

Supplementary material of the paper:**Key factors determining the presence of Tree-related Microhabitats: a synthesis of potential factors at site, stand and tree scales, and proposal for further research**

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Table 1SM. Main features of the TreM datasets used in this study

| Dataset name (reference if published) | Country | Climate zone | Ecoregion | Elevation (m): mean (range) | Number of plots | Number of trees |
|---------------------------------------|---|--|---|-----------------------------|-----------------|-----------------|
| BC_ALPES_Ref3 | France | Alpine | Western European broadleaf forests | 1324 (1200-1455) | 3 | 1162 |
| EFI | Belgium, Czech Republic, Denmark, France, Germany, Hungary, Ireland, Luxembourg, Poland, Serbia, Slovakia, Slovenia; Spain, Sweden, Switzerland | Alpine; Atlantic, Boreal, Continental; Mediterranean | Alps conifer and mixed forests; Baltic mixed forests; Carpathian montane coniferous forests; Dinaric Mountains mixed forests; Italian sclerophyllous and semi-deciduous forests; Northern Temperate Atlantic; Pyrenees conifer and mixed forests; Southern Temperate Atlantic; Western European broadleaf forests | 488 (13-1818) | 47 | 18886 |
| IRSTEALP | France | Alpine | Alps conifer and mixed forests | 1568 (1468-1715) | 10 | 1377 |

| Dataset name (reference if published) | Country | Climate zone | Ecoregion | Elevation (m): mean (range) | Number of plots | Number of trees |
|---------------------------------------|--|--|---|-----------------------------|-----------------|-----------------|
| JM_IRAN | Iran | NA (outside Europe) | Hyrcanian Forest, Montane broadleaf forest | 1334 (862-1802) | 25 | 424 |
| LL_CLIMTREE_BAVARIA | Germany | Alpine | Western European broadleaf forests | 1084 (660-1352) | 29 | 767 |
| LL_CLIMTREE_PYRENEES | France | Alpine | Pyrenees conifer and mixed forests | 1163 (705-1570) | 56 | 1857 |
| LL_HECHES | France | Alpine; Atlantic | Pyrenees conifer and mixed forests | 1053 (883-1173) | 40 | 1252 |
| LL_LISIERE | France | Atlantic | Western European broadleaf forests | 313 (185-358) | 56 | 2023 |
| LL_MARTELOSOPES | France | Atlantic | Western European broadleaf forests | 341 (203-464) | 16 | 2630 |
| LL_PLAINE | France | Atlantic | Western European broadleaf forests | 387 (245-1863) | 279 | 5492 |
| LL_PNM_MELEZE | France | | Alps conifer and mixed forests | 2080 (1918-2177) | 50 | 164 |
| LL_ROMANIA | Romania | | Carpathian montane coniferous forests | 905 (757-1118) | 20 | 892 |
| LL_VFP | France | Alpine; Atlantic | Pyrenees conifer and mixed forests | 1561 (603-2137) | 62 | 1905 |
| MS_PrimaryBeech | Albania; Bosnia; Bulgaria; Croatia; Romania; Slovakia; Ukraine | Alpine; Continental; Mediterranean | Carpathian montane coniferous forests; Dinaric Mountains mixed forests; Pannonian mixed forests; Rodope montane mixed forests | 1192 (591-1667) | 522 | 16607 |
| MS_PrimaryBeech_2018_19_NewTypo | Albania; Bosnia; Bulgaria; Croatia; Romania; Slovakia; Ukraine | Alpine; Continental; Mediterranean | Carpathian montane coniferous forests; Dinaric Mountains mixed forests; Pannonian mixed forests; Rodope montane mixed forests | 1324 (769-1713) | 386 | 17698 |
| TL_2007 | Switzerland | Continental | Western European broadleaf forests | 762 (460-1407) | 88 | 1760 |

| Dataset name (reference if published) | Country | Climate zone | Ecoregion | Elevation (m): mean (range) | Number of plots | Number of trees |
|---------------------------------------|-------------|--|---|-----------------------------|-----------------|-----------------|
| TL_2008 | Switzerland | Alpine; Continental | Alps conifer and mixed forests; Western European broadleaf forests | 771 (336-1592) | 192 | 4800 |
| TL_2020 | Switzerland | Alpine; Continental | Alps conifer and mixed forests; Western European broadleaf forests | 730 (427-1209) | 176 | 7060 |
| TL_JURA2017 | Switzerland | Continental | Western European broadleaf forests | 547 (436-682) | 48 | 570 |
| TL_PRATTIGAU | Switzerland | Alpine | Alps conifer and mixed forests | 1211 (698-1535) | 15 | 344 |
| TL_TOXYWA | Switzerland | Continental | Western European broadleaf forests | 662 (462-866) | 70 | 1244 |
| UH_HAP | Ukraine | Alpine | Carpathian montane coniferous forests | 778 (735-835) | 36 | 2488 |
| UH_SP | Ukraine | Alpine | Carpathian montane coniferous forests | 857 (478-1276) | 314 | 7285 |
| YP_GNB | France | Alpine; Atlantic; Continental; Mediterranean | Alps conifer and mixed forests; Northeastern Spain & Southern France Mediterranean; Southern Temperate Atlantic; Western European broadleaf forests | 597 (59-1653) | 232 | 7529 |

Table 2SM. Typology of Tree-related microhabitats (TreMs) for temperate and Mediterranean forests (Larrieu et al. 2018)

| Forms | Groups | Group definition | TreM types |
|---------------|------------------------------|------------------|----------------------------------|
| Cavities s.l. | Woodpecker breeding cavities | | Small woodpecker breeding cavity |

| | | |
|------------------|--|--|
| | Cavity excavated by a woodpecker for nesting | <p>Medium-sized woodpecker breeding cavity</p> <p>Large woodpecker breeding cavity</p> <p>Woodpecker “flute” (breeding cavity string)</p> |
| Rot holes | Cavity containing tree-hole mould (a mixture of decomposing wood, animal excretions and remains) | <p>Trunk base rot hole</p> <p>Trunk rot hole</p> <p>Semi-open trunk rot hole</p> <p>Chimney trunk base rot hole</p> <p>Chimney trunk rot hole</p> <p>Hollow branch</p> |
| Insect galleries | Holes and galleries excavated by saproxylic insect larvae | Insect galleries and bore holes |
| Concavities | Hole or hollow in the wood, either wet or dry, or a sheltered spot with no mould and which was not | <p>Dendrotelm (phytotelmata, water-filled hole)</p> <p>Woodpecker foraging excavation</p> |

| | | | |
|--------------------------------|-------------------------------|---|---|
| | | excavated by insect activity | Trunk bark-lined concavity Buttress-root concavity |
| Tree injuries and exposed wood | Exposed sapwood only | Bark loss exposing the sapwood only | Bark loss Fire scar Bark shelter Bark pocket |
| | Exposed sapwood and heartwood | Breakage or splitting exposing both sapwood and heartwood | Stem breakage Limb breakage (heartwood exposed) Crack Lightning scar Fork split at the intersection |
| Crown deadwood | Crown deadwood | Deadwood located in the crown of the tree | Dead branches Dead top Remaining broken limb |
| Excrescences | Twig tangles | Excrescence forming a dense packet of small twigs | Witch broom Epicormic shoots |

| | | | |
|--|---|---|---|
| | Burrs and cankers | Ball-shaped excrescences of more or less dense woody material | Burr Canker |
| Fruiting bodies of saproxylic fungi and slime moulds | Perennial fungal fruiting bodies | The fruiting bodies of saproxylic fungi that develop over several years | Perennial polypore |
| | Ephemeral fungal fruiting bodies and slime moulds | The fruiting bodies of saproxylic fungi that develop over only one year, or slime mould plasmodia | Annual polypore Pulpy agaric Large pyrenomycete Myxomycetes |
| Epiphytic and epixylic structures | Epiphytic and parasitic crypto- and phanerogams | Vascular plants, mosses and lichens that use the tree as a physical support | Bryophytes Foliose and fruticose lichens Ivy and lianas Ferns Mistletoe |
| | Nests | Vertebrate or invertebrate nests (excluding woodpecker breeding | Vertebrate nest Invertebrate nest |

| | | | |
|----------|------------|--|-----------------------------------|
| | | cavities) placed in the tree or in a cavity | |
| | Microsoils | Small amount of newly-created soil originating from the decomposition of organic matter from twigs, leaves, bark or mosses | Bark microsoil Crown microsoil |
| Exudates | Exudates | Fresh sap runs or resinosis | Sap run Heavy resinosis |

Statistical analysis

Example of command in R to call brm (package brms) for complete model: Rot Holes

```
modtot0= brm(pres~dbh*time+dbh*status+time*status-1+(1+status+dbh|siteplot)+(1+status+dbh|species), data=tot0,family=bernoulli(), prior = c(set_prior("normal(0,2)",class="b"), set_prior("exponential(1)",class="sd"), set_prior("lkj(6)",class="cor")),control=list(adapt_delta=0.9), chains=4, iter=3000, warmup=1000, cores=4)
```

command to get the variance information

```
TZ=predict(modtot0); 1-mean((TZ[,1]-tot0$pres)^2)/var(tot0$pres)
```

summary of the complete fit

Family: bernoulli

Links: mu = logit

Formula: pres ~ dbh * time + dbh * status + time * status - 1 + (1 + status + dbh | siteplot) + (1 + status + dbh | species)

Data: tot0 (Number of observations: 104377)

Draws: 4 chains, each with iter = 3000; warmup = 1000; thin = 1;

total post-warmup draws = 8000

Group-Level Effects:

~species (Number of levels: 24)

| | Estimate | Est.Error | l-95% CI | u-95% CI | Rhat | Bulk_ESS | Tail_ESS |
|------------------------|----------|-----------|----------|----------|------|----------|----------|
| sd(Intercept) | 0.91 | 0.17 | 0.65 | 1.31 | 1.00 | 2681 | 3723 |
| sd(status5) | 0.87 | 0.24 | 0.49 | 1.43 | 1.00 | 3631 | 4764 |
| sd(dbh) | 0.70 | 0.16 | 0.44 | 1.08 | 1.00 | 3534 | 4703 |
| cor(Intercept,status5) | -0.36 | 0.20 | -0.71 | 0.06 | 1.00 | 6662 | 6522 |
| (Intercept,dbh) | 0.22 | 0.18 | -0.16 | 0.56 | 1.00 | 3562 | 4752 |
| cor(status5,dbh) | -0.07 | 0.22 | -0.48 | 0.37 | 1.00 | 2775 | 4049 |

~siteplot (Number of levels: 2466)

| | Estimate | Est.Error | l-95% CI | u-95% CI | Rhat | Bulk_ESS | Tail_ESS |
|---------------|----------|-----------|----------|----------|------|----------|----------|
| sd(Intercept) | 1.75 | 0.05 | 1.66 | 1.84 | 1.00 | 2284 | 3910 |
| sd(status5) | 1.85 | 0.11 | 1.65 | 2.08 | 1.00 | 2790 | 4957 |

| | | | | | | | |
|------------------------|-------|------|-------|-------|------|------|------|
| sd(dbh) | 0.43 | 0.03 | 0.38 | 0.48 | 1.00 | 2639 | 4940 |
| cor(Intercept,status5) | -0.56 | 0.05 | -0.65 | -0.45 | 1.00 | 2857 | 4535 |
| (Intercept,dbh) | -0.33 | 0.05 | -0.43 | -0.22 | 1.00 | 4790 | 5614 |
| cor(status5,dbh) | 0.23 | 0.08 | 0.07 | 0.39 | 1.00 | 1427 | 2640 |

Population-Level Effects:

| | Estimate | Est.Error | l-95% CI | u-95% CI | Rhat | Bulk_ESS | Tail_ESS |
|---------------|----------|-----------|----------|----------|------|----------|----------|
| dbh | 0.65 | 0.18 | 0.31 | 1.01 | 1.00 | 3197 | 4692 |
| time1 | -3.36 | 0.22 | -3.78 | -2.91 | 1.00 | 1467 | 2536 |
| time2 | -4.66 | 0.25 | -5.13 | -4.15 | 1.00 | 1650 | 2421 |
| time3 | -4.76 | 0.25 | -5.23 | -4.26 | 1.00 | 1615 | 2532 |
| time4 | -4.01 | 0.24 | -4.47 | -3.52 | 1.00 | 1514 | 2705 |
| status5 | -0.30 | 0.31 | -0.94 | 0.28 | 1.00 | 3779 | 5666 |
| dbh:time2 | 0.48 | 0.08 | 0.32 | 0.64 | 1.00 | 7485 | 6265 |
| dbh:time3 | 0.59 | 0.08 | 0.44 | 0.74 | 1.00 | 6164 | 5633 |
| dbh:time4 | 0.83 | 0.07 | 0.70 | 0.96 | 1.00 | 8192 | 6851 |
| dbh:status5 | 0.02 | 0.06 | -0.10 | 0.14 | 1.00 | 5500 | 5977 |
| time2:status5 | 0.28 | 0.28 | -0.27 | 0.80 | 1.00 | 5721 | 5712 |
| time3:status5 | -0.17 | 0.34 | -0.84 | 0.48 | 1.00 | 5982 | 6279 |
| time4:status5 | -0.09 | 0.27 | -0.63 | 0.45 | 1.00 | 5782 | 6169 |

Draws were sampled using sampling (NUTS = No-U-Turn Sample).

For each parameter, Bulk_ESS and Tail_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

Example of command for model excluding variable: dbh

```
modtot0= brm(pres~time*status-1 +(1+status | siteplot)+(1+ status + dbh | species), data=tot0,family=bernoulli(), prior = c(set_prior(
"normal(0,2)",class="b"), set_prior("exponential(1)",class="sd"), set_prior("lkj(6)",class="cor")),control=list(adapt_delta=0.9), chains=4, iter=3000,
warmup=1000, cores=4)
```