**README**

**Data sets**

**dat2 = TraitDifferentiation.csv**

**Content:** Data and meta data extracted from the 70 included studies.

**Variables:**

*StudyID* = unique ID for each study with: 4 first letter of Author, year and 4 letters for journal

*SiteID* = unique ID for each study site (each common garden/transplant site is one site): StudyID.number (numbering goes from 1-n within StudyID)

*study\_type* = common.garden or reciprocal transplant

*species* = species name (Genus\_species)

*Trait* = Trait name

*studyunit* = SiteID\_species\_Trait

*ID* = SiteID\_species

*mean.elev* = mean elevation of study populations within StudyID

*r.elev* = range of elevation of study populations within StudyID

*mean.lat* = mean latitude of study populations within StudyID

*mean.long* = mean longitude of study populations within StudyID

*mean.temp* = mean annual temperature of study populations within StudyID from WorldClim <http://worldclim.org/bioclim>)

*r.temp* = range of mean annual temperature of study populations within StudyID from WorldClim <http://worldclim.org/bioclim>)

*mean seasonality* = mean seasonality of study populations within StudyID from WorldClim <http://worldclim.org/bioclim>)

*dist.km* = maximal distance in km of study populations within StudyID

*mean.dist.km* = mean distance in km of study populations within StudyID

*studysite* = Garden, greenhouse, climate\_chamber

*family* = plant family

*generation* = generation of plants used in common garden (F0: rhizomes, tillers, cuttings or seedlings collected in the field; F1: progeny of field-collected seed; F2+: progeny of plants grown for at least one generation under common environmental conditions)

*duration\_exp* = duration of experiment

*longevity* = longevity of study species

*growthform* = growthform of study species

*intro* = introduction status of study species

*country\_of\_origin* = country of origin of study species

*country\_of\_exp* = country of experiment

*region* = region of experiment

*elevation\_site* = elevation of transplant site

*breed* = breeding system of study species

*Year* = Year of the study

*TRAIT\_CAT1-4* = categories on different levels for traits

*n* = sample size

*estimate* = estimate of regression slopes (regression of mean annual temperature on trait mean within studyunit)

*p.value* = p value of regression of mean annual temperature on trait mean within studyunit

**LA = LocalAdaptation.csv**

**Content:** Data and meta data extracted from the 14 reciprocal transplant experiments.

**Variables:**

*StudyID* = unique ID for each study with: 4 first letter of Author, year and 4 letters for journal

*SiteID* = unique ID for each study site (each common garden/transplant site is one site): *study\_type* = common.garden or reciprocal transplant

*species* = species name (Genus\_species)

*Trait* = Trait name

*Year* = Year of experiment

*PopID* = unique ID for each population within study

*elev* = elevation (m a.s.l.) of population

*traitmean* = population mean of trait value

*traitvar* = population variation of trait value (if available)

*lat.pop* = mean latitude of study populations within StudyID

*long.pop* = mean longitude of study populations within StudyID

*studyunit* = SiteID\_species\_Trait

*ID* = SiteID\_species

*mean.elev* = mean elevation of study populations within StudyID

*r.elev* = range of elevation of study populations within StudyID

*family* = plant family

*generation* = generation of plants used in common garden (F0: rhizomes, tillers, cuttings or seedlings collected in the field; F1: progeny of field-collected seed; F2+: progeny of plants grown for at least one generation under common environmental conditions)

*duration\_exp* = duration of experiment

*longevity* = longevity of study species

*growthform* = growthform of study species

*intro* = introduction status of study species

*country\_of\_origin* = country of origin of study species

*country\_of\_exp* = country of experiment

*region* = region of experiment

*latitude\_site* = latitude of transplant site

*longitude\_site* = longitude of transplant site

*elevation\_site* = elevation of transplant site

*breed* = breeding system of study species

*elev.diff* = elevational difference between transplant site and population origin

*symp* = home vs. foreign site

*direction* = direction of transplant (> 0 = up; < 0 = down)

Create site information: which site is low, mid and high. factor.site2 is for the second analysis to check interaction symp \* site (needs to exclude mid elevation sites, but for Halbritter studies high elevation sites are different for 3 species)

*p.factor.site* = factor for site (low vs. high)

*p.factor.site2* = factor for site (low, mid and high)

*p.factor.pop* = factor for population (low vs. high)

*st.traitmean* = standardized population mean of trait value

*sample.size* = sample size