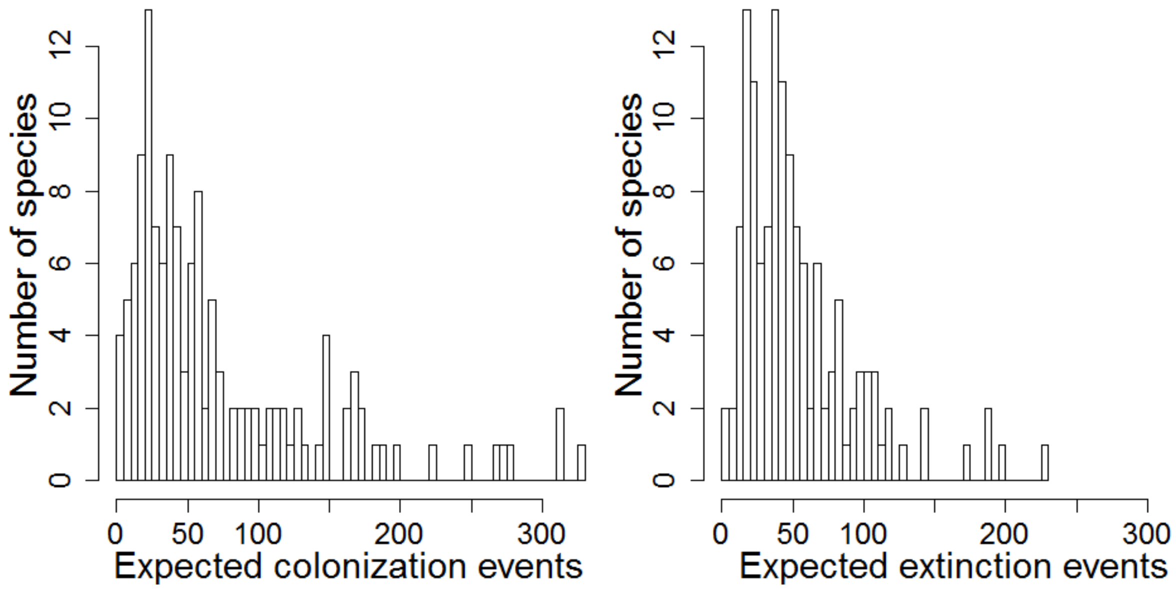
<u>Supplementary Information</u>

Extinction debts and colonization credits of non-forest plants in the European Alps

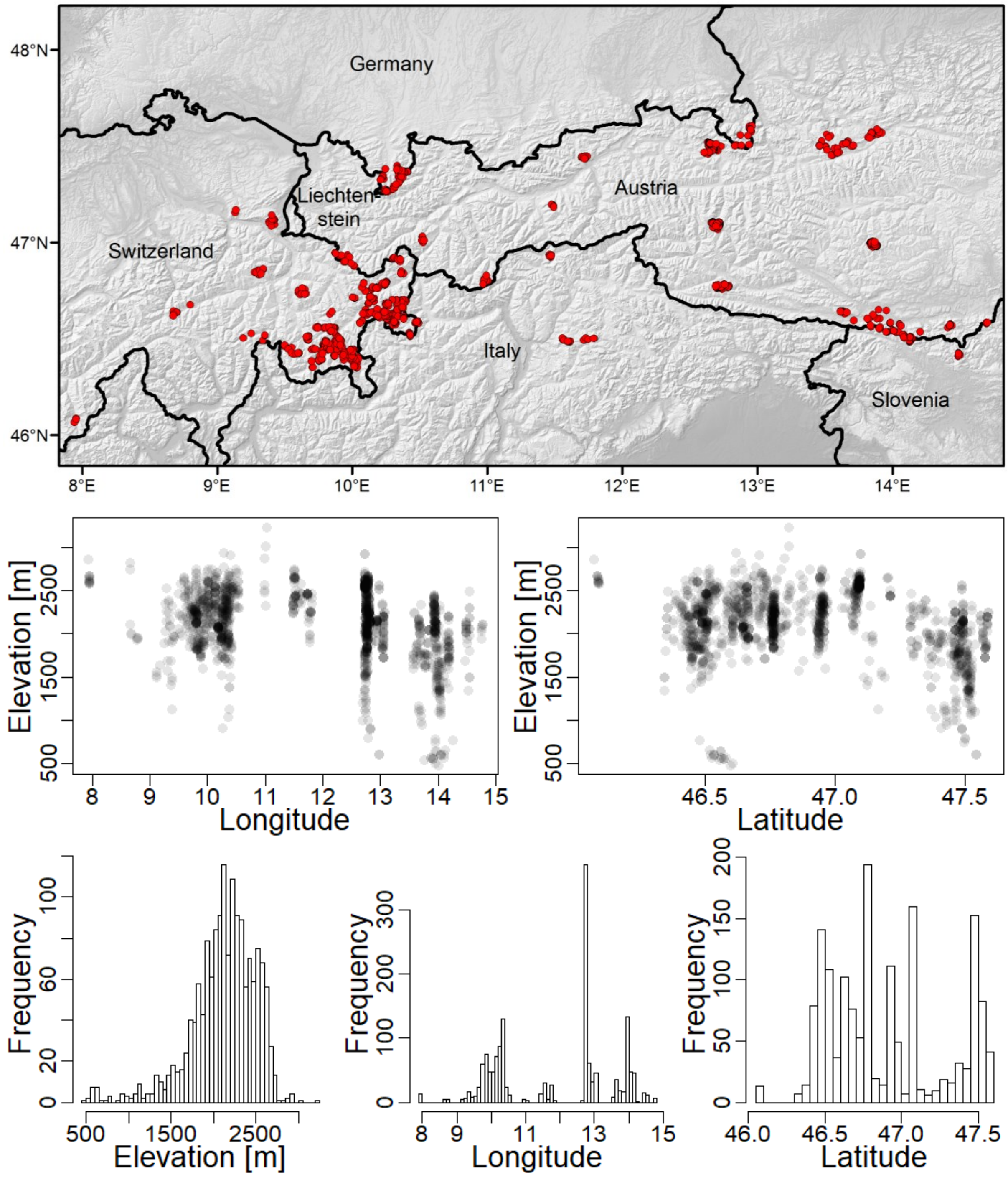
Rumpf *et al.*

Supplementary Table 1 Relations between disequilibria and species-specific properties of 135 vascular Alpine plants species. Extinction debts and colonization credits are relative to expected extinction and colonization events, respectively. Estimates were derived from beta-distributed linear regressions with a logit link for which values of extinction debts and colonization credits were transformed following Smithson and Verkuilen[1] to include zeros (see Methods). For dispersal capability high values represent higher dispersal capability of species by wind and animals, and for persistence capability high values represent competitive, long-living and dominant species. Temperature indicators represent alpine to nival (1), lower alpine to upper subalpine (1.5), subalpine (2), lower subalpine to upper montane (2.5), and montane (3) species. Values for dispersal and persistence capability were derived from own measurements, literature[2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15] and online data bases[16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31]. Temperature indicator values were derived from Landolt *et al.*[8].

Type of disequilibrium	Predictor	Estimate ± SE	df	z-value	p-value	pseudo R^2
Colonization credit	Intercept	-1.36 ± 0.13				
	Dispersal capability	-0.13 ± 0.06	131	-2.10	0.036	0.07
Extinction debt	Intercept	-2.16 ± 0.11				
	Dispersal capability	0.10 ± 0.05	131	1.92	0.055	0.03
Colonization credit	Intercept	-1.35 ± 0.13				
	Persistence capability	0.03 ± 0.09	131	0.33	0.741	<0.01
Extinction debt	Intercept	-2.16 ± 0.11				
	Persistence capability	-0.10 ± 0.07	131	-1.31	0.192	0.02
Colonization credit	Intercept	4.89 ± 1.05				
	Historical optimum	-2.84e-3 ± 0.48e-3	132	-5.94	<0.001	0.36
Extinction debt	Intercept	-6.87 ± 0.90				
	Historical optimum	2.10e-3 ± 0.40e-3	132	5.31	<0.001	0.20
Colonization credit	Intercept	-3.06 ± 0.35				
	Temperature indicator	0.98 ± 0.19	127	5.21	<0.001	0.28
Extinction debt	Intercept	-1.09 ± 0.27				
	Temperature indicator	-0.65 ± 0.16	127	-4.17	<0.001	0.14



Supplementary Figure 1 Number of re-surveyed plots in which colonization (left) and extinction (right) events were expected for 135 vascular plant species of the European Alps. On average across all species, colonization events were expected in 73 of the 1576 re-surveyed plots and extinction events in 54. Nine and four species had an expected colonization and extinction event in less than 10 plots, respectively (colonization: *Carex rupestris*, *Gentiana orbicularis*, *Gentianella aspera*, *Leontodon montanus*, *Pedicularis aspleniifolia*, *Phyteuma globulariifolium*, *Primula integrifolia*, *Saxifraga moschata*, and *Sesleria ovata*; extinction: *Laserpitium halleri*, *Potentilla grandiflora*, *Rumex scutatus*, and *Valeriana celtica*), and no species had none expected colonization or extinction event.



Supplementary Figure 2 Spatial distribution of the 1576 re-surveyed plots. Historical species distribution data were obtained from 26 historical publications[32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57], were first recorded between 1911-1970, and none of these plots was re-surveyed multiple times. Below the tree line, plots were typically located on extensively used pastures during both the historical and recent survey. In the historical survey, the number of species per plot ranged from 1 to 70 with a mean of 24 species, while the number of species per plot ranged from 2 to 81 with a mean of 29 in the recent re-survey. Potential sources of sampling bias and observer error were reduced as far as possible by a rigid re-location and re-survey design (see Rumpf *et al.*[58] for further details). The topographic background of the map was derived from Copernicus data of the European Environmental Agency.

Supplementary Methods

SDM calibration

```
BIOMOD_Modeling(myBiomodData,
                models              = c("GLM", "GAM", "GBM","CTA", "ANN",
                                        "SRE", "FDA", "MARS", "RF"),
                models.options      = *myBiomodOption*,
                NbRunEval           = 3,
                DataSplit           = 80,
                Prevalence          = 0.5,
                VarImport           = 3,
                models.eval.meth    = c("TSS", "ROC", "KAPPA"),
                SaveObj             = F,
                rescal.all.models   = T,
                do.full.models      = F)
```

where **myBiomodOption** are the default settings as follows:

```
GLM =   list( type = 'quadratic',
        interaction.level = 0,
        myFormula = NULL,
        test = 'AIC',
        family = binomial(link = 'logit'),
        mustart = 0.5,
        control = glm.control(epsilon = 1e-08, maxit = 50, trace = FALSE) ),
GAM =   list( algo = 'GAM_mgcv',
        type = 's_smoother',
        k = -1,
        interaction.level = 0,
        myFormula = NULL,
        family = binomial(link = 'logit'),
        method = 'GCV.Cp',
        optimizer = c('outer','newton'),
        select = FALSE,
        knots = NULL,
        paraPen = NULL,
        control = list(nthreads = 1, irls.reg = 0, epsilon = 1e-07, maxit = 200, trace = FALSE, mgc
                v.tol = 1e-07, mgcv.half = 15, rank.tol = 1.49011611938477e-08, nlm = list(ndi
                git=7, gradtol=1e-06, stepmax=2, steptol=1e-04, iterlim=200, check.analytical
                s=0), optim = list(factr=1e+07), newton = list(conv.tol=1e-06, maxNstep=5, m
                axSstep=2, maxHalf=30, use.svd=0), outerPIsteps = 0, idLinksBases = TRUE,
                scalePenalty = TRUE, keepData = FALSE, scale.est = pearson) ),
GBM =   list( distribution = 'bernoulli',
        n.trees = 2500,
        interaction.depth = 7,
        n.minobsinnode = 5,
        shrinkage = 0.001,
        bag.fraction = 0.5,
        train.fraction = 1,
        cv.folds = 3,
        keep.data = FALSE,
        verbose = FALSE,
        perf.method = 'cv'),
```

```
CTA =     list( method = 'class',
          parms = 'default',
          cost = NULL,
          control = list(xval = 5, minbucket = 5, minsplit = 5, cp = 0.001, maxdepth = 25) ),
ANN =     list( NbCV = 5,
          size = NULL,
          decay = NULL,
          rang = 0.1,
          maxit = 200),
SRE =     list( quant = 0.025),
FDA =     list( method = 'mars'),
MARS =    list( degree = 2,
          nk = NULL,
          penalty = 2,
          thresh = 0.001,
          prune = TRUE),
RF =      list( do.classif = TRUE,
          ntree = 500,
          mtry = 'default',
          nodesize = 5,
          maxnodes = NULL)
```

Ensemble modelling

```
BIOMOD_EnsembleModeling(modeling.output                  = myBiomodModelOut,
                        chosen.models                    = "all",
                        em.by                            = "all",
                        eval.metric                      = c("TSS"),
                        eval.metric.quality.threshold    = c(0.6),
                        prob.mean                        = T,
                        prob.cv                          = T,
                        prob.ci                          = F,
                        prob.ci.alpha                    = 0.05,
                        prob.median                      = F,
                        committee.averaging              = F,
                        prob.mean.weight                 = T,
                        prob.mean.weight.decay           = "proportional")
```

Projections

```
BIOMOD_Projection(modeling.output       = myBiomodModelOut,
                  new.env               = *environmental_data*,
                  proj.name             = *running_name*,
                  selected.models       = "all",
                  binary.meth           = "TSS",
                  compress              = "xz",
                  keep.in.memory        = FALSE,
                  on_0_1000             = TRUE,
                  build.clamping.mask   = T)
```

where **environmental_data** refers to either historic or recent environmental data of the data set, and **running_name** to an arbitrary name to save the output.

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