Fireveg-DB : summary of available data for Blue Table

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30 April, 2021

Brief (and very preliminary) summary of fire-related plant traits extracted from literature and unpublished references by two main sources: the NSW Flora Fire Response Database (v2.1, 2010, updated 2014), and Austraits (data provided by Will Cornwell, 23 April 2021). This document is currently under development.

# Data sources and formats

We first read the data from the NSW FFRD spreadsheet. This is in wide tabular format: each column is a variable.

nswffrd.data <- read\_excel(sprintf("%s/NSWFFRDv2.1.xlsx",input.dir), sheet=2, skip=1)

## Warning in read\_fun(path = enc2native(normalizePath(path)), sheet\_i = sheet, :  
## Expecting numeric in BT2108 / R2108C72: got '1-2'

# nswffrd.data

The data exported from Austraits by Will is in a long format: column trait\_name give the variable names and the value column has the trait values:

austrait.data <- read\_csv(sprintf("%s/blue-table-v0.0.2.csv",input.dir), col\_types="cccccccccccc")  
# austrait.data

# Traits

## Fire response

In the NSWFFRDv2 spreadsheet the variable Firesponse is coded in the following way:

S=seeder, R=resprouter. r=usually killed but sometimes resprouts, s=usually resprouts but sometimes killed; these may indicate a variable response seen by one observer, or a conflict between different observers (see comments column). When an equal number of references list the species as seeder or resprouter, this column reads as ‘S/R’ and details are given in the comments cloumn. Ideally fire response should be defined by mortality >70%=seeder, mortality <30%=resprouter [Gill & Bradstock, 1992].

nswffrd.data %>% select(Fireresponse) %>% table

## .  
## R Rs S S/R Sr SR   
## 1447 163 1113 179 183 1

We can rescale these values as suggested by David:

Resprouting <- c("S"="None", "Sr"="Few", "S/R"="Half", "SR"="Half", "Rs"="Most", "R"="All")  
nswffrd.data %>% transmute(fire\_response=Resprouting[Fireresponse]) %>% table

## .  
## All Few Half Most None   
## 1447 183 180 163 1113

Austraits data includes observations from the NSWFFRDv2 spreadsheet (dataset\_id=Auld\_2014) but the values are coded differently:

austrait.data %>% filter(dataset\_id %in% "Auld\_2014" & trait\_name %in% "fire\_response") %>% pull(value) %>% table

## .  
## fire\_killed fire\_killed resprouts resprouts   
## 1113 526 1451

Data for the same trait but from other data sources has following values in Austraits dataset:

austrait.data %>% filter(!dataset\_id %in% "Auld\_2014" & trait\_name %in% "fire\_response") %>% pull(value) %>% table

## .  
## fire\_killed   
## 5605   
## fire\_killed fire\_not\_relevant   
## 11   
## fire\_killed resprouts   
## 10   
## fire\_not\_relevant   
## 8   
## fire\_not\_relevant not\_fire\_killed\_does\_not\_resprout   
## 4   
## fire\_not\_relevant resprouts   
## 28   
## not\_fire\_killed\_does\_not\_resprout   
## 1232   
## resprouts   
## 8355   
## unknown   
## 3

## Resprouting organ

In the NSWFFRDv2 spreadsheet the variable resprout location is coded in the following way:

Source of buds for vegetative regenerators. Plum text indicates that the source of this information is from the fire response category given by one or more references (see Fire Response columns); a- indicates this is an assumption based on the species morphology. Where multiple methods are given: seperated by & both methods recorded by one observer; seperated by / different methods recorded by different observers. Where a category 4 fire response is given without specifying root suckers or rhizome, root suckers is listed here.

There are many possible values, sometimes used in combination:

nswffrd.data %>% distinct(`Resprout location`) %>% head

## # A tibble: 6 x 1  
## `Resprout location`   
## <chr>   
## 1 <NA>   
## 2 root buds   
## 3 basal buds   
## 4 basal   
## 5 root suckers   
## 6 root suckers / basal

We can use a similar approach as before in order to translate the most common values, but some fixed are required to adjust some fields and extract multiple values :

RegenerativeOrgan <- c("epicormic"="Epicormic",  
 "stemp buds"="Epicormic",  
 "apical"="Apical",  
 "lignotuber"="Lignotuber",  
 "rootstock"="Lignotuber",  
 "root stock"="Lignotuber",  
 "basal"="Basal",  
 "coppice"="Basal",  
 "tuber"="Tuber",  
 "taproot"="Tuber",  
 "tussock"="Tussock",  
 "rhizome"="Long rhizome or root sucker",  
 "root sucker"="Long rhizome or root sucker",  
 "rootucker"="Long rhizome or root sucker",  
 "root buds"="Long rhizome or root sucker",  
 "rhizome"="Short rhizome",  
 "stolon"="Stolon",  
 "stolons"="Stolon")  
 nswffrd.data %>% transmute(regen\_organ= RegenerativeOrgan[`Resprout location`]) %>% table(.,useNA='always')

## .  
## Apical Basal   
## 10 413   
## Epicormic Lignotuber   
## 39 85   
## Long rhizome or root sucker Stolon   
## 174 2   
## Tuber <NA>   
## 42 2321

Austraits data includes observations from the NSWFFRDv2 spreadsheet (dataset\_id=Auld\_2014) and other references using several distinct values. For example reference Clarke\_2015 has 2223 observations from 2093 distinct taxa and uses 6 different categories ranging from ‘aboveground\_caudex’ to ‘underground’:

austrait.data %>% filter(trait\_name %in% "regen\_strategy" ) %>% group\_by(dataset\_id) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n values`=n\_distinct(value), `n obs`=n(), min=min(value), max=max(value))

## # A tibble: 19 x 6  
## dataset\_id `n taxa` `n values` `n obs` min max   
## <chr> <int> <int> <int> <chr> <chr>   
## 1 Auld\_2014 1218 39 1263 aboveground\_oth… woody\_rootstock c…  
## 2 Baker\_2019 53 2 53 basal rhizome   
## 3 Clarke\_2015 2093 6 2223 aboveground\_cau… underground   
## 4 Denton\_2007 9 3 9 lignotuber rhizome   
## 5 French\_2017 12 3 12 basal fire\_killed   
## 6 Groom\_1997 94 6 95 bud-bearing\_root lignotuber   
## 7 Leishman\_1992 299 2 300 no\_storage\_organ storage\_organ   
## 8 Meers\_2007 127 7 127 bud-bearing\_root stolon   
## 9 Metcalfe\_2009 285 3 285 aboveground none   
## 10 Metcalfe\_202… 40 1 40 underground underground   
## 11 Metcalfe\_202… 141 3 142 aboveground underground   
## 12 Moore\_2019\_2 52 3 52 rhizome stolon   
## 13 Nicolle\_2006 985 4 1031 epicormic lignotuber   
## 14 Pekin\_2011 183 3 185 fleshy\_undergro… woody\_rootstock\_o…  
## 15 Prior\_2016 7 3 7 basal fire\_killed   
## 16 Rye\_2015 22 3 22 lignotuber unknown   
## 17 Schmidt\_1997 14 1 14 lignotuber lignotuber   
## 18 White\_2020 3055 2 3710 resprouts resprouts\_non\_fir…  
## 19 Williams\_2011 943 7 958 aboveground\_oth… stolon

## Maximum bark thickness

Austraits data reports this as quantitative values:

austrait.data %>% filter(trait\_name %in% "bark\_thickness" ) %>% group\_by(dataset\_id) %>% mutate(value=as.numeric(value)) %>% summarise(min=min(value),max=max(value),mean=mean(value),sd=sd(value),count=n())

## # A tibble: 9 x 6  
## dataset\_id min max mean sd count  
## <chr> <dbl> <dbl> <dbl> <dbl> <int>  
## 1 Cernusak\_2006 2.21 4.84 3.49 0.948 12  
## 2 Knox\_2011 0.15 1.55 0.501 0.316 27  
## 3 Kotowska\_2020 1.8 38.9 9.29 8.00 76  
## 4 Lawes\_2012 1 32 8.96 5.16 900  
## 5 Lee\_2019 0.27 6.88 2.02 1.18 65  
## 6 Onoda\_2010 0.178 2.20 0.831 0.397 155  
## 7 Rosell\_2014 0.245 5.11 1.39 1.13 62  
## 8 Wright\_2002 0.425 2.74 0.986 0.361 64  
## 9 Wright\_2019 0.46 3.4 1.60 0.618 187

## Seed mass

Austraits data report quantitative data from several sources:

austrait.data %>% filter(trait\_name %in% "seed\_mass" ) %>% group\_by(dataset\_id) %>% mutate(value=as.numeric(value)) %>% summarise(min=min(value),max=max(value),mean=mean(value),sd=sd(value),count=n())

## # A tibble: 49 x 6  
## dataset\_id min max mean sd count  
## <chr> <dbl> <dbl> <dbl> <dbl> <int>  
## 1 ANBG\_2019 0.003 7575 22.3 253. 3463  
## 2 Angevin\_2011 0.001 61.6 3.35 8.95 78  
## 3 Briggs\_2010 5 848 252. 399. 4  
## 4 Catford\_2014 0.00005 38 2.11 5.79 143  
## 5 Cross\_2009 0.02 15.7 2.43 3.16 44  
## 6 Denton\_2007 19 125 51.2 33.1 36  
## 7 Dwyer\_2017 0.00133 11.3 0.918 1.50 150  
## 8 Everingham\_2020 0.05 53.3 11.0 9.98 3224  
## 9 Falster\_2005\_1 0.07 48000 2733. 9214. 29  
## 10 Falster\_2005\_2 0.1 62 18.4 22.0 16  
## # … with 39 more rows

## Propagule dispersal model

From the NSWFFRDv2 spreadsheet:

Seed Dispersal mechanism: Known vector for dispersal (wind, bird, ants, mammal, adhesion, etc); a- indicates seed is adapted for dispersal by the given vector (but not necessarily shown to use this vector); ? indicates possible vector

nswffrd.data %>% group\_by(`Seed dispersal mechanism`) %>% summarise(count=n())

## # A tibble: 81 x 2  
## `Seed dispersal mechanism` count  
## <chr> <int>  
## 1 a-adhesion 29  
## 2 a-adhesion? 1  
## 3 a-ant 240  
## 4 a-ant (55) wind (96) 1  
## 5 a-ant / explosive capsule 14  
## 6 a-ant & a-vertebrate 3  
## 7 a-ant? 14  
## 8 a-ant? / a-vertebrate 1  
## 9 a-ingestion 8  
## 10 a-vertebrate 26  
## # … with 71 more rows

This could be transformed into a value with two attributes to indicate (a) if it is based on “adaptations” or if it is a known dispersal vector, and (b) the certainty of the observation.

In Austraits this is coded as trait dispersal\_syndrome with several possible values but no attributes:

austrait.data %>% filter(trait\_name %in% "dispersal\_syndrome" ) %>% group\_by(dataset\_id) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n values`=n\_distinct(value), `n obs`=n(), min=min(value), max=max(value))

## # A tibble: 28 x 6  
## dataset\_id `n taxa` `n values` `n obs` min max   
## <chr> <int> <int> <int> <chr> <chr>   
## 1 Angevin\_2011 87 8 87 adhesion wind   
## 2 Auld\_2014 909 34 934 adhesion wind   
## 3 Barlow\_1981 13 1 13 aril aril   
## 4 BRAIN\_2007 41 3 44 anemochory unassisted   
## 5 Catford\_2014 48 10 48 anemochory animal\_vec… wind   
## 6 Cooper\_2004 20 2 21 anemochory endozoocho…  
## 7 Forster\_1995 4 2 4 anemochory endozoocho…  
## 8 Gallagher\_2012 4 2 4 animal\_vector hydrochory   
## 9 Gross\_1993 1 1 1 hydrochory hydrochory   
## 10 Grubb\_1996 52 2 52 anemochory animal\_vec…  
## # … with 18 more rows

## Seedbank type

In the NSWFFRDv2 spreadsheet the trait Seed storage is coded in following way:

The following definitions have been used for seed-bank type. Soil seedbank: persistent=some carry over of viable seeds from year to year, transient=no viable seeds persist for more than 1 year [Thompson & Grime 1979 JEc 67:893-921]; Canopy seedbank: serotinous=most seed retained for a few years (released by fire, death, drying over time) [Lamont et al 1991 BotRev 57:277-317] canopy transient=retained on plant for short period only. Plum text indicates that the source of this information is from the fire response category given by one or more references (see Fire Response columns); blue text indicates this is an assumption based on the species morphology.

nswffrd.data %>% group\_by(`Seed storage`) %>% summarise(count=n())

## # A tibble: 47 x 2  
## `Seed storage` count  
## <chr> <int>  
## 1 a-canopy 57  
## 2 a-persistent soil 118  
## 3 canopy 126  
## 4 canopy - transient 50  
## 5 canopy (>1y) & soil 1  
## 6 canopy (1; 9) / soil (6) 1  
## 7 canopy (released before next flowering period) 1  
## 8 canopy (remains on stem for several years) 1  
## 9 canopy (retained several years, very low density of seed in soil; 32) 1  
## 10 canopy / persistent soil 1  
## # … with 37 more rows

Some attributes (coded as text colors, references in hyperlinks) are lost when reading the data in this way. Some fields start with a- or have multiple values joined by & or /, others have notes in parenthesis.

In Austraits: according to the Sync table suggested by Will and Mark this is currently represented in three columns: serotiny + soil\_seedbank + seed\_storage\_location.

*Canopy seedbank*: Seeds retained in serotinos or bradysporous woody fruits in the plant canopy and released after scorch (may also be released spontaneously) Some species of Banksia, Hakea, Allocasuarina, Leptosperum, Eucalypts, Callitris

*Soil-persistent seedbank*: Seeds or fruits released from the parent plant at maturity, with a non-trivial fraction that remains viable in the soil for more than one year and able to germinate after fire Many species of Fabaceae, Ericaceae, Rutaceae, Rhamnaceae, Grevillea, Persoonia

*Transient seedbank*: Seeds or fruits released from the parent plant at maturity and do not remain viable in the soil for more than one year (i.e. germinate or die within one year) Some grasses, figs, orchids, most lilioid genera, Syzygium, Loranthaceae

*Non-canopy*: Not a canopy seedbank, but could be with soil persistent ot transient No evidence of serotinous fruits, but otherwsie uncertain

*Soil seedbank* is reported in Austraits as a binary variable per species:

austrait.data %>% filter(trait\_name %in% "soil\_seedbank" ) %>% group\_by(dataset\_id,value,unit) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id', 'value'. You can override using the `.groups` argument.

## # A tibble: 8 x 5  
## # Groups: dataset\_id, value [8]  
## dataset\_id value unit `n taxa` `n obs`  
## <chr> <chr> <chr> <int> <int>  
## 1 Gosper\_2012 0 <NA> 100 100  
## 2 Gosper\_2012 1 <NA> 175 175  
## 3 Gosper\_2018 0 <NA> 20 20  
## 4 Gosper\_2018 1 <NA> 39 39  
## 5 Kirkpatrick\_2020 0 <NA> 40 40  
## 6 Kirkpatrick\_2020 1 <NA> 38 38  
## 7 Williams\_2005 0 <NA> 53 53  
## 8 Williams\_2005 1 <NA> 57 57

*Seed storage location*

austrait.data %>% filter(trait\_name %in% "seed\_storage\_location" ) %>% group\_by(dataset\_id,value) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id'. You can override using the `.groups` argument.

## # A tibble: 7 x 4  
## # Groups: dataset\_id [2]  
## dataset\_id value `n taxa` `n obs`  
## <chr> <chr> <int> <int>  
## 1 Auld\_2014 canopy 252 546  
## 2 Auld\_2014 canopy soil 5 10  
## 3 Auld\_2014 none 9 18  
## 4 Auld\_2014 not\_canopy 1 2  
## 5 Auld\_2014 soil 1029 2106  
## 6 Standish\_2019 canopy 61 61  
## 7 Standish\_2019 soil 523 526

*Serotiny* is recorded as a variable with either binary values (not\_serotinous vs. serotinous) or ordinal scale (low, moderate, high):

austrait.data %>% filter(trait\_name %in% "serotiny" ) %>% group\_by(dataset\_id,value) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id'. You can override using the `.groups` argument.

## # A tibble: 19 x 4  
## # Groups: dataset\_id [8]  
## dataset\_id value `n taxa` `n obs`  
## <chr> <chr> <int> <int>  
## 1 Denton\_2007 serotinous 6 6  
## 2 Denton\_2007 serotiny\_low 2 2  
## 3 Denton\_2007 serotiny\_moderate 1 1  
## 4 Gosper\_2012 not\_serotinous 245 245  
## 5 Gosper\_2012 serotinous 99 99  
## 6 Gosper\_2018 not\_serotinous 106 108  
## 7 Gosper\_2018 serotinous 11 11  
## 8 Groom\_1997 not\_serotinous 1 1  
## 9 Groom\_1997 serotiny\_high 4 4  
## 10 Groom\_1997 serotiny\_low 13 13  
## 11 Groom\_1997 serotiny\_moderate 76 77  
## 12 Groom\_2010 not\_serotinous 12 12  
## 13 Groom\_2010 serotiny\_high 15 18  
## 14 Groom\_2010 serotiny\_low 9 11  
## 15 Hughes\_1992 not\_serotinous 213 213  
## 16 Hughes\_1992 serotinous 21 21  
## 17 Kirkpatrick\_2020 not\_serotinous 92 92  
## 18 Kirkpatrick\_2020 serotinous 32 32  
## 19 Nicolle\_2006 serotinous 82 82

## Recruitment pattern

This variable is reported in Austraits from a single source with one or more observations per species:

austrait.data %>% filter(trait\_name %in% "fire\_and\_establishing" ) %>% group\_by(dataset\_id,value) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id'. You can override using the `.groups` argument.

## # A tibble: 5 x 4  
## # Groups: dataset\_id [1]  
## dataset\_id value `n taxa` `n obs`  
## <chr> <chr> <int> <int>  
## 1 Cheal\_2017 establish\_anytime 1088 1120  
## 2 Cheal\_2017 establish\_intermediate\_age 5 5  
## 3 Cheal\_2017 establish\_intermediate\_to\_over\_mature\_vegetation 22 22  
## 4 Cheal\_2017 establish\_just\_after\_fire\_and\_mature\_vegetation 16 16  
## 5 Cheal\_2017 establish\_just\_after\_fire\_only 446 449

## Germination cue

In the NSWFFRDv2 spreadsheet the trait Germination cue is coded in following way:

Germination is stimulated by a fire-related (e.g. heat, smoke) or other (e.g. stratification, leaching) cue; a- indicates seed is adapted for given cue (ie hard seed coat adapted for heat cue)

nswffrd.data %>% group\_by(`Germination cue`) %>% summarise(count=n())

## # A tibble: 89 x 2  
## `Germination cue` count  
## <chr> <int>  
## 1 a-heat 244  
## 2 after ripening 3  
## 3 after ripening / smoke 1  
## 4 after ripening / stratification (93), heat & smoke combined (88) 1  
## 5 after ripening period of several months required 1  
## 6 cold stratification 1  
## 7 dark 1  
## 8 germ after rain 1  
## 9 germinates readily 1  
## 10 germination decreased with fire; possibly lethal heat effect 3  
## # … with 79 more rows

This variable is reported in Austraits from several sources with different coding of values (Check with Will?)

austrait.data %>% filter(trait\_name %in% "fire\_cued\_seeding" ) %>% group\_by(dataset\_id) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n values`=n\_distinct(value), `n obs`=n(), min=min(value), max=max(value))

## # A tibble: 4 x 6  
## dataset\_id `n taxa` `n values` `n obs` min max   
## <chr> <int> <int> <int> <chr> <chr>   
## 1 Auld\_2014 594 68 602 0.5seedlings/10m2 i… prone to detrime…  
## 2 Baker\_2019 5 1 5 fire\_cued\_seeding fire\_cued\_seeding  
## 3 Cheal\_2017 893 2 904 fire\_cued\_seeding\_c… fire\_cued\_seedin…  
## 4 Clarke\_2015 2281 2 2420 fire\_cued\_seeding no\_fire\_cued\_see…

## Fire\_response\_juvenile

This is reported in Austraits from a single source as a variable with two possible values:

austrait.data %>% filter(trait\_name %in% "fire\_response\_juvenile" ) %>% group\_by(dataset\_id,value,unit) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id', 'value'. You can override using the `.groups` argument.

## # A tibble: 2 x 5  
## # Groups: dataset\_id, value [2]  
## dataset\_id value unit `n taxa` `n obs`  
## <chr> <chr> <chr> <int> <int>  
## 1 Cheal\_2017 juvenile\_fire\_killed <NA> 826 839  
## 2 Cheal\_2017 juvenile\_resprout <NA> 456 467

## Fire\_response\_on\_maturity

This is reported in Austraits from a single source as a variable with three possible values:

austrait.data %>% filter(trait\_name %in% "fire\_response\_on\_maturity" ) %>% group\_by(dataset\_id,value,unit) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id', 'value'. You can override using the `.groups` argument.

## # A tibble: 3 x 5  
## # Groups: dataset\_id, value [3]  
## dataset\_id value unit `n taxa` `n obs`  
## <chr> <chr> <chr> <int> <int>  
## 1 Cheal\_2017 mature\_do\_not\_resprout <NA> 384 389  
## 2 Cheal\_2017 mature\_to\_juvenile <NA> 466 474  
## 3 Cheal\_2017 remain\_mature <NA> 434 443

## Germination treatment

This is reported in Austraits from three different sources and many possible values (Check with Will?):

austrait.data %>% filter(trait\_name %in% "germination\_treatment" ) %>% group\_by(dataset\_id) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n values`=n\_distinct(value), `n obs`=n(), min=min(value), max=max(value))

## # A tibble: 3 x 6  
## dataset\_id `n taxa` `n values` `n obs` min max   
## <chr> <int> <int> <int> <chr> <chr>   
## 1 ANBG\_2019 136 29 902 apply\_chemi… stratification   
## 2 Auld\_2014 594 50 607 after ripen… wash / remove seedcoat / …  
## 3 Kew\_2019\_6 1015 19 2628 excise\_peri… sterilise\_domestos

## Lifespan

This is reported in Austraits from few sources and several possible values:

austrait.data %>% filter(trait\_name %in% "lifespan" ) %>% group\_by(dataset\_id,value,unit) %>% summarise(count=n())

## `summarise()` has grouped output by 'dataset\_id', 'value'. You can override using the `.groups` argument.

## # A tibble: 20 x 4  
## # Groups: dataset\_id, value [20]  
## dataset\_id value unit count  
## <chr> <chr> <chr> <int>  
## 1 Cheal\_2017 <10 <NA> 13  
## 2 Cheal\_2017 <100 <NA> 1182  
## 3 Cheal\_2017 <20 <NA> 36  
## 4 Cheal\_2017 <3 <NA> 3  
## 5 Cheal\_2017 <50 <NA> 305  
## 6 Gosper\_2012 <6 <NA> 26  
## 7 Gosper\_2012 >6 <NA> 318  
## 8 Jurado\_1993 ? year 1  
## 9 Jurado\_1993 <1 year 66  
## 10 Jurado\_1993 <10 year 48  
## 11 Jurado\_1993 <100 year 19  
## 12 Jurado\_1993 <20 year 21  
## 13 Jurado\_1993 <5 year 29  
## 14 Jurado\_1993 <50 year 21  
## 15 Jurado\_1993 >100 year 25  
## 16 White\_2020 <1 <NA> 691  
## 17 White\_2020 <10 <NA> 904  
## 18 White\_2020 <50 <NA> 3616  
## 19 White\_2020 >500 <NA> 1418  
## 20 White\_2020 50-500 <NA> 1309

## Time\_from\_fire\_to\_fruit

This is reported in Austraits from two sources and four possible values:

austrait.data %>% filter(trait\_name %in% "time\_from\_fire\_to\_fruit" ) %>% group\_by(dataset\_id,value,unit) %>% summarise(`n taxa`=n\_distinct(taxon\_name), `n obs`=n())

## `summarise()` has grouped output by 'dataset\_id', 'value'. You can override using the `.groups` argument.

## # A tibble: 4 x 5  
## # Groups: dataset\_id, value [4]  
## dataset\_id value unit `n taxa` `n obs`  
## <chr> <chr> <chr> <int> <int>  
## 1 Gosper\_2012 240 months 2 2  
## 2 Gosper\_2012 72 months 1 1  
## 3 Gosper\_2012 96 months 6 6  
## 4 Gosper\_2018 228 months 1 1