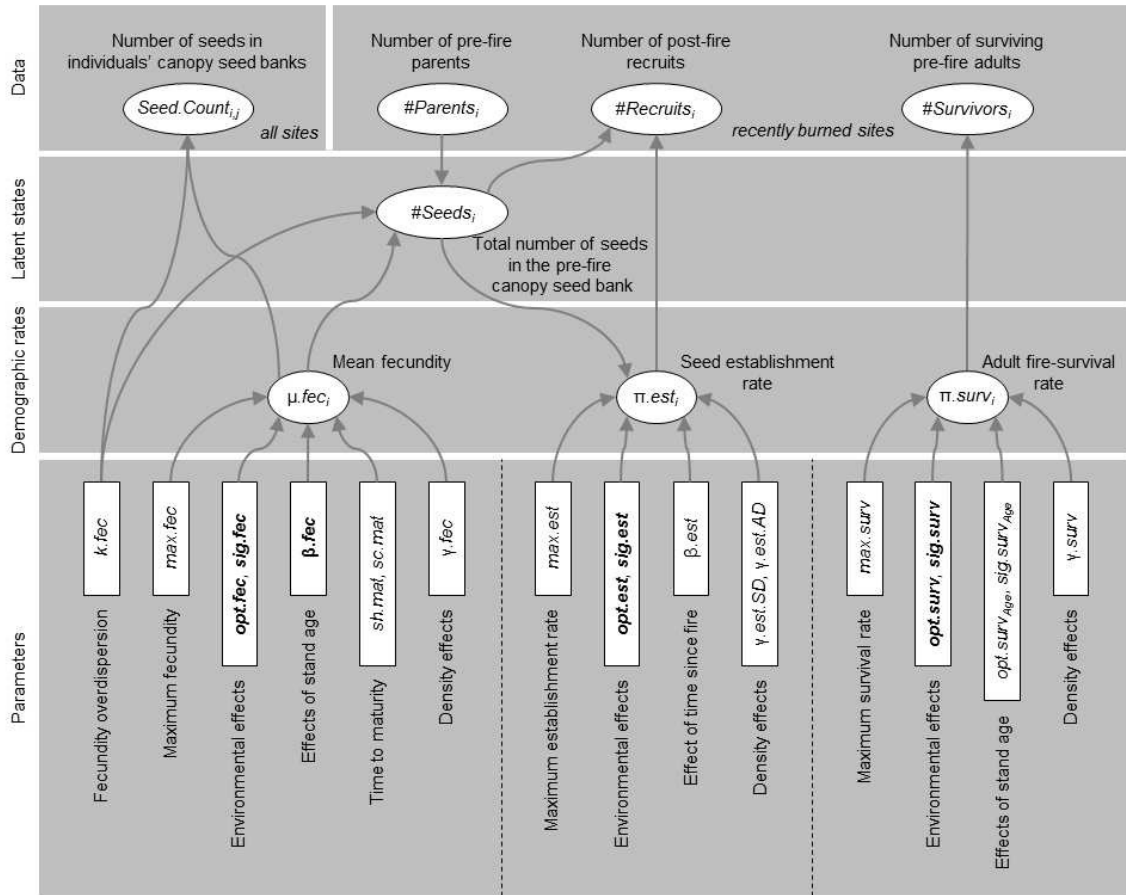


Fig. S6. Hierarchical structure of the demographic response model. The model structure is depicted as a directed acyclic graph (DAG) showing the hierarchical relations between model parameters, demographic rates, latent states and the recorded demographic data. The latent state variable $\#Seeds$ is included for the inference of per-seed establishment rates from the observed number of recruits on recently burned sites. On these sites the number of pre-fire parents can be determined by combining counts of burned skeletons and fire-surviving adults, but no data on the pre-fire canopy seed bank is available. Hence the size of the pre-fire canopy seed bank on these sites is predicted from the fecundity submodel. See the Methods for a detailed description of all variables and their statistical relations and Tab. S6 for prior distributions of the model parameters.

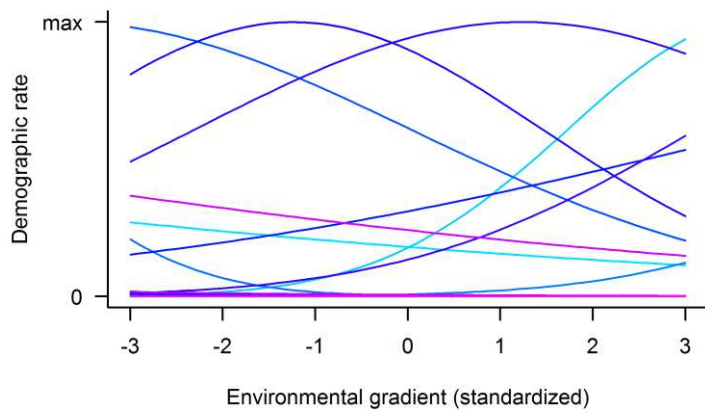


Fig. S7. 100 samples from the prior predictions of demographic response curves. The possible predictions apply to all combinations of demographic rates and environmental variables, since responses of each demographic rate to environmental gradients are proportional to a respective maximum rate and all environmental variables were centred and scaled. Lines show demographic response curves based on 100 random samples from the prior distributions of the environmental optimum ($opt.fec_k$, $opt.est_k$ or $opt.surv_k$) and of the environmental response strength ($sig.fec^2_k$, $sig.est^2_k$ or $sig.surv^2_k$), respectively, and a fixed value of the maximum demographic rate ($max.fec$, $max.est$ or $max.surv$). Note that for most of the 100 parameter combinations the predictions are close to zero throughout the depicted environmental range (mean \pm three standard deviations) because of extreme (positive or negative) values of the environmental optimum.

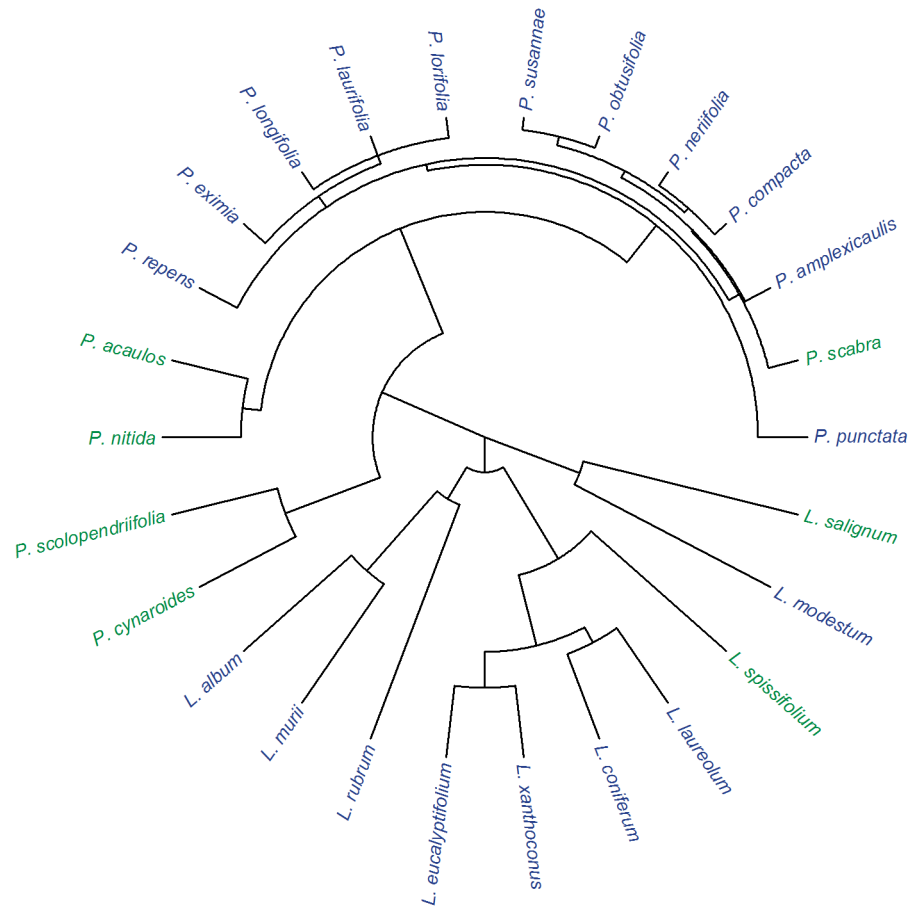


Fig. S8. Phylogenetic tree of the study species. The phylogenetic reconstruction is based on 18 DNA markers for 291 taxa of the Proteaceae family. Here only the trimmed phylogenetic tree for the 26 study species is shown (blue: nonsprouters, green: resprouters).