

Appendices: Tree species vary widely in their tolerance for liana infestation: a case study of differential host response to generalist parasites.

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S1 SPECIES INCLUDED AND THEIR SAMPLE SIZES IN DIFFERENT DATASETS

S1 SPECIES INCLUDED AND THEIR SAMPLE SIZES IN DIFFERENT DATASETS

Table S1.1. Overview of species used in each analysis, ordered alphabetically. A cross (X) indicates a species was included. Columns fecundity, reproduction, growth and survival respectively refer to the annual probability of reproducing; fraction of the crown bearing reproductive structures; growth; and survival.

Species	Fecundity	Reproduction	Growth	Survival
<i>Acalypha diversifolia</i>	X	X		
<i>Alchornea costaricensis</i>	X	X	X	X
<i>Alseis blackiana</i>	X	X	X	X
<i>Anacardium excelsum</i>	X	X	X	X
<i>Apeiba membranacea</i>	X	X	X	X
<i>Apeiba tibourbou</i>	X	X	X	X
<i>Aspidosperma spruceanum</i>	X	X		
<i>Astrocaryum standleyanum</i>	X	X	X	X
<i>Astronium graveolens</i>	X	X	X	X
<i>Beilschmiedia pendula</i>	X	X	X	X
<i>Brosimum alicastrum</i>	X	X		
<i>Calophyllum longifolium</i>	X	X		
<i>Casearia aculeata</i>	X	X		
<i>Casearia arborea</i>	X	X	X	X
<i>Cassipourea elliptica</i>	X	X		
<i>Cecropia insignis</i>	X	X		
<i>Cecropia obtusifolia</i>	X	X	X	X
<i>Ceiba pentandra</i>	X	X	X	X
<i>Chrysophyllum argenteum</i>	X	X	X	X
<i>Chrysophyllum cainito</i>	X	X	X	X
<i>Cordia alliodora</i>	X	X		
<i>Cordia bicolor</i>	X	X		
<i>Coussarea curvigemma</i>	X	X		
<i>Croton billbergianu</i>	X	X		
<i>Cupania seemannii</i>	X	X	X	X
<i>Desmopsis panamensis</i>	X	X	X	X
<i>Dipteryx oleifera</i>	X	X		
<i>Drypetes standleyi</i>	X	X		
<i>Eugenia galalonensis</i>	X	X	X	X
<i>Eugenia nesiotica</i>	X	X		
<i>Eugenia oerstediana</i>	X	X	X	X
<i>Faramea occidentalis</i>	X	X	X	X
<i>Garcinia intermedia</i>	X	X	X	X
<i>Guapira standleyana</i>	X	X		
<i>Guarea guidonia</i>	X	X	X	X
<i>Gutteria dumetorum</i>	X	X		
<i>Guettarda foliacea</i>	X	X	X	X
<i>Gustavia superba</i>	X	X	X	X
<i>Hasseltia floribunda</i>	X	X	X	X
<i>Heisteria concinna</i>	X	X		
<i>Hirtella triandra</i>	X	X	X	X
<i>Hura crepitans</i>	X	X		
<i>Hieronyma alchorneoide</i>	X	X	X	X
<i>Inga marginata</i>	X	X	X	X
<i>Jacaranda copaia</i>	X	X	X	X

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S1 SPECIES INCLUDED AND THEIR SAMPLE SIZES IN DIFFERENT DATASETS

Table S1.1. Continued

<i>Laetia thamnia</i>	X	X		
<i>Lindackeria laurina</i>	X	X		
<i>Lonchocarpus heptaphyllus</i>	X	X	X	X
<i>Luehea seemannii</i>	X	X		
<i>Macrocnemum roseum</i>	X	X		
<i>Mosannonna garwoodii</i>	X	X		
<i>Miconia affinis</i>	X	X	X	X
<i>Miconia argentea</i>	X	X	X	X
<i>Miconia nervosa</i>	X	X		
<i>Mouriri myrtilloides</i>	X	X	X	X
<i>Nectandra cissiflora</i>	X	X		
<i>Ocotea cernua</i>	X	X	X	X
<i>Ocotea oblonga</i>	X	X	X	X
<i>Ocotea whitei</i>	X	X	X	X
<i>Oenocarpus mapora</i>	X	X		
<i>Platymiscium pinnatum</i>	X	X		
<i>Platypodium elegans</i>	X	X	X	X
<i>Pachira sessilis</i>	X	X	X	X
<i>Poulsenia armata</i>	X	X		
<i>Pouteria reticulata</i>	X	X	X	X
<i>Prioria copaiifera</i>	X	X		
<i>Protium costaricense</i>	X	X		
<i>Protium panamense</i>	X	X	X	X
<i>Protium tenuifolium</i>	X	X	X	X
<i>Pseudobombax septenatum</i>	X	X		
<i>Pterocarpus rohrii</i>	X	X	X	X
<i>Quararibea asterolepis</i>	X	X	X	X
<i>Randia armata</i>	X	X	X	X
<i>Rinorea sylvatica</i>	X	X	X	X
<i>Attalea butyracea</i>	X	X		
<i>Simarouba amara</i>	X	X		
<i>Sloanea terniflora</i>	X	X	X	X
<i>Socratea exorrhiza</i>	X	X	X	X
<i>Spondias radlkoferi</i>	X	X	X	X
<i>Tabebuia guayacan</i>	X	X	X	X
<i>Tabebuia rosea</i>	X	X	X	X
<i>Tabernaemont arborea</i>	X	X	X	X
<i>Tachigali versicolor</i>	X	X	X	X
<i>Talisia nervosa</i>	X	X		
<i>Terminalia amazonia</i>	X	X	X	X
<i>Terminalia oblonga</i>	X	X		
<i>Tetragastris panamensis</i>	X	X		
<i>Trattinnicki aspera</i>	X	X	X	X
<i>Trichilia pallida</i>	X	X		
<i>Trichilia tuberculata</i>			X	X
<i>Triplaris cumingiana</i>			X	X
<i>Unonopsis pittieri</i>			X	X
<i>Virola sebifera</i>			X	X
<i>Virola multiflora</i>			X	X
<i>Virola surinamensis</i>			X	X
<i>Vochysia ferruginea</i>			X	X
<i>Xylopia macrantha</i>			X	X
<i>Zanthoxylum ekmanii</i>			X	X
<i>Zanthoxylum panamense</i>			X	X

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S1 SPECIES INCLUDED AND THEIR SAMPLE SIZES IN DIFFERENT DATASETS

Table S1.1. Continued

S1 SPECIES INCLUDED AND THEIR SAMPLE SIZES IN DIFFERENT DATASETS

Table S1.2. The focal species used to build integral projection models, and their sample sizes in the various datasets (described in the maintext). The columns seeds, recruits, seedlings, trees, and reproduction correspond to the number of individual records of seeds (dataset 2), new recruits (dataset 3) from the seedling census (dataset 4), BCI 50ha FDP census and towerplot data (dataset 1), and the data on the reproduction and liana census (dataset 6). A total of 33 have enough data - including information on liana loads > 1 cm dbh

Species	Seeds	Recruits	Seedlings	Trees	Reproduction
<i>Alchornea costaricensi</i>	10187	77	336	828	260
<i>Alseis blackiana</i>	152070	70	2060	13182	1261
<i>Apeiba membranacea</i>	8028	127	298	570	307
<i>Beilschmiedi pendula</i>	1708	1935	16382	4056	115
<i>Brosimum alicastrum</i>	6687	97	1558	1194	403
<i>Cecropia insignis</i>	80899	187	834	2551	742
<i>Chrysophyllu argenteum</i>	39	33	407	1119	92
<i>Chrysophyllu cainito</i>	919	220	908	271	42
<i>Cordia alliodora</i>	5188	105	477	433	227
<i>Cordia bicolor</i>	5770	63	641	2222	561
<i>Drypetes standleyi</i>	639	81	1122	3080	169
<i>Eugenia oerstediana</i>	1717	883	6906	4039	91
<i>Garcinia intermedia</i>	328	85	971	6945	961
<i>Guarea guidonia</i>	1213	184	1013	3134	721
<i>Guatteria dumetorum</i>	1237	53	191	2293	242
<i>Gustavia superba</i>	216	365	1589	1187	99
<i>Heisteria concinna</i>	907	505	1072	1189	368
<i>Hirtella triandra</i>	741	222	1360	6587	870
<i>Jacaranda copaia</i>	79938	160	284	783	479
<i>Luehea seemannii</i>	116071	182	540	648	508
<i>Miconia argentea</i>	3385	115	728	2884	177
<i>Ocotea whitei</i>	117	186	4715	1566	283
<i>Platypodium elegans</i>	482	10	105	312	132
<i>Pouteria reticulata</i>	646	340	3869	2705	253
<i>Quararibea asterolepis</i>	18090	1349	7317	3207	124
<i>Simarouba amara</i>	1472	98	784	3787	471
<i>Tabebuia guayacan</i>	3729	58	254	132	132
<i>Tabebuia rosea</i>	3262	133	464	573	280
<i>Tabernaemont arborea</i>	730	44	365	2544	128
<i>Tetragastris panamensis</i>	2343	575	3909	7213	511
<i>Trichilia pallida</i>	366	49	146	1157	662
<i>Trichilia tuberculata</i>	28841	3756	9577	20309	758
<i>Triplaris cumingiana</i>	716	154	247	640	380

S2 R CODE

We provide the code used to build the integral projection models as an unofficial R-package (IPM2s). This package can be installed locally from the archive downloaded from the Smithsonian repository¹, or it can be directly installed from github using the package devtools in R. Note that maintained official R packages exist on CRAN (e.g. IPMpack).

```
## devtools is required
require(devtools)
install_github("MarcoDVisser/IPM2s")
```

An example code on how to fit models and build IPMs is supplied below. A text file with the example code below can be found in the package source code in the /int/example folder as a textfile.

```
#####
#####
## Example script for building IPMs for a given species list
## (object SpFitList) from fitted models
#####
## Update 20.01.2017, Princeton, NJ

## Load all fit model objects
require(lme4)
require(IPM2s)

#####
#####
## Step 1: Simulate datasets
#####
#####
## Species
SpFitList <- c("A", "B", "C")

#####
## < 1 cm dbh Individuals = Seedlings
#####

## Number of seedlings per species
N <- 1000
Seedlings <- data.frame(
  id=paste0(rep(SpFitList,each=N),rep(1:N,length(SpFitList))),
  height=rep(seq(1,2000,length.out=N),length(SpFitList)),
  sp=rep(SpFitList,each=N))

#####
## 1 cm dbh + Individuals = Trees
#####
cat("\t ##### \n ")
cat("\t \t \t Creating example datasets \n")
cat("\t ##### \n ")
```

¹<https://repository.si.edu/handle/10088/32629>

```

## Number of trees per species
N <- 1000
Trees <- data.frame(
  id=paste0(rep(SpFitList,each=N),rep(1:N,length(SpFitList))),
  dbh=rep(1:N,length(SpFitList)),
  sp=rep(SpFitList,each=N)

## Survival & growth per species
sB0 <- rep(c(1.3,1.6,1.8),each=N) # Seedlings
sB1 <- rep(c(0.001,0.002,0.003),each=N) # Seedlings
B0 <- rep(c(1.7,2.2,3),each=N) # Trees
B1 <- rep(c(0.004,0.003,0.003),each=N) # Trees
B2 <- rep(c(-1.5,-1,-1),each=N) # Trees

## Reproduction curve
B3 <- rep(c(-5,-10,-50),each=N) # Trees
B4 <- rep(c(0.02,0.03,0.08),each=N) # Trees
B5 <- rep(c(-2,-1,-1),each=N) # Trees

## Seedling annual survival
Seedlings$S <- rbinom(N*length(SpFitList),1,
  prob=plogis(sB0+sB1*Seedlings$height))
## Seedling annual growth
Seedlings$G <- rnorm(N*length(SpFitList),
  mean=rev(B0)+rev(B1)*Seedlings$height,sd=1)

## random liana score
Trees$liana <- sample(0:4,3*N,prob=c(.6,.1,.1,.1,.1),replace=TRUE)

## Tree annual survival
Trees$S <- rbinom(N*length(SpFitList),1,
  prob=plogis(B0+B1*Trees$dbh+B2*Trees$liana))
## Tree annual growth
Trees$G <- rnorm(N*length(SpFitList),
  mean=rev(B0)+rev(B1)*Trees$dbh+rev(B2)*Trees$liana,sd=1)

## Tree annual reproduction
Trees$R <- rbinom(N*length(SpFitList),1,
  prob=plogis(B3+B4*Trees$dbh+B5*Trees$liana))

## Tree annual crown fraction
Trees$C <- plogis(B3+B4*Trees$dbh+B5*Trees$liana)

## Tree dbh height allometry
Trees$H <- SLogis(Trees$dbh,rev(2e4*B0)+rev(10*B1)*Trees$dbh,400,410)

## All other vital rates are kept constant for simplicity
## (as not to needlessly increase complexity of an example)

cat("\t ##### \n ")
cat("\t \t \t Done creating example datasets \n")
cat("\t ##### \n ")

```



```

#####
#####
## Step 2: Fit vital rate models
#####
#####

## Timing starts.. this may take some time (about 3-4 min on most systems)
## Speed up by setting N lower above

StartT <- Sys.time()
cat("\t ##### \n ")
cat( "\t \t \t Fitting vital rate models \n")
cat("\t ##### \n ")

## First Seedlings
## Standardize size (aids in model convergence)
## Growth
Seedlings$size <- scale(Seedlings$height)
temp <- unlist(attributes(Seedlings$size)[2:3])
sdlgrownorm <- list(size=c(temp[1],temp[2]))
sdlgrowmain.saved <- lmer(G~size+(1+size|sp),data=Seedlings)

## Check the linear assumption of the model
## Red lines should be centred around zero
## and show no trend, or curves
linearityCheck(sdlgrowmain.saved,"size")

##in this case sigma is equal among species
sdlsigmas <- array(rep(sigma(sdlgrowmain.saved),
                        length(SpFitList)))
names(sdlsigmas) <- SpFitList

## Survival
sdlsurvmain.saved <- glmer(S~size+(1+size|sp),data=Seedlings,family=binomial)
sdlsurvnorm <- sdlgrownorm

## Note that whenever models warn about convergence problems.
## This can be caused by scale differences between variables.
## The tolerance is optimal for variables on a scale
## close to -1 to 1. Some models here have
## other scales, and may converge on the correct
## solution despite the warning.
## User can test this by checking the relative
## tolerance and seeing if it is acceptable.
## User can also update the model to
## test if more iterations solves this.
## The models above and below seem to have found the correct parameters
## (the ones used to create the data), despite the
## warnings.

## Warnings on convergence, update model to run try again
sdlsurvmain.saved <- update(sdlsurvmain.saved)

## still complaining check relative values
relgrad <- with(sdlsurvmain.saved@optinfo$derivs,solve(Hessian,gradient))

```

```

## Check if the gradient is fine
max(abs(relgrad))<0.001 ## model can be assumed to have converged

## Check the linear assumption of the model
linearityCheck(sdl survmain.saved, "size")

## Now Trees

## Growth
Trees$size <- scale(Trees$dbh) # Normalization again
growmain.saved <- lmer(G~size+as.factor(liana)+(1+size+as.factor(liana)|sp),
                      data=Trees)

## Check the linear assumption of the model
linearityCheck(growmain.saved, "size")

temp <- unlist(attributes(Trees$size)[2:3]) ##L
grownorm <- list(size=c(temp[1],temp[2]))

##in this case sigma is equal among species
treesigmas <- array(rep(sigma(sdl growmain.saved),
                        length(SpFitList)))
names(treesigmas) <- SpFitList

## Survival
survmain.saved <- glmer(S~size+as.factor(liana)+(1+size+as.factor(liana)|sp),
                      data=Trees,family=binomial)

## Check the linear assumption of the model
linearityCheck(survmain.saved, "size")

survnorm <- grownorm

## Reproduction
repmain.saved <- glmer(R~size+as.factor(liana)+(1+size+as.factor(liana)|sp),
                      data=Trees,family=binomial)
repnorm <- grownorm

## Check the linear assumption of the model
linearityCheck(repmain.saved, "size")

## crown fraction
fecmain.saved <- lmer(C~size+as.factor(liana)+(1+size+as.factor(liana)|sp),
                    data=Trees)
fecnorm <- grownorm

## here we see linearity problems (created on purpose, to illustrate)
linearityCheck(fecmain.saved, "size")

## Allometric model
s2tmod.saved <- lmer(dbh~H+(1+dbh|sp), data=Trees)

## CONSTANT VITAL RATES (for simplicity)
## seed production
seedprod.saved <- data.frame(sp=SpFitList, fec=rep(1,length(SpFitList)))
## recruitment and height distributions

```

```

recruirate.saved <- data.frame(sp=SpFitList, rrater=rep(.1,length(SpFitList)))

sdlheightresults.saved <- data.frame(sp=SpFitList, v=rep(1.05,length(SpFitList)),
                                     lambda=rep(12.5,length(SpFitList)),
                                     shape=rep(1.05,length(SpFitList)),
                                     scale=rep(1.05,length(SpFitList)))

## Size ranges
Sizeranges <- data.frame(sp=SpFitList, maxdbh=rep(2000,length(SpFitList)))

EndT <- Sys.time()

cat("\t ##### \n ")
cat( "\t \t All models fit. Work started at \n")
cat( "\t \t",format(StartT),"\n")
cat( "\t \t Work ended at \n")
cat( "\t \t",format(EndT),"\n")
cat( "\t \t Which took \n")
cat( "\t \t",format(EndT-StartT),"\n")
cat("\t ##### \n ")
cat("\n")

#####
## Setup bootstrap

Nboots <- 10
LianaEigenvalues <- array(dim=c(length(SpFitList),5,Nboots),
                          dimnames=list(SpFitList,
                                          c("10","11","12","13","14"),
                                          1:Nboots))

## Start bootstrap operations
merModSamplerFE <- function(mod,n=1) {
  mvrnorm(n,fixef(mod),vcov(mod))
}

cat("\t ##### \n ")
cat("\t Starting bootstrap with",Nboots, " iterations for ",length(SpFitList), "Species \n ")
cat("\t ##### \n ")

## time the execution
StartT <- Sys.time()

for(j in 1:Nboots){

#####
  ## iterate model parameters
#####
  ## NON MerMod

```

```

## subset all fit objects to focal species
seedprod <- seedprod.saved
recruitrate <- recruitrate.saved
sdlheightresults <- sdlheightresults.saved

## MerMod

## allometric equations
s2tmod <- s2tmod.saved
s2tmod@beta <- merModSamplerFE(s2tmod)
IPM_s2t <- data.frame(sp=rownames(ranef(s2tmod)$sp),
                     intercept=fixef(s2tmod)[1]+ranef(s2tmod)$sp[,1],
                     slope=fixef(s2tmod)[2]+ranef(s2tmod)$sp[,2])

## structure list(modelname, list(modelobject, norms))
## or list(modelname, modelobject) if no norms
repmain <- repmain.saved
fecmain <- fecmain.saved
repmain@beta <- merModSamplerFE(repmain)
fecmain@beta <- merModSamplerFE(fecmain)

sdlgrowmain <- sdlgrowmain.saved
sdlgrowmain@beta <- merModSamplerFE(sdlgrowmain)
sdlsurvmain <- sdlsurvmain.saved
sdlsurvmain@beta <- merModSamplerFE(sdlsurvmain)
growmain <- growmain.saved
growmain@beta <- merModSamplerFE(growmain)
survmain <- survmain.saved
survmain@beta <- merModSamplerFE(survmain)

## Start building all IPMs
#####
DimSdl <- 100
DimTree <- 400

for(i in 1: length(SpFitList)) {

  foc.sp <- SpFitList[i]

  cat("\r \t Bootstrap ", j, "Species # ", i, " ")

  sizerange<-c(0,Sizeranges$maxdbh[Sizeranges$sp==foc.sp]*1.1)

  hghtdbhthreshold <- sdl2splg(dbh=10,model=IPM_s2t
                             ,sp=SpFitList[i])
  dbhthreshold <- sdl2splg(hght=hghtdbhthreshold,model=IPM_s2t
                          ,sp=SpFitList[i])

  seedlingclasses <- seq(sizerange[1],hghtdbhthreshold,length.out=DimSdl)
                    # remove final class
  seedlingclasses <- seedlingclasses[-length(seedlingclasses)]
  seedlingclasswidth<-mean(diff(seedlingclasses))

```

```

treeclasses<-seq(dbhthreshold,sizerange[2],length.out=DimTree)
treeclasswidth<-mean(diff(treeclasses))

classes<-c(seedlingclasses,treeclasses)

## subset all fit objects to focal species
f.sp <- seedprod[seedprod$sp==foc.sp,c("fec","sp")]
f.sts <- recruitrate[recruitrate$sp==foc.sp,c("rrate","sp")]

## structure list(modelname, list(modelobject, norms))
## or list(modelname, modelobject) if no norms
f.repro <- list("lmepredict",repro,
              list("lmepredict",list(fecmain,as.numeric(fecnorm$size))))

f.sdlhght <- data.frame("dweibull",
                      sdlheightresults$shape[sdlheightresults$sp==foc.sp],
                      sdlheightresults$scale[sdlheightresults$sp==foc.sp])
names(f.sdlhght) <- c("bestmod", "p_1", "p_2")

f.s2t <- IPM_s2t[IPM_s2t$sp==foc.sp,]

f.sg <- list(list(sdlgrowmain,sdlgrownorm$size,
                sdsigmamain[sdsigmamain==foc.sp]),
            "lmepredict")

f.ss <- list(list(sdlurvmain,sdlurvnorm$size), "lmepredict")

f.tg <- list(list(growmain,grownorm$size,treesigmamain[names(treesigmamain)==foc.sp]),
            "lmepredict")
f.ts <- list(list(survmain,survnorm$size), "lmepredict")

## No elasticity calculations needed for this step
Imat <- ItMat(vitalrate="tree growth",delta=1,size=1,
             seedlingclasses,treeclasses)

## set the liana infestation level
GlobalLianaLevel <- NULL

## Build the IPM
fullIPM <- constructIPM(seedlingclasses,treeclasses,
                      seedlingclasseswidth,treeclasseswidth,
                      sizerange,hghtdbhthreshold,dbhthreshold,
                      f.sp,f.sts,f.repro,f.sdlhght,f.s2t,f.sg,
                      f.ss,f.tg,f.ts,Imat=Imat)

## set the liana infestation level
GlobalLianaLevel <- 1
## Build the IPM
Liana1fullIPM <- constructIPM(seedlingclasses,treeclasses,
                              seedlingclasseswidth,treeclasseswidth,
                              sizerange,hghtdbhthreshold,dbhthreshold,
                              f.sp,f.sts,f.repro,f.sdlhght,f.s2t,f.sg,
                              f.ss,f.tg,f.ts,Imat=Imat)[c("IPM","GSM")]

## Build the IPM
GlobalLianaLevel <- 2

```

```

Liana2fullIPM <- constructIPM(seedlingclasses,treeclasses,
                             seedlingclasseswidth,treeclasseswidth,
                             sizerange,hghtdbhthreshold,dbhthreshold,
                             f.sp,f.sts,f.repro,f.sdlhght,f.s2t,f.sg,
                             f.ss,f.tg,f.ts,Imat=Imat)[c("IPM","GSM")]

## Build the IPM
GlobalLianaLevel <- 3
Liana3fullIPM <- constructIPM(seedlingclasses,treeclasses,
                             seedlingclasseswidth,treeclasseswidth,
                             sizerange,hghtdbhthreshold,dbhthreshold,
                             f.sp,f.sts,f.repro,f.sdlhght,f.s2t,f.sg,
                             f.ss,f.tg,f.ts,Imat=Imat)[c("IPM","GSM")]

## Build the IPM
GlobalLianaLevel <- 4
Liana4fullIPM <- constructIPM(seedlingclasses,treeclasses,
                             seedlingclasseswidth,treeclasseswidth,
                             sizerange,hghtdbhthreshold,dbhthreshold,
                             f.sp,f.sts,f.repro,f.sdlhght,f.s2t,f.sg,
                             f.ss,f.tg,f.ts,Imat=Imat)[c("IPM","GSM")]

Lianaeigenvalues [i,,j] <- c(lambda(fullIPM[["IPM"]]),
                             lambda(Liana1fullIPM[["IPM"]]),
                             lambda(Liana2fullIPM[["IPM"]]),
                             lambda(Liana3fullIPM[["IPM"]]),
                             lambda(Liana4fullIPM[["IPM"]]))

}

}
EndT <- Sys.time()

cat("\t ##### \n ")
cat( "\t \t Calculations complete. Work started at \n")
cat( "\t \t",format(StartT),"\n")
cat( "\t \t Work ended at \n")
cat( "\t \t",format(EndT),"\n")
cat( "\t \t Which took \n")
cat( "\t \t",format(EndT-StartT),"\n")
cat("\t ##### \n ")
cat("\n")

```

S3 JUSTIFICATION OF THE STATISTICAL MODELLING APPROACH

We fit hierarchical mixed models in which model parameters are fit simultaneously across species (fixed parameters), and to each species separately (random effects). We then use the across species effect of lianas (β_2) in combination with the species-specific estimates (γ_s) as a measure of the additive impact of lianas on baseline growth, mortality and reproduction (see maintext, eq. 1), and evaluate their correlations with two axis of life-history variation. This analysis is similar to fitting a separate model for each species in sequence, and then relating each liana-effect coefficient to the two axes of life-history variation, but the hierarchical approach should almost invariably lead to more robust and unbiased predictions (i.e. BLUP estimates; Robinson 1991, *Statistical Science* 6; Gelman 2006, *Technometrics* 48). Nevertheless, estimates will be subject to shrinkage (movement towards the overall mean or fixed effect). We therefore evaluated whether our result could be influenced by shrinkage (i.e. significance being driven by species estimates with low sample size pulled close to the fixed effect or overall mean). We assessed the effect of shrinkage in two ways. First, we regressed the species-specific random effects (regarding the effects of lianas; γ_s) against sample size to detect if there was any strong pull towards zero (i.e. the fixed effect) at low sample size (Figure S3.1). This shows that shrinkage does not appear to affect the results (Fig. S3.1). Second we redid all analysis using single species models for the 11 species for which the most data were available. These species had at least 10 individuals observed in each infestation class (Fig. S3.2). Rerunning all analysis, with vital rates fit separately for each of these species, showed no qualitative change our results (Figure S3.2). We also note that including traits directly as 3-way interactions (liana-trait-size) results in the same trends, levels of significance, and conclusions.

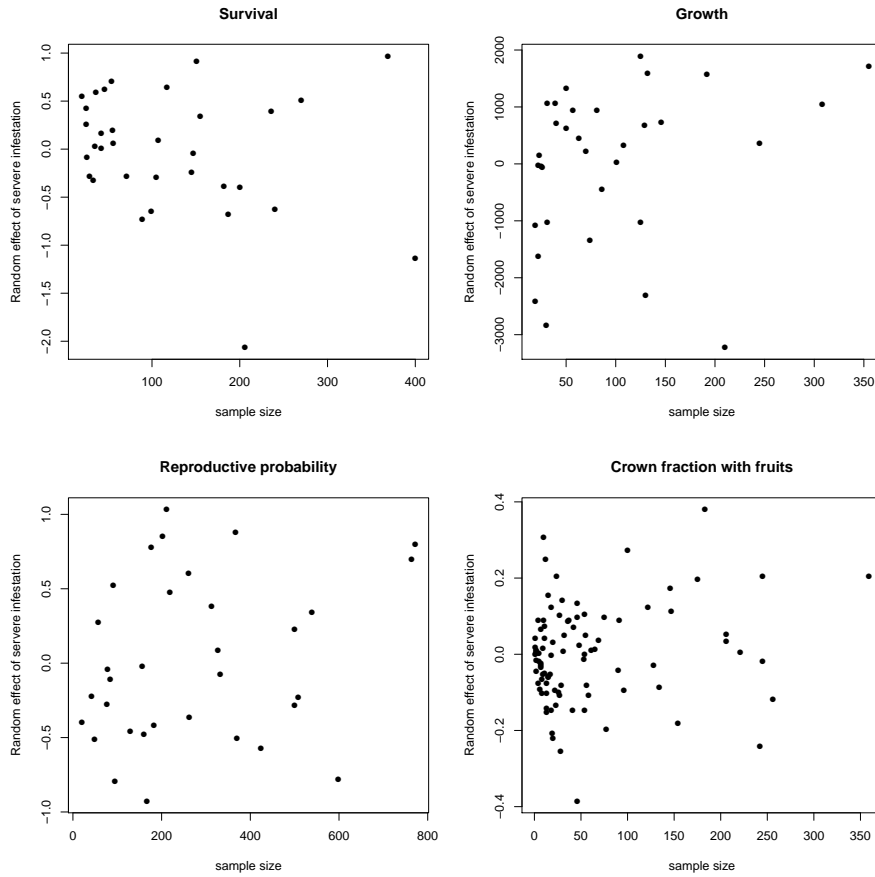


Figure S3.1. Estimates of the additive species-specific impact of lianas associated with heavy liana infestation (γ_s , y-axis) plotted against each species' sample size (x-axis). Here γ_s is the species-specific random effect (see eq. 1 in maintext). We detected no significant effect of sample size on γ_s .

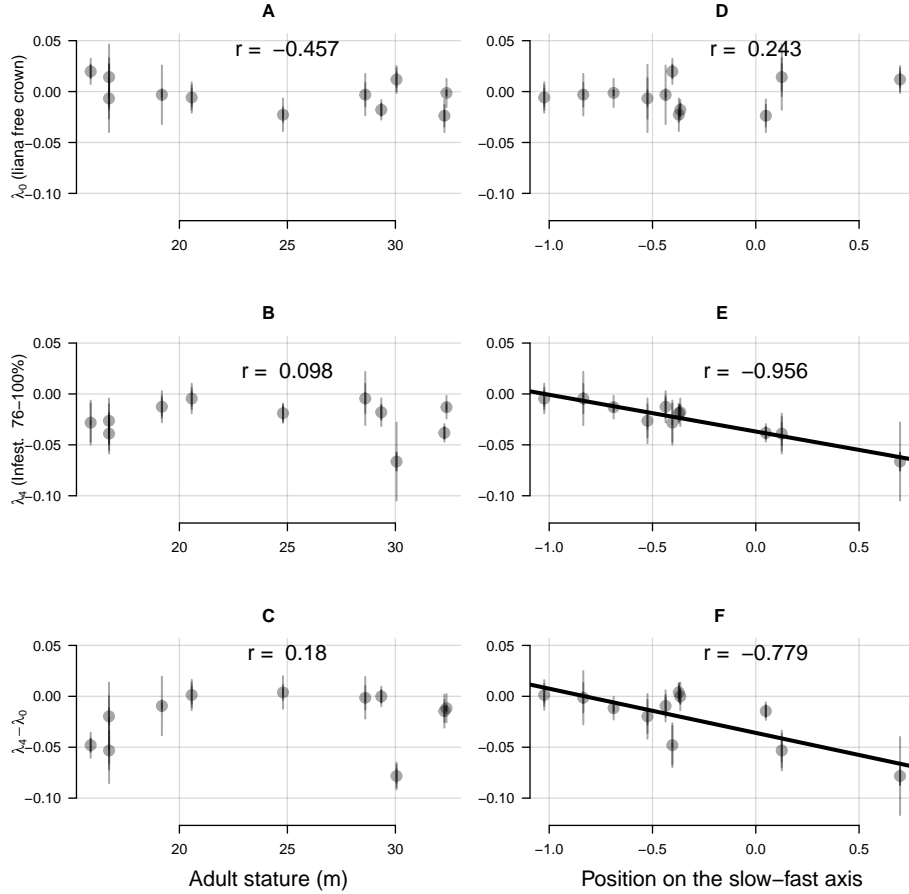


Figure S3.2. Analysis and results from figure 4, when fitting species-specific models for the 11 most numerous species (i.e. a single glm or lm fit per species per vital rate). The 11 species had at least 10 individuals in each infestation class. Figure description identical to main text, and results remain qualitatively the same.

S4 AIC VALUES OF FITTED MODELS AND MODEL COEFFICIENTS

AIC values for the models of different vital rates, including Δ AIC values are presented in the tables below. Model null, size, main and full correspond to mixed effect models including no predictor variables, using only size, size including additive effects of liana load, and full interactions between size and liana load, respectively.

Table S4.3. AIC values for the size-dependent fraction of reproductive individuals.

Model	AIC	Δ AIC
Null	19219	3512
Size	16498	791
Main	15710	3
Full	15707	0

Table S4.4. AIC values for the size-dependent seed production (fraction of crown bearing reproductive structures).

Model	AIC	Δ AIC
Null	3012	484
Size	2773	244
Main	2528	0
Full	2553	25

Table S4.5. AIC values for the size-dependent basal area growth.

Model	AIC	Δ AIC
Null	94670	11665
Size	94543	11538
Main	83062	57
Full	83005	0

Table S4.6. AIC values for the size-dependent survival.

Model	AIC	Δ AIC
Null	5191	587
Size	5075	471
Main	4603	0
Full	4609	6

Table S4.7. Fit coefficients (fixed effects) of the AIC-selected mixed models (and standard errors). Intercept and size (slope) values are the "species mean" coefficients relating to size-dependent reproduction, fecundity, growth and survival for liana free trees. Columns reproduction, fecundity, growth and survival respectively refer to the annual probability of reproducing; fraction of the crown bearing reproductive structures; basal area growth ($mm^2 \cdot year^{-1}$); and survival (10 year). Coefficients L1-L4 relate to main effects of lianas for each crown infestation class, while the L(1-4):size are the coefficients relating to size - infestation class interactions.

	Reproduction	Fecundity	Growth	Survival
Intercept	-0.4628 (0.2924)	0.6833 (0.0224)	2772.214 (308.1966)	2.067 (0.1346)
size	2.8014 (0.2603)	0.1762 (0.0218)	-37.3389 (193.466)	-0.1963 (0.1003)
L1	0.034 (0.0909)	-0.0763 (0.0132)	-443.3472 (135.146)	0.1746 (0.1549)
L2	-0.2458 (0.1182)	-0.1141 (0.0215)	-855.2915 (199.6878)	0.0702 (0.1717)
L3	-0.5911 (0.1321)	-0.167 (0.0233)	-999.2213 (179.128)	-0.2263 (0.1926)
L4	-1.9947 (0.1899)	-0.1895 (0.0338)	-1337.3534 (200.4283)	-0.5799 (0.179)
L1:size			103.2487 (127.7744)	
L2:size			395.7886 (159.3142)	
L3:size			-529.8031 (175.0574)	
L4:size			-207.356 (160.3242)	

S5 *FITTED ESTIMATES, VITAL RATES AND COMPARISONS TO
OBSERVED DATA*

S5 FITTED ESTIMATES, VITAL RATES AND
COMPARISONS TO OBSERVED DATA

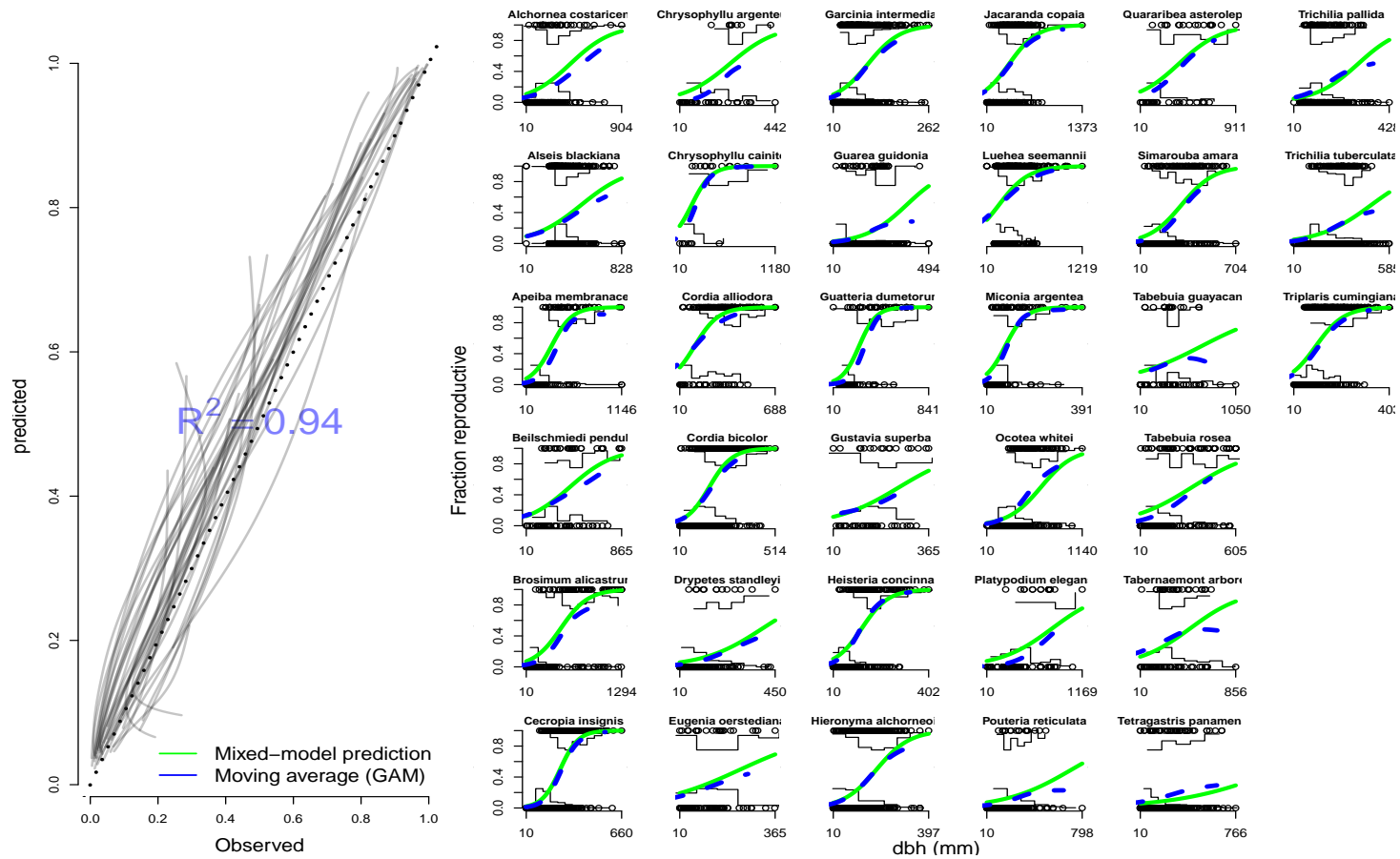


Figure S5.3. The proportion of reproductive individuals as a function of tree size (dbh). The large panel on the left shows the agreement between the model predictions from the best fit mixed-model (y-axis; see maintext) and a general additive model (x-axis; GAM) for each species. The smaller panels on the right show model fits per species over size (dbh in mm). Here, the green line shows the predicted values by the fitted mixed effect model (corresponding to the y-axis on the large left panel), while the blue lines indicates a GAM predicted moving average (corresponding to the x-axis on the large left panel). The step-wise lines are indicative of the relative density of the reproductive status at a given size.

S5 FITTED ESTIMATES, VITAL RATES AND COMPARISONS TO OBSERVED DATA

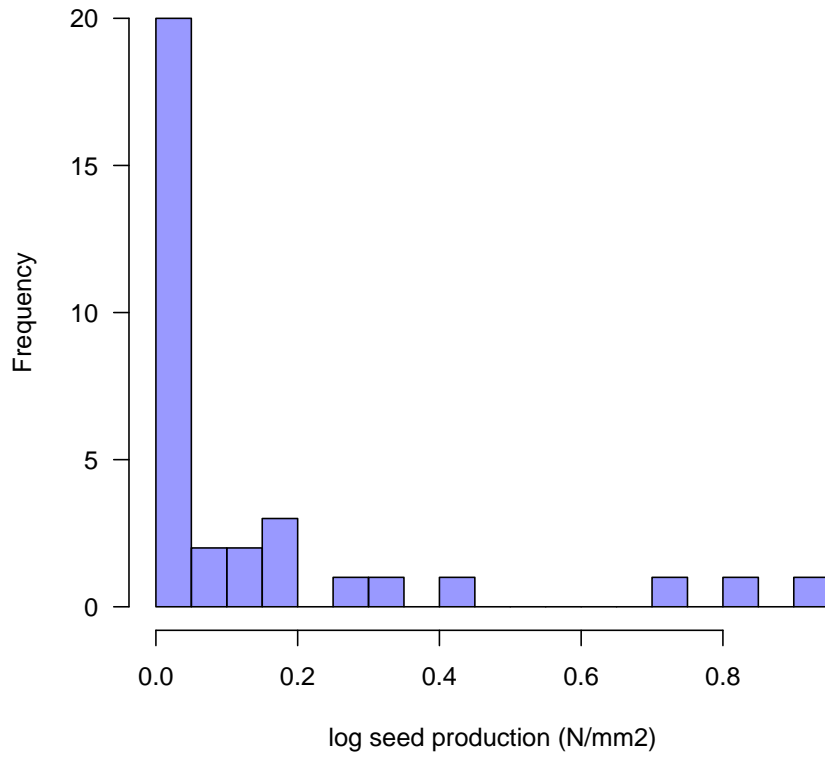


Figure S5.4. Distribution of seed production, in numbers of seeds produced per unit basal area

S5 FITTED ESTIMATES, VITAL RATES AND COMPARISONS TO OBSERVED DATA

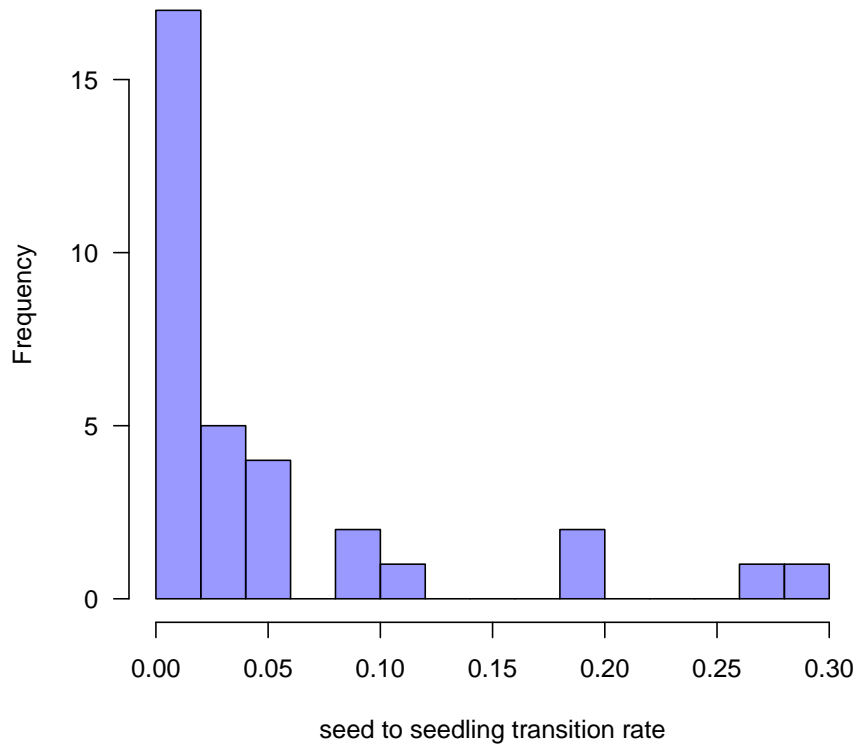


Figure S5.5. Distribution of estimates of the annual seed to seedling transition rate

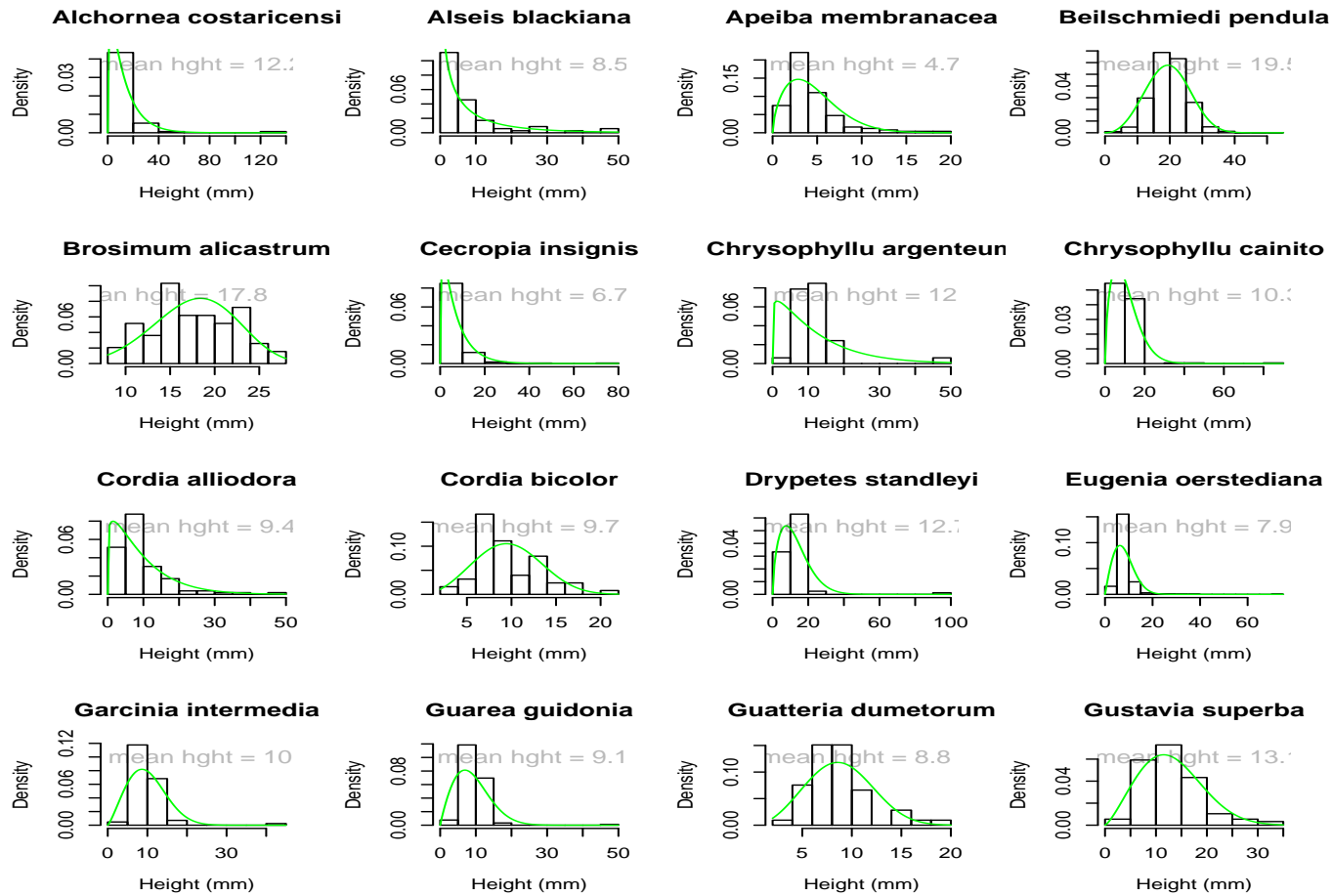


Figure S5.6. Distribution of initial heights of seedlings, with fit models (green lines). Seedling heights of zero indicate very small seedlings that could not be measured without danger of inflicting damage. The above multi-panel graph is number 1 of 3 plots containing all species.

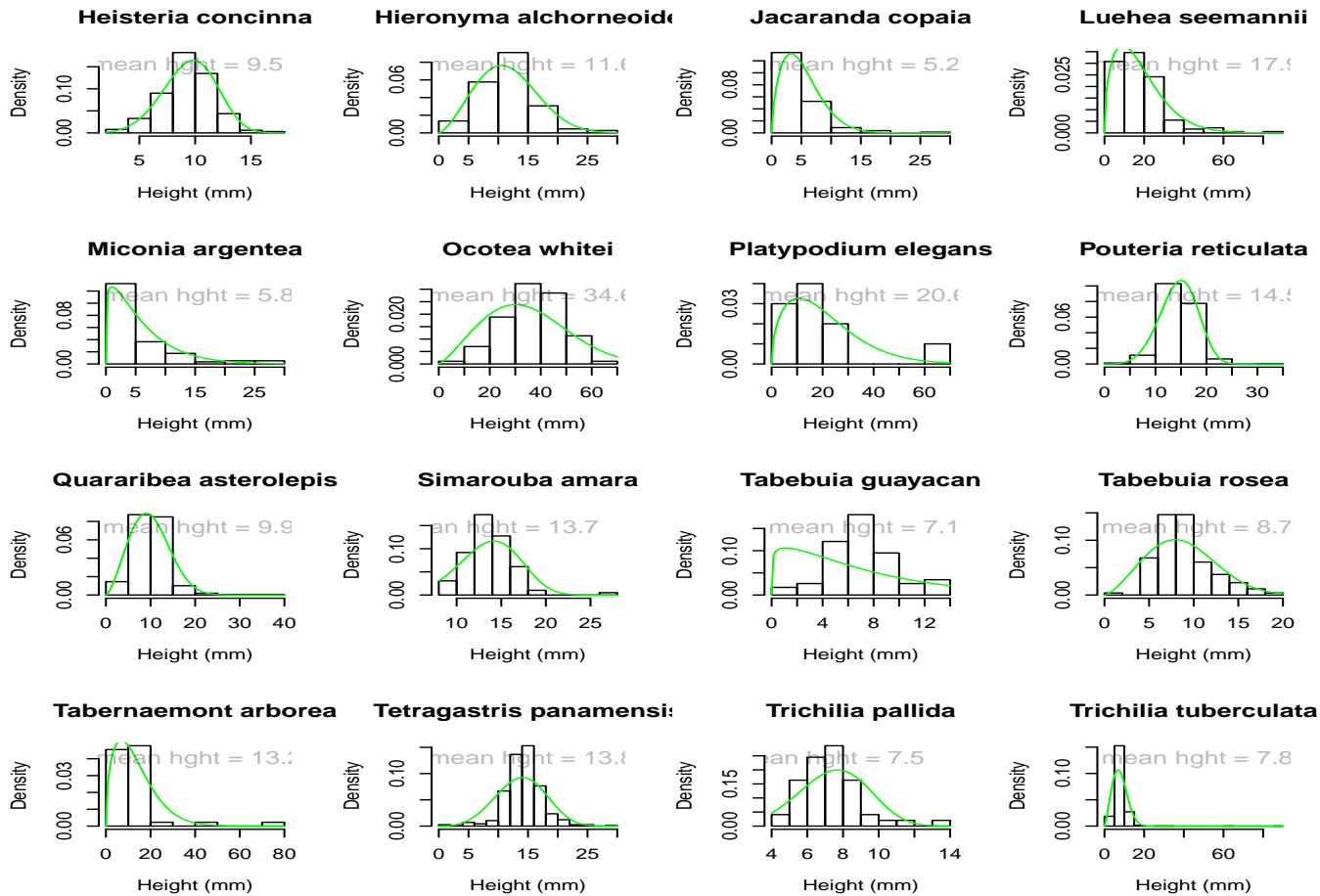


Figure S5.7. Distribution of initial heights of seedlings, with fit models (green lines). Seedling heights of zero indicate very small seedlings that could not be measured without danger of inflicting damage. The above multi-panel graph is number 2 of 3 plots containing all species.

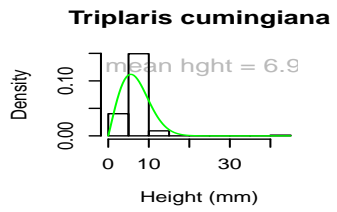


Figure S5.8. Distribution of initial heights of seedlings, with fit models (green lines). Seedling heights of zero indicate very small seedlings that could not be measured without danger of inflicting damage. The above multi-panel graph is number 3 of 3 plots containing all species.

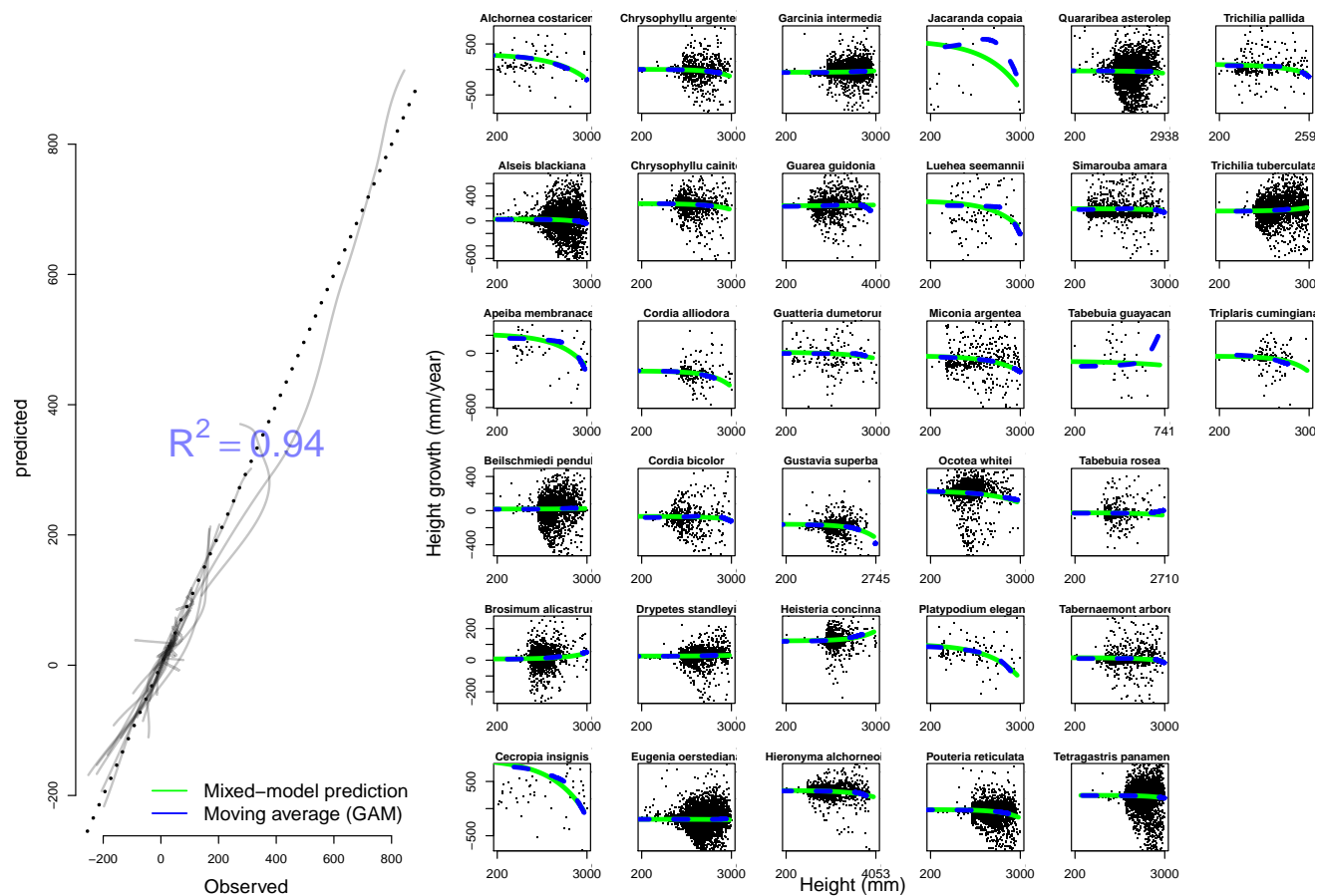


Figure S5.9. Yearly height growth of seedlings as a function of seedling height (mm). The large panel on the left shows the agreement between the model predictions from the best fit mixed-model (y-axis; see maintext) and a general additive model (x-axis; GAM) for each species. The smaller panels on the right show model fits per species over size (height in mm). Here, the green line shows the predicted values by the fitted mixed effect model (corresponding to the y-axis on the large left panel), while the blue lines indicates a GAM predicted moving average (corresponding to the x-axis on the large left panel). The histograms are indicative of the relative density of the data at a given size.

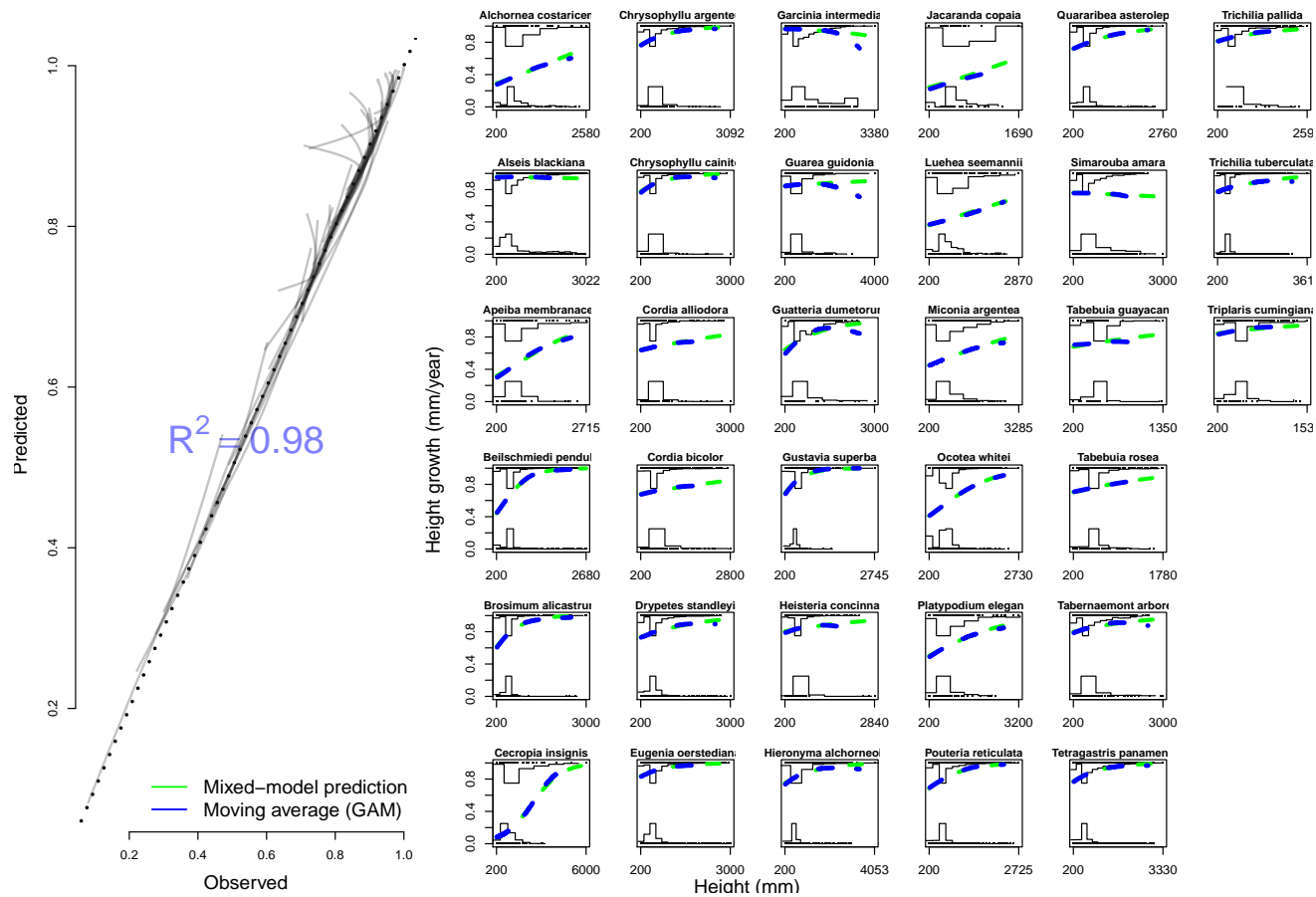


Figure S5.10. Yearly survival of seedlings as a function of seedling height (mm). The large panel on the left shows the agreement between the model predictions from the best fit mixed-model (y-axis; see maintext) and a general additive model (x-axis; GAM) for each species. The smaller panels on the right show model fits per species over size (height in mm). Here, the green line shows the predicted values by the fitted mixed effect model (corresponding to the y-axis on the large left panel), while the blue lines indicates a GAM predicted moving average (corresponding to the x-axis on the large left panel). The histograms are indicative of the relative density of the data at a given size. Individual survival and mortality states (1 and 0 values) are plotted as black dots that have been slightly jittered.

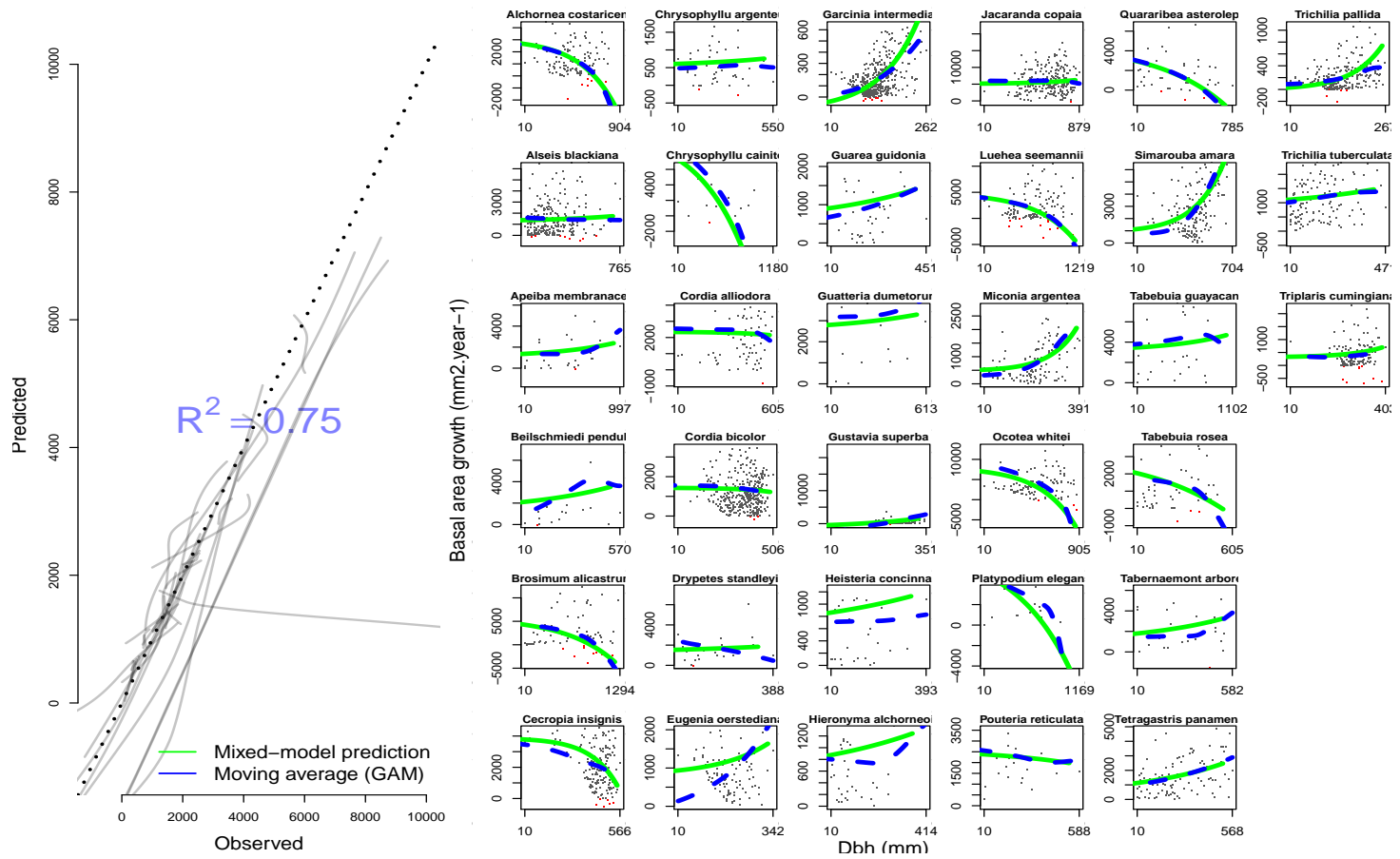


Figure S5.11. Yearly basal area growth of trees (mm^2), as a function of dbh (mm). The large panel on the left shows the agreement between the model predictions from the best fit mixed-model (y-axis; see maintext) and a general additive model (x-axis; GAM) for each species. The smaller panels on the right show model fits per species over size (height in mm). Here, the green line shows the predicted values by the fitted mixed effect model (corresponding to the y-axis on the large left panel), while the blue lines indicates a GAM predicted moving average (corresponding to the x-axis on the large left panel).

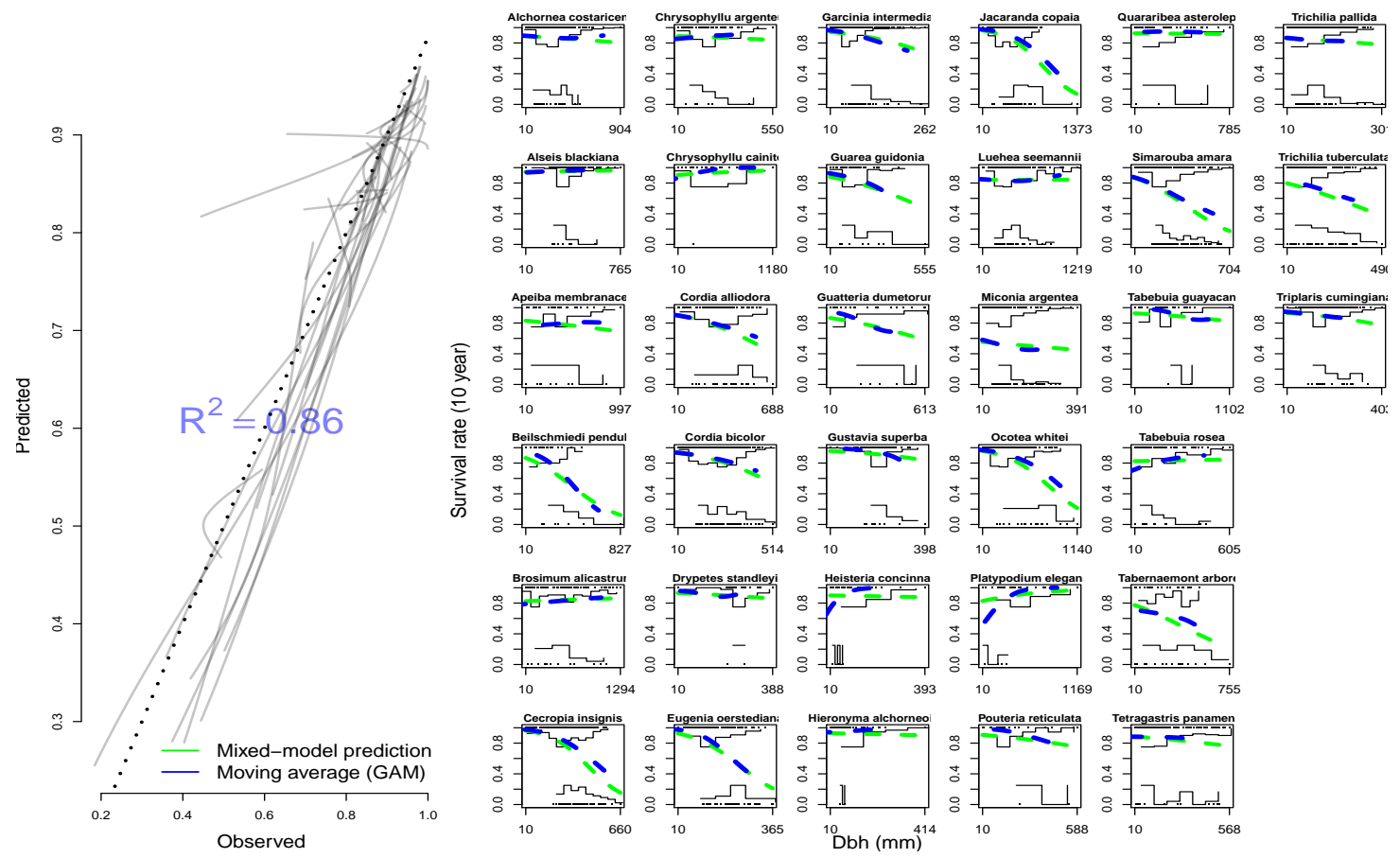


Figure S5.12. Decadal survival of trees as a function of dbh (mm). The large panel on the left shows the agreement between the model predictions from the best fit mixed-model (y-axis; see maintext) and a general additive model (x-axis; GAM) for each species. The smaller panels on the right show model fits per species over size (height in mm). Here, the green line shows the predicted values by the fitted mixed effect model (corresponding to the y-axis on the large left panel), while the blue lines indicates a GAM predicted moving average (corresponding to the x-axis on the large left panel). The stepwise lines show the relative density of mortality and survival events at different sizes classes. Individual survival and mortality states (1 and 0 values) are plotted as black dots that have been slightly jittered.

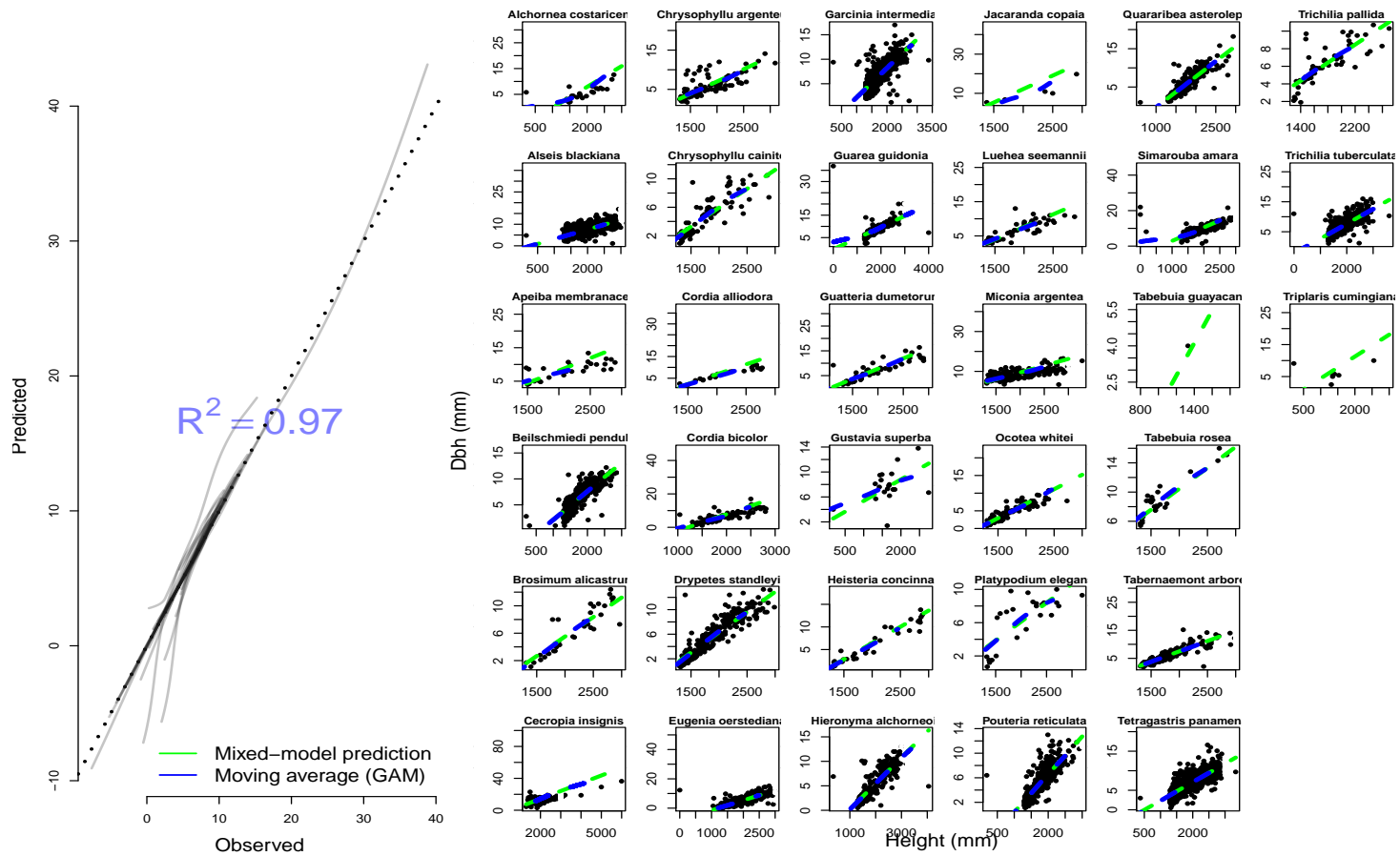


Figure S5.13. The diameter at breast height (dbh in mm) plotted against seedling height (mm), measured at the same time for each species. The large panel on the left shows the agreement between the model predictions from the best fit mixed-model (y-axis; see maintext) and a general additive model (x-axis; GAM) for each species. The smaller panels on the right show model fits per species over size (height in mm). Here, the green line shows the predicted values by the fitted mixed effect model (corresponding to the y-axis on the large left panel), while the blue lines indicates a GAM predicted moving average (corresponding to the x-axis on the large left panel). Individual survival and mortality states (1 and 0 values) are plotted as black dots that have been slightly jittered.

*S6 LIANAS EFFECTS ON POPULATION GROWTH RATES ALONG
TRAIT AXES FOR DIFFERENT LEVELS OF LIANA INFESTATION*

**S6 LIANAS EFFECTS ON POPULATION GROWTH
RATES ALONG TRAIT AXES FOR DIFFERENT
LEVELS OF LIANA INFESTATION**

Main text figure 6 shows how tree species adult stature and position on the fast-slow axis relates to effects of heavy liana infestation. Here we show parallel figures for other levels of liana infestation.

S6 LIANAS EFFECTS ON POPULATION GROWTH RATES ALONG TRAIT AXES FOR DIFFERENT LEVELS OF LIANA INFESTATION

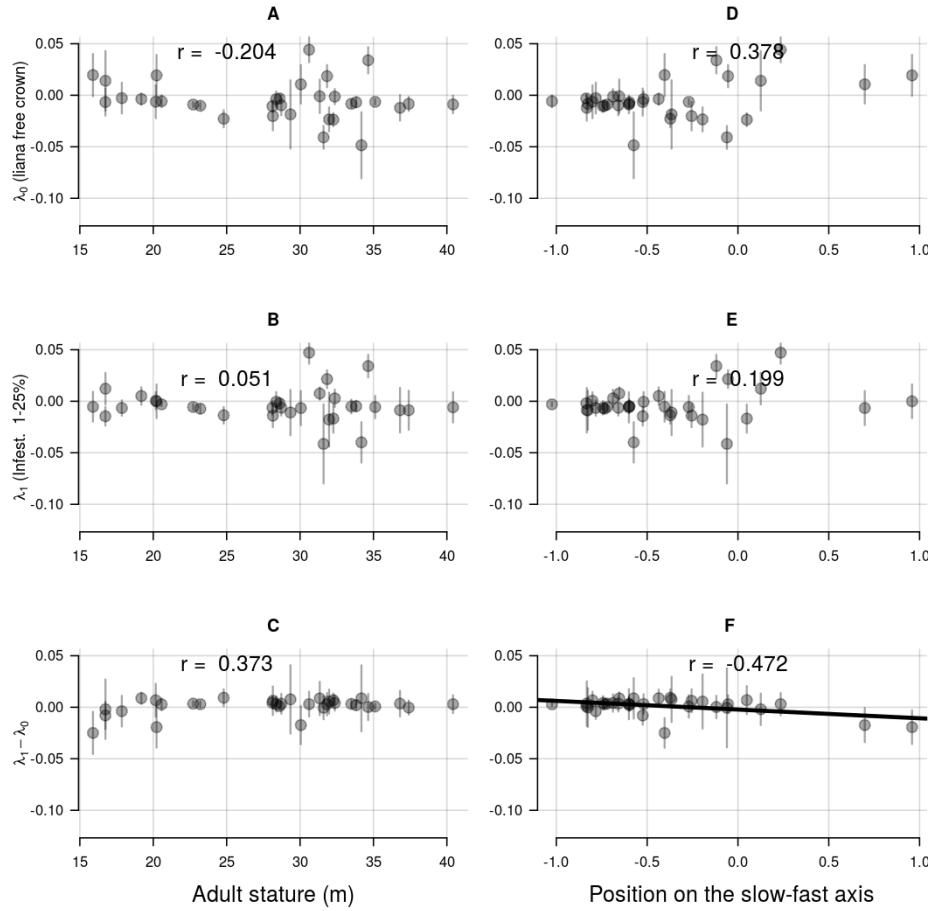


Figure S6.14. Relationship of tree species' adult stature (A,B,C) and position on the slow-fast axis (D,E,F) to projected population growth rates, λ , of host trees when liana-free (A,D; $\lambda_{L=0}$) and when **lightly infested** by lianas (B,E; $\lambda_{L=1}$), and to the difference between the two (C,F; $\lambda_{L=1} - \lambda_{L=0}$). Larger values on the slow-fast axis correspond to faster growth and lower survival, and species with larger scores on this axis tended to be more sensitive to liana infestation. Solid lines indicate a statistically significant relationship (Bonferoni corrected significance level set to 0.0083) and r is the Pearson correlation coefficient. Vertical lines are standard deviations estimated by sampling from model posterior distributions.

S6 LIANAS EFFECTS ON POPULATION GROWTH RATES ALONG TRAIT AXES FOR DIFFERENT LEVELS OF LIANA INFESTATION

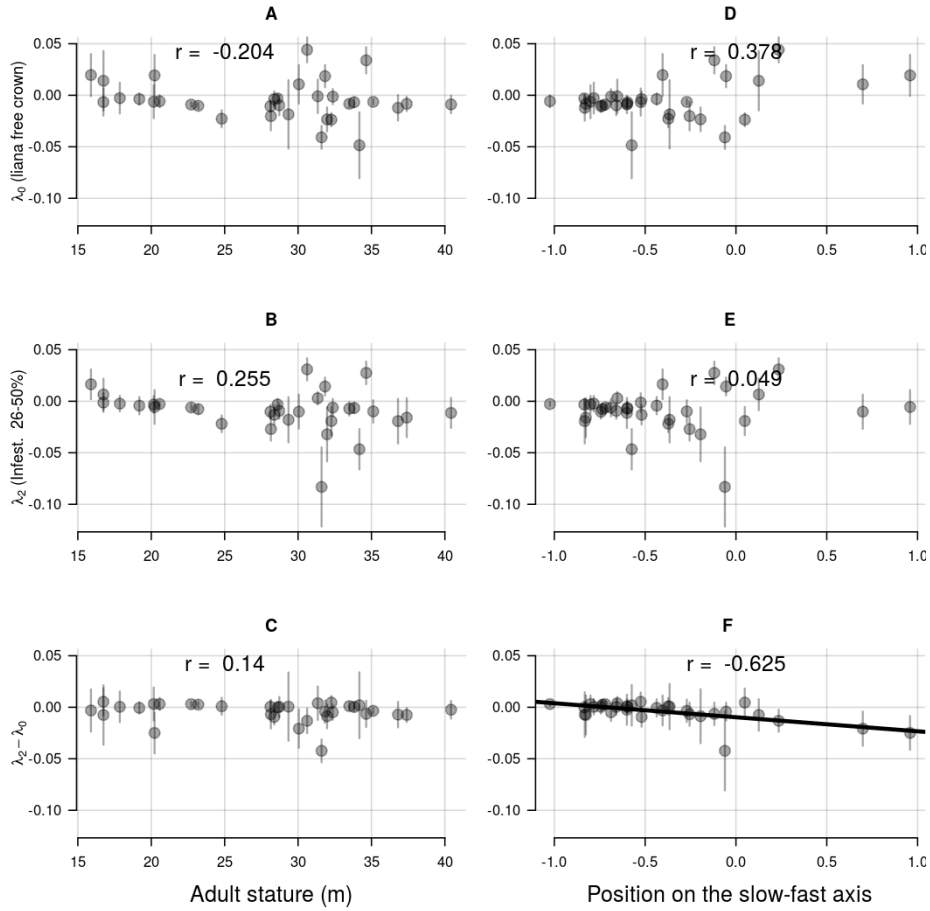


Figure S6.15. Relationship of tree species' adult stature (A,B,C) and position on the slow-fast axis (D,E,F) to projected population growth rates, λ , of host trees when liana-free (A,D; $\lambda_{L=0}$) and when **moderately infested** by lianas (B,E; $\lambda_{L=2}$), and to the difference between the two (C,F; $\lambda_{L=2} - \lambda_{L=0}$). Larger values on the slow-fast axis correspond to faster growth and lower survival, and species with larger scores on this axis tended to be more sensitive to liana infestation. Solid lines indicate a statistically significant relationship (Bonferoni corrected significance level set to 0.0083) and r is the Pearson correlation coefficient. Vertical lines are standard deviations estimated by sampling from model posterior distributions.

S6 LIANAS EFFECTS ON POPULATION GROWTH RATES ALONG TRAIT AXES FOR DIFFERENT LEVELS OF LIANA INFESTATION

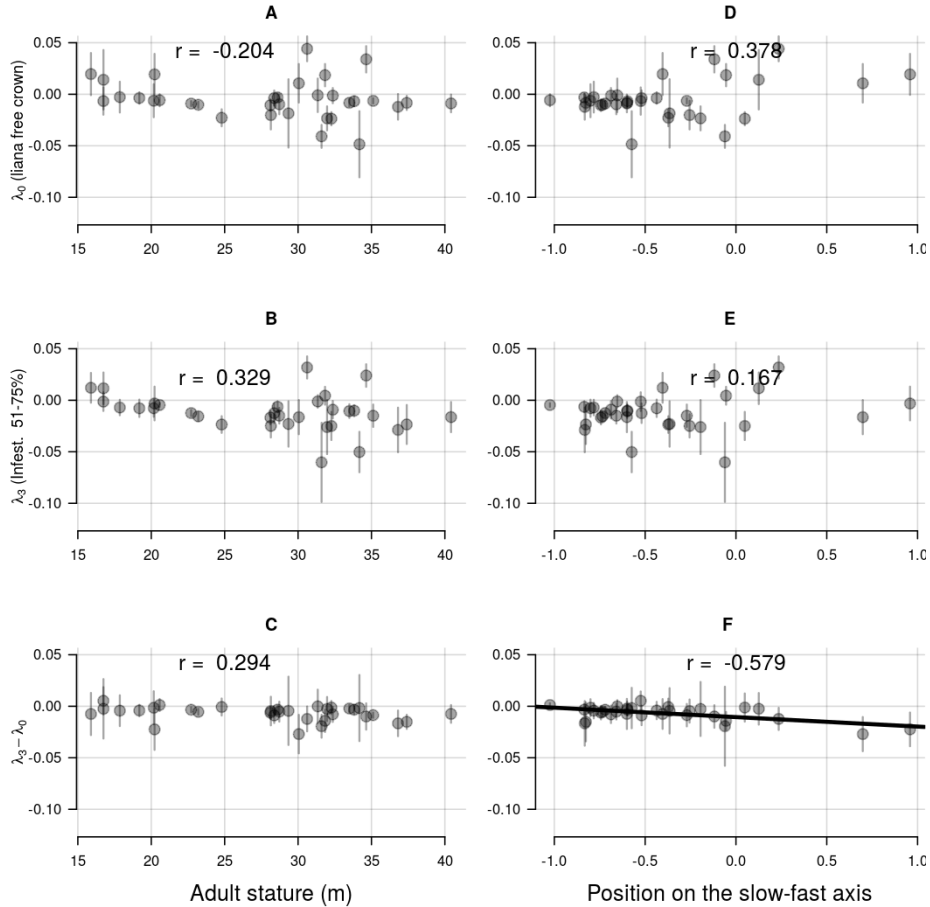


Figure S6.16. Relationship of tree species' adult stature (A,B,C) and position on the slow-fast axis (D,E,F) to projected population growth rates, λ , of host trees when liana-free (A,D; $\lambda_{L=0}$) and when **moderate-severely infested** by lianas (B,E; $\lambda_{L=3}$), and to the difference between the two (C,F; $\lambda_{L=3} - \lambda_{L=0}$). Larger values on the slow-fast axis correspond to faster growth and lower survival, and species with larger scores on this axis tended to be more sensitive to liana infestation. Solid lines indicate a statistically significant relationship (Bonferoni corrected significance level set to 0.0083) and r is the Pearson correlation coefficient. Vertical lines are standard deviations estimated by sampling from model posterior distributions.

S7 LIANA LETHALITY, SURVIVORSHIP BIAS AND LIANA PREVALENCE

We demonstrate that increasing rates of liana-induced mortality (lethality) can cause survivorship bias, or the phenomenon that species more heavily affected by lianas will have lower proportions of infected individuals (all else being equal). We present the following Markov-chain model, which models the liana-tree interaction as a two state susceptible-infested model. Trees can be in one of two states (1) liana free or (2) infested. Trees then transition between these states over time according to the matrix:

$$\mathbf{A} = \begin{bmatrix} (1-C)(1-M) & R(1-(M+L)) \\ C(1-M) & (1-R)(1-(M+L)) \end{bmatrix} \quad (1)$$

Where M is mortality in liana-free trees, L is lethality or the additional mortality in liana-infested trees, C is liana colonization of liana-free trees colonization and R is the loss of lianas from liana-infested trees (recovery). We parameterized the matrix with the mean observed mortality among study species, with the rates of colonization and recovery taken from Ingwell et al. (2010, referenced in main text) - which were kept constant. Note that the result given below do not depend on the exact values of M, C or R . We then varied the lethality parameter between 0 and 1 (Figure S7.17), and calculated the asymptotic stable state distribution (i.e. the dominant right eigenvector) to estimate the proportion infested. The R code is supplied below.

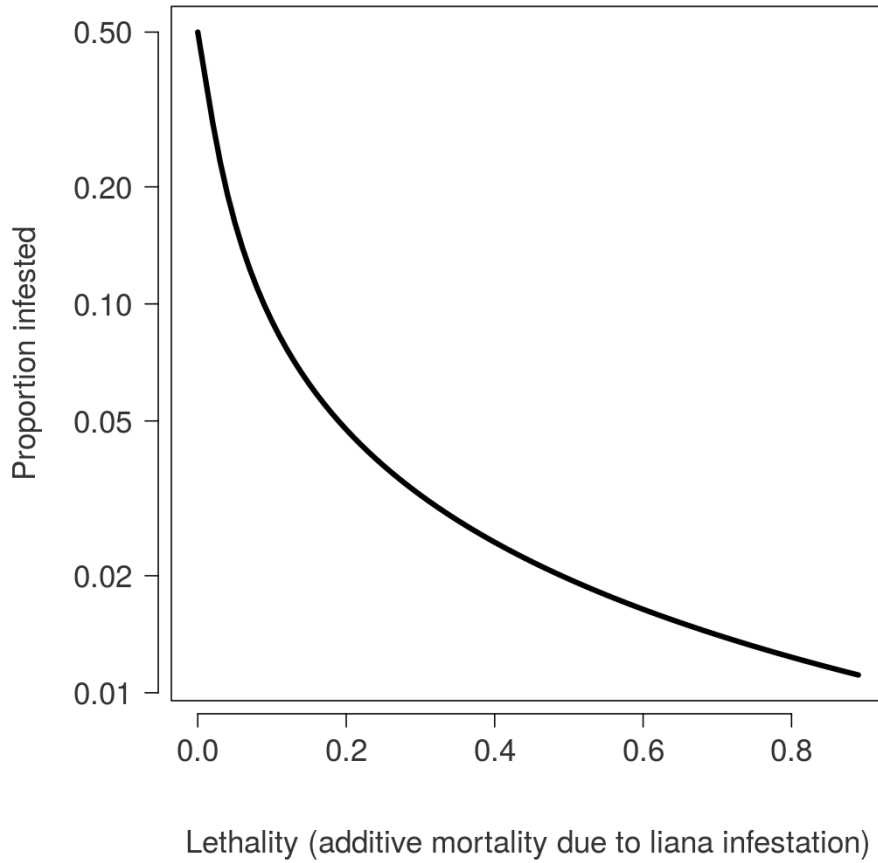


Figure S7.17. Predicted proportion of infested individuals, when only the lethality of lianas differs (additive effect of infestation on mortality) - and the rates of colonization, recovery and mortality are kept equal. The model shows that in theory, simply the differential effects of lianas on mortality is enough to cause differences in the proportion infested among species.

S7 LIANA LETHALITY, SURVIVORSHIP BIAS AND LIANA
PREVALENCE

```
## Simple Markov chain (SI) model shows that only a shift in lethality
## can cause decrease in proportion infested - all else equal.
## default pl and p0 values are from Ingwel et al 2010.
infestMat <- function(M,L,C=1-(1-0.056)^(1/10),R=1-(1-0.106)^(1/10),
                      ret.mat=FALSE){
  A <- matrix(c((1-M)*(1-C), (1-(M+L))*(R), (1-M)*(C), (1-(M+L))*(1-R)),ncol=2,byrow=T)
  u <- eigen(A)$vectors[,1]
  if(ret.mat) {return(A)} else {return(u/sum(u))}
}

par(mfrow=c(1,1),las=1
     ,bg="white",fg="black",
     col.lab="grey20",col.axis="grey20",
     cex.axis=1.4,cex.lab=1.4,
     mar=c(6.5,6.8,2,1),mgp=c(5,1,.5))

M <- 0.01 ## M
C <- 0.01 ## colonization
R <- 0.01 ## recovery
L <- seq(0,.89,0.01) ## lethality (L)
Pinf <- L

for(i in 1:length(L)) Pinf[i] <- infestMat(M,L[i],C,R)[2]

plot(L,Pinf,type="l",log="y",
      ylab="Proportion infested",
      xlab="Lethality (additive mortality due to liana infestation)",lwd=4)
```