

# Package ‘finalfit’

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**Type** Package

**Title** Quickly Create Elegant Regression Results Tables and Plots when Modelling

**Version** 1.0.2

**Maintainer** Ewen Harrison <ewen.harrison@ed.ac.uk>

**Description** Generate regression results tables and plots in final format for publication. Explore models and export directly to PDF and 'Word' using 'RMarkdown'.

**License** MIT + file LICENCE

**Encoding** UTF-8

**LazyData** true

**BugReports** <https://github.com/ewenharrison/finalfit/issues>

**URL** <https://github.com/ewenharrison/finalfit>

**Imports** bdsmatrix, boot, broom, dplyr, forcats, GGally, ggplot2, grid, gridExtra, lme4, magrittr, mice, pillar, pROC, purrr, scales, stats, stringr, survival, tidyr (>= 1.0.0)

**RoxygenNote** 6.1.1

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**Author** Ewen Harrison [aut, cre],  
Tom Drake [aut],  
Riinu Ots [aut]

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**R topics documented:**

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finalfit-package	<i>finalfit: Quickly create elegant final results tables and plots when modelling.</i>
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## Description

finalfit: Quickly create elegant final results tables and plots when modelling.

### finalfit model wrappers

[glmuni](#), [glmmulti](#), [glmmulti\\_boot](#), [glmmixed](#), [lmuni](#), [lmmulti](#), [lmmixed](#), [coxphuni](#), [coxphmulti](#), [crruni](#), [crrmulti](#), [svyglmuni](#), [svyglmmulti](#).

### finalfit model extractor

Generic: [fit2df](#)

Methods (not called directly): [fit2df.glm](#), [fit2df.glm1ist](#), [fit2df.glmboot](#), [fit2df.lm](#), [fit2df.lm1ist](#), [fit2df.lmerMod](#), [fit2df.lmerMod](#), [fit2df.coxph](#), [fit2df.coxph1ist](#), [fit2df.crr](#), [fit2df.crr1ist](#), [fit2df.stanfit](#).

### finalfit all-in-one function

Generic: [finalfit](#), [finalfit\\_permute](#).

Methods (not called directly): [finalfit.glm](#), [finalfit.lm](#), [finalfit.coxph](#).

### finalfit plotting functions

[coefficient\\_plot](#), [or\\_plot](#), [hr\\_plot](#), [surv\\_plot](#), [ff\\_plot](#).

### finalfit helper functions

[ff\\_glimpse](#), [ff\\_label](#), [ff\\_merge](#), [ff\\_interaction](#).

**finalfit prediction functions**[boot\\_predict](#), [finalfit\\_newdata](#).Methods (not called directly): [boot\\_compare](#).**finalfit missing data functions**[missing\\_glimpse](#), [missing\\_pattern](#), [missing\\_compare](#), [missing\\_plot](#), [missing\\_pairs](#).

---

boot_compare	<i>Compare bootstrapped distributions</i>
--------------	---

---

**Description**

Not usually called directly. Included in [boot\\_predict](#). Usually used in combination with A function that takes the output from [summary\\_factorlist\(..., fit\\_id=TRUE\)](#) and merges with any number of model dataframes, usually produced with a model wrapper followed by the [fit2df\(\)](#) function (see examples).

**Usage**

```
boot_compare(bs.out, confint_sep = " to ", comparison = "difference",
             condense = TRUE, compare_name = NULL, digits = c(2, 3),
             ref_symbol = 1)
```

**Arguments**

bs.out	Output from <code>boot::boot</code> ,
confint_sep	String separating lower and upper confidence interval
comparison	Either "difference" or "ratio".
condense	Logical. FALSE gives numeric values, usually for plotting. TRUE gives table for final output.
compare_name	Name to be given to comparison metric.
digits	Rounding for estimate values and p-values, default c(2,3).
ref_symbol	Reference level symbol

**Value**

A dataframe of first differences or ratios for bootstrapped distributions of a metric of interest.  
finalfit predict functions

**See Also**[boot\\_predict](#) [finalfit\\_newdata](#)**Examples**

```
# See boot_predict.
```

---

boot_predict	<i>Bootstrap simulation for model prediction</i>
--------------	--

---

### Description

Generate model predictions against a specified set of explanatory levels with bootstrapped confidence intervals. Add a comparison by difference or ratio of the first row of newdata with all subsequent rows.

### Usage

```
boot_predict(fit, newdata, type = "response", R = 100,
  estimate_name = NULL, confint_sep = " to ", condense = TRUE,
  boot_compare = TRUE, compare_name = NULL,
  comparison = "difference", ref_symbol = "-", digits = c(2, 3))
```

### Arguments

fit	A model generated using <code>lm</code> , <code>glm</code> , <code>lmmulti</code> , and <code>glmmulti</code> .
newdata	Dataframe usually generated with <code>finalfit_newdata</code> .
type	the type of prediction required, see <code>predict.glm</code> . The default for <code>glm</code> models is on the scale of the response variable. Thus for a binomial model the default predictions are predicted probabilities.
R	Number of simulations. Note default R=100 is very low.
estimate_name	Name to be given to prediction variable $\hat{y}$ .
confint_sep	String separating lower and upper confidence interval
condense	Logical. FALSE gives numeric values, usually for plotting. TRUE gives table for final output.
boot_compare	Include a comparison with the first row of newdata with all subsequent rows. See <code>boot_compare</code> .
compare_name	Name to be given to comparison metric.
comparison	Either "difference" or "ratio".
ref_symbol	Reference level symbol
digits	Rounding for estimate values and p-values, default <code>c(2,3)</code> .

### Details

To use this, first generate newdata for specified levels of explanatory variables using `finalfit_newdata`. Pass model objects from `lm`, `glm`, `lmmulti`, and `glmmulti`. The comparison metrics are made on individual bootstrap samples distribution returned as a mean with confidence intervals. A p-value is generated on the proportion of values on the other side of the null from the mean, e.g. for a ratio greater than 1.0, p is the number of bootstrapped predictions under 1.0, multiplied by two so is two-sided.

**Value**

A dataframe of predicted values and confidence intervals, with the option of including a comparison of difference between first row and all subsequent rows of newdata.

**See Also**

[finalfit\\_newdata](#)

/codefinalfit predict functions

**Examples**

```
library(finalfit)
library(dplyr)

# Predict probability of death across combinations of factor levels
explanatory = c("age.factor", "extent.factor", "perfor.factor")
dependent = 'mort_5yr'

# Generate combination of factor levels
colon_s %>%
  finalfit_newdata(explanatory = explanatory, newdata = list(
    c("<40 years", "Submucosa", "No"),
    c("<40 years", "Submucosa", "Yes"),
    c("<40 years", "Adjacent structures", "No"),
    c("<40 years", "Adjacent structures", "Yes")
  )) -> newdata

# Run simulation
colon_s %>%
  glmulti(dependent, explanatory) %>%
  boot_predict(newdata, estimate_name = "Predicted probability of death",
    compare_name = "Absolute risk difference", R=100, digits = c(2,3))

# Plotting
explanatory = c("nodes", "extent.factor", "perfor.factor")
colon_s %>%
  finalfit_newdata(explanatory = explanatory, rowwise = FALSE, newdata = list(
    rep(seq(0, 30), 4),
    c(rep("Muscle", 62), rep("Adjacent structures", 62)),
    c(rep("No", 31), rep("Yes", 31), rep("No", 31), rep("Yes", 31))
  )) -> newdata

colon_s %>%
  glmulti(dependent, explanatory) %>%
  boot_predict(newdata, boot_compare = FALSE, R=100, condense=FALSE) -> plot

library(ggplot2)
theme_set(theme_bw())
plot %>%
  ggplot(aes(x = nodes, y = estimate, ymin = estimate_conf.low,
    ymax = estimate_conf.high, fill=extent.factor))+
```

```

geom_line(aes(colour = extent.factor))+
geom_ribbon(alpha=0.1)+
facet_grid(.~perfor.factor)+
xlab("Number of postive lymph nodes")+
ylab("Probability of death")+
labs(fill = "Extent of tumour", colour = "Extent of tumour")+
ggtitle("Probability of death by lymph node count")

```

---

check\_recode

*Check accurate recoding of variables*


---

## Description

This was written a few days after the retraction of a paper in JAMA due to an error in recoding the treatment variable (<https://jamanetwork.com/journals/jama/fullarticle/2752474>). This takes a data frame or tibble, fuzzy matches variable names, and produces crosstables of all matched variables. A visual inspection should reveal any miscoding.

## Usage

```

check_recode(.data, dependent = NULL, explanatory = NULL,
             include_numerics = TRUE, ...)

```

## Arguments

.data	Data frame or tibble.
dependent	Optional character vector: name(s) of dependent variable(s).
explanatory	Optional character vector: name(s) of explanatory variable(s).
include_numerics	
	Logical. Include numeric variables in function.
...	Pass other arguments to <code>agrep</code> .

## Value

List of length two. The first is an index of variable combinations. The second is a nested list of crosstables as tibbles.

## Examples

```

library(dplyr)
data(colon_s)
colon_s_small = colon_s %>%
  select(-id, -rx, -rx.factor) %>%
  mutate(
    age.factor2 = forcats::fct_collapse(age.factor,
      "<60 years" = c("<40 years", "40-59 years")),
    sex.factor2 = forcats::fct_recode(sex.factor,
      # Intentional miscode

```

```

      "F" = "Male",
      "M" = "Female")
    )

# Check
colon_s_small %>%
  check_recode(include_numerics = FALSE)

out = colon_s_small %>%
  select(-extent, -extent.factor, -time, -time.years) %>%
  check_recode()
out

# Select a tibble and expand
out$counts[[9]]
# Note this variable (node4) appears miscoded in original dataset survival::colon.

# Choose to only include variables that you actually use.
# This uses standard Finalfit grammar.
dependent = "mort_5yr"
explanatory = c("age.factor2", "sex.factor2")
colon_s_small %>%
  check_recode(dependent, explanatory)

```

---

coefficient\_plot

*Produce a coefficient table and plot*


---

## Description

Produce a coefficient and plot from a `lm()` model.

## Usage

```

coefficient_plot(.data, dependent, explanatory, random_effect = NULL,
  factorlist = NULL, lmfit = NULL, confint_type = "default",
  remove_ref = FALSE, breaks = NULL, column_space = c(-0.5, -0.1,
  0.5), dependent_label = NULL, prefix = "",
  suffix = ": Coefficient, 95% CI, p-value)", table_text_size = 5,
  title_text_size = 18, plot_opts = NULL, table_opts = NULL, ...)

```

## Arguments

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1: name of dependent variable (must be numeric/continuous).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>random_effect</code>	Character vector of length 1, name of random effect variable.
<code>factorlist</code>	Option to provide output directly from <code>summary_factorlist()</code> .
<code>lmfit</code>	Option to provide output directly from <code>lmmulti()</code> and <code>lmmixed()</code> .



confint_type	For for lmer models, one of c("default", "Wald", "profile", "boot") Note "default" == "Wald".
remove_ref	Logical. Remove reference level for factors.
breaks	Manually specify x-axis breaks in format c(0.1, 1, 10).
column_space	Adjust table column spacing.
dependent_label	Main label for plot.
prefix	Plots are titled by default with the dependent variable. This adds text before that label.
suffix	Plots are titled with the dependent variable. This adds text after that label.
table_text_size	Alter font size of table text.
title_text_size	Alter font size of title text.
plot_opts	A list of arguments to be appended to the ggplot call by "+".
table_opts	A list of arguments to be appended to the ggplot table call by "+".
...	Other parameters.

**Value**

Returns a table and plot produced in ggplot2.

**See Also**

Other finalfit plot functions: [ff\\_plot](#), [hr\\_plot](#), [or\\_plot](#), [surv\\_plot](#)

**Examples**

```
library(finalfit)
library(ggplot2)

# Coefficient plot
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "nodes"
colon_s %>%
  coefficient_plot(dependent, explanatory)

colon_s %>%
  coefficient_plot(dependent, explanatory, table_text_size=4, title_text_size=14,
    plot_opts=list(xlab("Beta, 95% CI"), theme(axis.title = element_text(size=12))))
```

---

colon_s	<i>Chemotherapy for Stage B/C colon cancer</i>
---------	--

---

**Description**

This is a modified version of `survival::colon`. These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence and one for death

**Usage**

```
data(colon_s)
```

**Format**

A data frame with 929 rows and 33 variables

**Source**

[colon](#)

---

coxphmulti	<i>Cox proportional hazards multivariable models: finalfit model wrapper</i>
------------	--

---

**Description**

Using `finalfit` conventions, produces multivariable Cox Proportional Hazard regression models for a set of explanatory variables against a survival object.

**Usage**

```
coxphmulti(.data, dependent, explanatory)
```

**Arguments**

<code>.data</code>	Data frame.
<code>dependent</code>	Character vector of length 1: name of survival object in form <code>Surv(time, status)</code> .
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.

**Details**

Uses `coxph` with `finalfit` modelling conventions. Output can be passed to `fit2df`.

**Value**

A multivariable [coxph](#) fitted model output. Output is of class `coxph`.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other finalfit model wrappers: [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```
# Cox Proportional Hazards multivariable analysis.
library(finalfit)
library(dplyr)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "Surv(time, status)"
colon_s %>%
  coxphmulti(dependent, explanatory) %>%
  fit2df()
```

---

coxphuni	<i>Cox proportional hazards univariable models: finalfit model wrapper</i>
----------	--

---

**Description**

Using finalfit conventions, produces multiple univariable Cox Proportional Hazard regression models for a set of explanatory variables against a survival object.

**Usage**

```
coxphuni(.data, dependent, explanatory)
```

**Arguments**

.data	Data frame.
dependent	Character vector of length 1: name of survival object in form <code>Surv(time, status)</code> .
explanatory	Character vector of any length: name(s) of explanatory variables.

**Details**

Uses [coxph](#) with finalfit modelling conventions. Output can be passed to [fit2df](#).

**Value**

A list of univariable [coxph](#) fitted model outputs. Output is of class `coxphlist`.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other finalfit model wrappers: [coxphmulti](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```
# Cox Proportional Hazards univariable analysis.
library(finalfit)
library(dplyr)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "Surv(time, status)"
colon_s %>%
  coxphuni(dependent, explanatory) %>%
  fit2df()
```

---

crrmulti

*Competing risks multivariable regression: finalfit model wrapper*

---

**Description**

Using finalfit conventions, produces multivariable Competing Risks Regression models for a set of explanatory variables.

**Usage**

```
crrmulti(.data, dependent, explanatory, ...)
```

**Arguments**

<code>.data</code>	Data frame or tibble.
<code>dependent</code>	Character vector of length 1: name of survival object in form <code>Surv(time, status)</code> . Status default values should be 0 censored (e.g. alive), 1 event of interest (e.g. died of disease of interest), 2 competing event (e.g. died of other cause).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>...</code>	Other arguments to <a href="#">crr</a>

**Details**

Uses [crr](#) with finalfit modelling conventions. Output can be passed to [fit2df](#).

**Value**

A multivariable [crr](#) fitted model class `crr`.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other finalfit model wrappers: [coxphmulti](#), [coxphuni](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```
library(dplyr)
melanoma = boot::melanoma
melanoma = melanoma %>%
  mutate(
    # Cox PH to determine cause-specific hazards
    status_coxph = ifelse(status == 2, 0, # "still alive"
      ifelse(status == 1, 1, # "died of melanoma"
        0)), # "died of other causes is censored"

    # Fine and Gray to determine subdistribution hazards
    status_crr = ifelse(status == 2, 0, # "still alive"
      ifelse(status == 1, 1, # "died of melanoma"
        2)), # "died of other causes"
    sex = factor(sex),
    ulcer = factor(ulcer)
  )

dependent_coxph = c("Surv(time, status_coxph)")
dependent_crr = c("Surv(time, status_crr)")
explanatory = c("sex", "age", "ulcer")

# Create single well-formatted table
melanoma %>%
  summary_factorlist(dependent_crr, explanatory, column = TRUE, fit_id = TRUE) %>%
  ff_merge(
    melanoma %>%
      coxphmulti(dependent_coxph, explanatory) %>%
      fit2df(estimate_suffix = " (Cox PH multivariable)")
  ) %>%
  ff_merge(
    melanoma %>%
      crrmulti(dependent_crr, explanatory) %>%
      fit2df(estimate_suffix = " (competing risks multivariable)")
  ) %>%
  select(-fit_id, -index) %>%
  dependent_label(melanoma, dependent_crr)
```

**Description**

Using `finalfit` conventions, produces univariable Competing Risks Regression models for a set of explanatory variables.

**Usage**

```
crruni(.data, dependent, explanatory, ...)
```

**Arguments**

<code>.data</code>	Data frame or tibble.
<code>dependent</code>	Character vector of length 1: name of survival object in form <code>Surv(time, status)</code> . Status default values should be 0 censored (e.g. alive), 1 event of interest (e.g. died of disease of interest), 2 competing event (e.g. died of other cause).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>...</code>	Other arguments to <code>crr</code>

**Details**

Uses `crr` with `finalfit` modelling conventions. Output can be passed to `fit2df`.

**Value**

A list of univariable `crr` fitted models class `crrlist`.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other `finalfit` model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [glmrmixed](#), [glmrmulti\\_boot](#), [glmrmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmrmulti](#), [svyglmuni](#)

**Examples**

```
library(dplyr)
melanoma = boot::melanoma
melanoma = melanoma %>%
  mutate(
    # Cox PH to determine cause-specific hazards
    status_coxph = ifelse(status == 2, 0, # "still alive"
      ifelse(status == 1, 1, # "died of melanoma"
        0)), # "died of other causes is censored"

    # Fine and Gray to determine subdistribution hazards
    status_crr = ifelse(status == 2, 0, # "still alive"
      ifelse(status == 1, 1, # "died of melanoma"
        2)), # "died of other causes"
    sex = factor(sex),
    ulcer = factor(ulcer)
  )
```

```

dependent_coxph = c("Surv(time, status_coxph)")
dependent_crr = c("Surv(time, status_crr)")
explanatory = c("sex", "age", "ulcer")

# Create single well-formatted table
melanoma %>%
  summary_factorlist(dependent_crr, explanatory, column = TRUE, fit_id = TRUE) %>%
  ff_merge(
    melanoma %>%
      coxphmulti(dependent_coxph, explanatory) %>%
      fit2df(estimate_suffix = " (Cox PH multivariable)")
  ) %>%
  ff_merge(
    melanoma %>%
      crrmulti(dependent_crr, explanatory) %>%
      fit2df(estimate_suffix = " (competing risks multivariable)")
  ) %>%
  select(-fit_id, -index) %>%
  dependent_label(melanoma, dependent_crr)

```

---

dependent_label	<i>Make a label for the dependent variable</i>
-----------------	--

---

### Description

Can be add dependent label to final results dataframe.

### Usage

```
dependent_label(df.out, .data, dependent, prefix = "Dependent: ",
  suffix = "")
```

### Arguments

df.out	Dataframe (results table) to be altered.
.data	Original dataframe.
dependent	Character vector of length 1: quoted name of dependent variable. Can be continuous, a binary factor, or a survival object of form <code>Surv(time, status)</code>
prefix	Prefix for dependent label
suffix	Suffix for dependent label

### Value

Returns the label for the dependent variable, if specified.

**Examples**

```

library(dplyr)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
explanatory_multi = c("age.factor", "obstruct.factor")
random_effect = "hospital"
dependent = 'mort_5yr'

# Separate tables
colon_s %>%
summary_factorlist(dependent, explanatory, fit_id=TRUE) -> example.summary

colon_s %>%
glmuni(dependent, explanatory) %>%
fit2df(estimate_suffix=" (univariable)") -> example.univariable

colon_s %>%
glmulti(dependent, explanatory) %>%
fit2df(estimate_suffix=" (multivariable)") -> example.multivariable

colon_s %>%
glmmixed(dependent, explanatory, random_effect) %>%
fit2df(estimate_suffix=" (multilevel)") -> example.multilevel

# Pipe together
example.summary %>%
  finalfit_merge(example.univariable) %>%
  finalfit_merge(example.multivariable) %>%
  finalfit_merge(example.multilevel) %>%
  select(-c(fit_id, index)) %>%
  dependent_label(colon_s, dependent) -> example.final
example.final

```

---

extract\_variable\_label

*Extract variable labels from dataframe*

---

**Description**

Variable labels can be created using [ff\\_label](#). Some functions strip variable labels (variable attributes), e.g. `forcats::fct_recode`. Use this function to create a vector of variable labels from a data frame. Then use [ff\\_relabel](#) to relabel variables in data frame.

**Usage**

```
extract_variable_label(.data)
```

**Arguments**

`.data`                    Dataframe containing labelled variables.



**Examples**

```
colon_s %>%
  extract_variable_label
```

---

ff_column_totals	<i>Add column totals to summary_factorlist() output</i>
------------------	---

---

**Description**

Add column totals to summary\_factorlist() output

**Usage**

```
ff_column_totals(df.in, .data, dependent, na_include_dependent = FALSE,
  percent = TRUE, digits = 1, label = NULL, prefix = "")
```

```
finalfit_column_totals(df.in, .data, dependent,
  na_include_dependent = FALSE, percent = TRUE, digits = 1,
  label = NULL, prefix = "")
```

**Arguments**

df.in	summary_factorlist() output.
.data	Data frame used to create summary_factorlist().
dependent	Character. Name of dependent variable.
na_include_dependent	Logical. When TRUE, missing data in the dependent variable is included in totals.
percent	Logical. Include percentage.
digits	Integer length 1. Number of digits for percentage.
label	Character. Label for total row.
prefix	Character. Prefix for column totals, e.g "N=".

**Value**

Data frame.

**Examples**

```
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  summary_factorlist(dependent, explanatory) %>%
  ff_column_totals(colon_s, dependent)

# Ensure works with missing data in dependent
```

```

colon_s = colon_s %>%
  dplyr::mutate(
    mort_5yr = forcats::fct_explicit_na(mort_5yr)
  )
colon_s %>%
  summary_factorlist(dependent, explanatory) %>%
  ff_column_totals(colon_s, dependent)

```

---

ff\_formula

*Generate formula as character string*


---

### Description

Useful when passing finalfit dependent and explanatory lists to base R functions

### Usage

```
ff_formula(dependent, explanatory, random_effect = NULL)
```

```
finalfit_formula(dependent, explanatory, random_effect = NULL)
```

### Arguments

dependent      Optional character vector: name(s) of dependent variable(s).  
explanatory      Optional character vector: name(s) of explanatory variable(s).  
random\_effect    Optional character vector: name(s) of random effect variable(s).

### Value

Character vector

### Examples

```

explanatory = c("age", "nodes", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
ff_formula(dependent, explanatory)

```

```

explanatory = c("age", "nodes", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
random_effect = "(age.factor | hospital)"
ff_formula(dependent, explanatory)

```

ff\_glimpse

*Descriptive statistics for dataframe***Description**

Everyone has a function like this, str, glimpse, glance etc. This one is specifically designed for use with finalfit language. It is different in dividing variables by numeric vs factor.

**Usage**

```
ff_glimpse(.data, dependent = NULL, explanatory = NULL, digits = 1,
           levels_cut = 5)
```

```
finalfit_glimpse(.data, dependent = NULL, explanatory = NULL,
                 digits = 1, levels_cut = 5)
```

**Arguments**

.data	Dataframe.
dependent	Optional character vector: name(s) of dependent variable(s).
explanatory	Optional character vector: name(s) of explanatory variable(s).
digits	Significant digits for continuous variable summaries
levels_cut	Max number of factor levels to include in factor levels summary (in order to avoid the long printing of variables with many factors).

**Value**

Dataframe on summary data.

**Examples**

```
library(finalfit)
dependent = 'mort_5yr'
explanatory = c("age", "nodes", "age.factor", "extent.factor", "perfor.factor")
colon_s %>%
  finalfit_glimpse(dependent, explanatory)
```

---

ff_interaction	<i>Make an interaction variable and add to dataframe</i>
----------------	--

---

### Description

Combine two factor variables to make an interaction variable. Factor level order is determined by the order in the variables themselves. Note, names of the factor variables should not be quoted. The name of the variable is created from the names of the two factors. The variable is also labelled with a name derived from any pre-existing labels.

### Usage

```
ff_interaction(.data, ..., levels_sep = "|", var_sep = "__",
              label_sep = ":")

finalfit_interaction(.data, ..., levels_sep = "|", var_sep = "__",
                    label_sep = ":")
```

### Arguments

.data	Data frame.
...	The unquoted names of two factors.
levels_sep	Quoted character: how levels are separated in new variable.
var_sep	Quoted character: how variable name is separated.
label_sep	Quoted character: how variable label is separated

### Value

Original data frame with new variable added via 'dplyr::mutate'.

### Examples

```
colon_s %>%
  ff_interaction(sex.factor, perfor.factor) %>%
  summary_factorlist("mort_5yr", "sex.factor__perfor.factor")
```

---

ff_label	<i>Label a variable</i>
----------	-------------------------

---

**Description**

Label a variable

**Usage**

```
ff_label(.var, variable_label)
finalfit_label(.var, variable_label)
```

**Arguments**

.var            Quoted variable name  
variable\_label Quoted variable label

**Value**

Labelled variable

**See Also**

[extract\\_variable\\_label](#) [ff\\_relabel](#)

**Examples**

```
colon_s$sex.factor %>%
  ff_label("Sex") %>%
  str()
```

---

ff_merge	<i>Merge a <a href="#">summary_factorlist()</a> table with any number of model results tables.</i>
----------	--

---

**Description**

A function that takes the output from [summary\\_factorlist\(..., fit\\_id=TRUE\)](#) and merges with any number of model dataframes, usually produced with a model wrapper followed by the [fit2df\(\)](#) function (see examples).

**Usage**

```
ff_merge(factorlist, fit2df_df, ref_symbol = "-", estimate_name = NULL,
         last_merge = FALSE)
```

```
finalfit_merge(factorlist, fit2df_df, ref_symbol = "-",
               estimate_name = NULL, last_merge = FALSE)
```

**Arguments**

factorlist	Output from <code>summary_factorlist(..., fit_id=TRUE)</code> .
fit2df_df	Output from model wrappers followed by <code>fit2df()</code> .
ref_symbol	Reference symbol for model reference levels, typically "-" or "1.0".
estimate_name	If you have chosen a new 'estimate name' (e.g. "Odds ratio") when running a model wrapper (e.g. 'glmuni'), then you need to pass this new name to 'finalfit_merge' to generate correct table. Defaults to OR/HR/Coefficient
last_merge	Logical. Set to try for the final merge in a series to remove index and fit_id columns.

**Value**

Returns a dataframe of combined tables.

**See Also**

[summary\\_factorlist](#) [fit2df](#)

**Examples**

```
library(finalfit)
library(dplyr)

data(colon_s)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
explanatory_multi = c("age.factor", "obstruct.factor")
random_effect = "hospital"
dependent = "mort_5yr"

# Create separate tables
colon_s %>%
  summary_factorlist(dependent, explanatory, fit_id=TRUE) -> example.summary

colon_s %>%
  glmuni(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (univariable)") -> example.univariable

colon_s %>%
  glmulti(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (multivariable)") -> example.multivariable
```

```
colon_s %>%
  glmmixed(dependent, explanatory, random_effect) %>%
  fit2df(estimate_suffix=" (multilevel)") -> example.multilevel

# Pipe together
example.summary %>%
  ff_merge(example.univariable) %>%
  ff_merge(example.multivariable) %>%
  ff_merge(example.multilevel, last_merge = TRUE)

# Using finalfit()
colon_s %>%
  finalfit(dependent, explanatory, keep_fit_id = TRUE) %>%
  ff_merge(example.multilevel, last_merge = TRUE)
```

---

ff\_metrics

*Generate common metrics for regression model results*

---

## Description

Generate common metrics for regression model results

## Usage

```
ff_metrics(.data)

## S3 method for class 'lm'
ff_metrics(.data)

## S3 method for class 'lmList'
ff_metrics(.data)

## S3 method for class 'glm'
ff_metrics(.data)

## S3 method for class 'glmList'
ff_metrics(.data)

## S3 method for class 'lmerMod'
ff_metrics(.data)

## S3 method for class 'glmerMod'
ff_metrics(.data)

## S3 method for class 'coxph'
ff_metrics(.data)

## S3 method for class 'coxphList'
ff_metrics(.data)
```

**Arguments**

.data            Model output.

**Value**

Model metrics vector for output.

**Examples**

```
library(finalfit)

# glm
fit = glm(mort_5yr ~ age.factor + sex.factor + obstruct.factor + perfor.factor,
  data=colon_s, family="binomial")
fit %>%
  ff_metrics()

# glmlist
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
colon_s %>%
  glmulti(dependent, explanatory) %>%
  ff_metrics()

# glmerMod
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
random_effect = "hospital"
dependent = "mort_5yr"
colon_s %>%
  glmmixed(dependent, explanatory, random_effect) %>%
  ff_metrics()

# lm
fit = lm(nodes ~ age.factor + sex.factor + obstruct.factor + perfor.factor,
  data=colon_s)
fit %>%
  ff_metrics()

# lmerMod
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
random_effect = "hospital"
dependent = "nodes"

colon_s %>%
  lmmixed(dependent, explanatory, random_effect) %>%
  ff_metrics()

# coxphlist
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "Surv(time, status)"
```



```

colon_s %>%
  coxphmulti(dependent, explanatory) %>%
  ff_metrics()

# coxph
fit = survival::coxph(survival::Surv(time, status) ~ age.factor + sex.factor +
  obstruct.factor + perfor.factor,
  data = colon_s)

fit %>%
  ff_metrics()

```

---

ff_newdata	<i>Generate newdata for simulations</i>
------------	---

---

## Description

Generate newdata while respecting the variable types and factor levels in the primary data frame used to run model.

## Usage

```

ff_newdata(.data, dependent = NULL, explanatory = NULL,
  rowwise = TRUE, newdata)

finalfit_newdata(.data, dependent = NULL, explanatory = NULL,
  rowwise = TRUE, newdata)

```

## Arguments

.data	Dataframe.
dependent	Optional character vector of length 1: name of dependent variable. Not usually specified in bootstrapping model predictions.
explanatory	Character vector of any length: name(s) of explanatory variables.
rowwise	Logical. Format newdata is provided in.
newdata	A list of rows or columns corresponding exactly to the order of explanatory variables. Useful errors generated if requirements not fulfilled

## Details

Generate model predictions against a specified set of explanatory levels with bootstrapped confidence intervals. Add a comparison by difference or ratio of the first row of newdata with all subsequent rows.

## Value

A list of multivariable [glm](#) fitted model outputs. Output is of class `glm1list`.

**See Also**

[boot\\_predict](#) [boot\\_compare](#)

**Examples**

```
# See boot_predict.
library(finalfit)
library(dplyr)

# Predict probability of death across combinations of factor levels
explanatory = c("age.factor", "extent.factor", "perfor.factor")
dependent = 'mort_5yr'

# Generate combination of explanatory variable levels rowwise
colon_s %>%
  finalfit_newdata(explanatory = explanatory, newdata = list(
    c("<40 years", "Submucosa", "No"),
    c("<40 years", "Submucosa", "Yes"),
    c("<40 years", "Adjacent structures", "No"),
    c("<40 years", "Adjacent structures", "Yes")
  )) -> newdata

# Generate combination of explanatory variable levels colwise.
explanatory = c("nodes", "extent.factor", "perfor.factor")
colon_s %>%
  finalfit_newdata(explanatory = explanatory, rowwise = FALSE, newdata = list(
    rep(seq(0, 30), 4),
    c(rep("Muscle", 62), rep("Adjacent structures", 62)),
    c(rep("No", 31), rep("Yes", 31), rep("No", 31), rep("Yes", 31))
  )) -> newdata
```

---

ff\_percent\_only

*Include only percentages for factors in [summary\\_factorlist](#) output*

---

**Description**

Include only percentages for factors in [summary\\_factorlist](#) output

**Usage**

```
ff_percent_only(.data)
```

```
finalfit_percent_only(.data)
```

**Arguments**

.data                    Output from [finalfit](#) or similar.

**Value**

Data frame.

**Examples**

```
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  summary_factorlist(dependent, explanatory) %>%
  ff_percent_only()
```

---

ff_permute	<i>Permute explanatory variables to produce multiple output tables for common regression models</i>
------------	---

---

**Description**

Permute explanatory variables to produce multiple output tables for common regression models

**Usage**

```
ff_permute(.data, dependent = NULL, explanatory_base = NULL,
  explanatory_permute = NULL, multiple_tables = FALSE,
  include_base_model = TRUE, include_full_model = TRUE,
  base_on_top = TRUE, ...)
```

```
finalfit_permute(.data, dependent = NULL, explanatory_base = NULL,
  explanatory_permute = NULL, multiple_tables = FALSE,
  include_base_model = TRUE, include_full_model = TRUE,
  base_on_top = TRUE, ...)
```

**Arguments**

.data	Data frame or tibble.
dependent	Character vector of length 1: quoted name of dependent variable. Can be continuous, a binary factor, or a survival object of form <code>Surv(time, status)</code> .
explanatory_base	Character vector of any length: quoted name(s) of base model explanatory variables.
explanatory_permute	Character vector of any length: quoted name(s) of explanatory variables to permute through models.
multiple_tables	Logical. Multiple model tables as a list, or a single table including multiple models.
include_base_model	Logical. Include model using explanatory_base variables only.

```

include_full_model      Logical. Include model using all explanatory_base and explanatory_permute
                        variables.
base_on_top             Logical. Base variables at top of table, or bottom of table.
...                    Other arguments to finalfit

```

### Value

Returns a list of data frame with the final model table.

### Examples

```

explanatory_base = c("age.factor", "sex.factor")
explanatory_permute = c("obstruct.factor", "perfor.factor", "node4.factor")

# Linear regression
colon_s %>%
  finalfit_permute("nodes", explanatory_base, explanatory_permute)

# Cox proportional hazards regression
colon_s %>%
  finalfit_permute("Surv(time, status)", explanatory_base, explanatory_permute)

# Logistic regression
# colon_s %>%
#   finalfit_permute("mort_5yr", explanatory_base, explanatory_permute)

# Logistic regression with random effect (glmer)
# colon_s %>%
#   finalfit_permute("mort_5yr", explanatory_base, explanatory_permute,
#     random_effect = "hospital")

```

---

ff\_plot

*Produce a table and plot*

---

### Description

Wraps `or_plot`, `hr_plot`, and `coefficient_plot` and sends to the appropriate method depending on the dependent variable type.

### Usage

```
ff_plot(.data, dependent, explanatory, ...)
```

```
finalfit_plot(.data, dependent, explanatory, ...)
```

**Arguments**

.data            Data frame.  
 dependent       Character vector of length 1.  
 explanatory     Character vector of any length: name(s) of explanatory variables.  
 ...              Pass arguments [or\\_plot](#), [hr\\_plot](#), or [coefficient\\_plot](#)

**Value**

A table and a plot using [ggplot2](#)

**See Also**

Other finalfit plot functions: [coefficient\\_plot](#), [hr\\_plot](#), [or\\_plot](#), [surv\\_plot](#)

**Examples**

```
# Coefficient plot
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "nodes"
colon_s %>%
  ff_plot(dependent, explanatory)

# Odds ratio plot
dependent = "mort_5yr"
colon_s %>%
  ff_plot(dependent, explanatory)

# Hazard ratio plot
dependent = "Surv(time, status)"
colon_s %>%
  ff_plot(dependent, explanatory, dependent_label = "Survival")
```

---

<code>ff_relabel</code>	<i>Relabel variables in a data frame</i>
-------------------------	--

---

**Description**

Variable labels can be created using [ff\\_label](#). Some functions strip variable labels (variable attributes), e.g. `forcats::fct_recode`. Use this function to create a vector of variable labels from a data frame. Then use [ff\\_relabel](#) to relabel variables in data frame.

**Usage**

```
ff_relabel(.data, .labels)

finalfit_relabel(.data, .labels)
```

**Arguments**

`.data`                Data frame to be relabelled

`.labels`             Vector of variable labels (usually created using [extract\\_variable\\_label](#)) of same length as `.data`.

**Examples**

```
# Label variable
colon_s$sex.factor %>%
  ff_label("Sex") %>%
  str()

# Make factor level "Unknown" NA
colon_s %>%
  dplyr::mutate_if(is.factor, forcats::fct_recode,
  NULL = "Unknown") %>%
  str()

# Reset data
data(colon_s)

# Extract variable labels
vlabels = colon_s %>% extract_variable_label()

# Run function where labels are lost
colon_s %>%
  dplyr::mutate_if(is.factor, forcats::fct_recode,
  NULL = "Unknown") %>%
  str()

# Relabel
colon_s %<>% ff_relabel(vlabels)
colon_s %>% str()
```

---

 ff\_relabel\_df

*Relabel variables from data frame after tidyverse functions*


---

**Description**

Relabel variables from data frame after tidyverse functions

**Usage**

```
ff_relabel_df(.data, .df)
```

```
finalfit_relabel_df(.data, .df)
```

**Arguments**

- .data            Data frame or tibble after applicaton of label stripping functions.  
.df              Original data frame which contains labels.

**Value**

Data frame or tibble

---

ff_remove_p	<i>Remove p-value from output</i>
-------------	-----------------------------------

---

**Description**

This will work with [finalfit](#) and any [fit2df](#) output.

**Usage**

```
ff_remove_p(.data)
finalfit_remove_p(.data)
```

**Arguments**

- .data            Output from [finalfit](#) or similar.

**Value**

Data frame.

**Examples**

```
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  finalfit(dependent, explanatory) %>%
  ff_remove_p()
```

---

ff_remove_ref	<i>Remove regression reference level row from table</i>
---------------	---

---

### Description

This looks for a column with a name including "Coefficient", "OR", or "HR" (`finalfit` defaults) and removes any rows with "-" (the default for the reference level). Can also be combined to produce an `or_plot`, see below.

### Usage

```
ff_remove_ref(.data, only_binary = TRUE)

finalfit_remove_ref(.data, only_binary = TRUE)
```

### Arguments

<code>.data</code>	Output from <code>finalfit</code> or similar.
<code>only_binary</code>	Logical. Remove reference level only for two-level factors. When set to false, reference level for all factors removed.

### Value

Data frame.

### Examples

```
# Table example
explanatory = c("age.factor", "age", "sex.factor", "nodes", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  finalfit(dependent, explanatory, add_dependent_label = FALSE) %>%
  ff_remove_ref() %>%
  dependent_label(colon_s, dependent)

# Plot example
explanatory = c("age.factor", "age", "sex.factor", "nodes", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  summary_factorlist(dependent, explanatory, total_col = TRUE, fit_id=TRUE) %>%
  ff_merge(
    glmuni(colon_s, dependent, explanatory) %>%
    fit2df()) %>%
  ff_remove_ref() %>%
  dplyr::select(-`OR`) -> factorlist_plot

colon_s %>%
  or_plot(dependent, explanatory, factorlist = factorlist_plot)
```



---

ff_row_totals	<i>Add row totals to summary_factorlist() output</i>
---------------	--

---

## Description

This adds a total and missing count to variables. This is useful for continuous variables. Compare this to `summary_factorlist(total_col = TRUE)` which includes a count for each dummy variable as a factor and mean (sd) or median (iqr) for continuous variables.

## Usage

```
ff_row_totals(df.in, .data, dependent, explanatory,
  missing_column = TRUE, na_include_dependent = FALSE,
  na_complete_cases = FALSE, total_name = "Total N",
  na_name = "Missing N")
```

```
finalfit_row_totals(df.in, .data, dependent, explanatory,
  missing_column = TRUE, na_include_dependent = FALSE,
  na_complete_cases = FALSE, total_name = "Total N",
  na_name = "Missing N")
```

## Arguments

<code>df.in</code>	summary_factorlist() output.
<code>.data</code>	Data frame used to create summary_factorlist().
<code>dependent</code>	Character. Name of dependent variable.
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>missing_column</code>	Logical. Include a column of counts of missing data.
<code>na_include_dependent</code>	Logical. When TRUE, missing data in the dependent variable is included in totals.
<code>na_complete_cases</code>	Logical. When TRUE, missing data counts for variables are for complete cases across all included variables.
<code>total_name</code>	Character. Name of total column.
<code>na_name</code>	Character. Name of missing column.

## Value

Data frame.

**Examples**

```

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  summary_factorlist(dependent, explanatory) %>%
  ff_row_totals(colon_s, dependent, explanatory)

```

---

ff\_stratify\_helper      *Help making stratified summary\_factorlist tables*

---

**Description**

Help making stratified summary\_factorlist tables

**Usage**

```
ff_stratify_helper(df.out, .data)
```

**Arguments**

df.out	Output from summary_factorlist
.data	Original data frame used for summary_factorlist.

**Examples**

```

library(dplyr)
explanatory = c("age.factor", "sex.factor")
dependent = "perfor.factor"

# Pick option below
split = "rx.factor"
split = c("rx.factor", "node4.factor")

# Piped function to generate stratified crosstabs table
colon_s %>%
  group_by(!!! syms(split)) %>% #Looks awkward, but avoids unquoted var names
  group_modify(~ summary_factorlist(.x, dependent, explanatory)) %>%
  ff_stratify_helper(colon_s)

```

finalfit

*Final output tables for common regression models***Description**

An "all-in-one" function that takes a single dependent variable with a vector of explanatory variable names (continuous or categorical variables) to produce a final table for publication including summary statistics. The appropriate model is selected on the basis of dependent variable and whether a random effect is specified.

`finalfit.lm` method (not called directly)

`finalfit.glm` method (not called directly)

`finalfit.coxph` method (not called directly)

**Usage**

```
finalfit(.data, dependent, explanatory, explanatory_multi = NULL,
        random_effect = NULL, column = FALSE, keep_models = FALSE,
        metrics = FALSE, add_dependent_label = TRUE,
        dependent_label_prefix = "Dependent: ", dependent_label_suffix = "",
        keep_fit_id = FALSE, ...)
```

```
finalfit.lm(.data, dependent, explanatory, explanatory_multi = NULL,
           random_effect = NULL, column = FALSE, keep_models = FALSE,
           metrics = FALSE, add_dependent_label = TRUE,
           dependent_label_prefix = "Dependent: ", dependent_label_suffix = "",
           keep_fit_id = FALSE, ...)
```

```
finalfit.glm(.data, dependent, explanatory, explanatory_multi = NULL,
            random_effect = NULL, column = FALSE, keep_models = FALSE,
            metrics = FALSE, add_dependent_label = TRUE,
            dependent_label_prefix = "Dependent: ", dependent_label_suffix = "",
            keep_fit_id = FALSE, ...)
```

```
finalfit.coxph(.data, dependent, explanatory, explanatory_multi = NULL,
              random_effect = NULL, column = TRUE, keep_models = FALSE,
              metrics = FALSE, add_dependent_label = TRUE,
              dependent_label_prefix = "Dependent: ", dependent_label_suffix = "",
              keep_fit_id = FALSE, ...)
```

**Arguments**

<code>.data</code>	Data frame or tibble.
<code>dependent</code>	Character vector of length 1: quoted name of dependent variable. Can be continuous, a binary factor, or a survival object of form <code>Surv(time, status)</code> .
<code>explanatory</code>	Character vector of any length: quoted name(s) of explanatory variables.

<code>explanatory_multi</code>	Character vector of any length: quoted name(s) of a subset of explanatory variables to generate reduced multivariable model (must only contain variables contained in <code>explanatory</code> ).
<code>random_effect</code>	Character vector of length 1: quoted name of random effects variable. When included mixed effects model generated ( <code>lme4::glmer</code> <code>lme4::lmer</code> ).
<code>column</code>	Logical: Compute margins by column rather than row.
<code>keep_models</code>	Logical: include full multivariable model in output when working with reduced multivariable model ( <code>explanatory_multi</code> ) and/or mixed effect models ( <code>random_effect</code> ).
<code>metrics</code>	Logical: include useful model metrics in output in publication format.
<code>add_dependent_label</code>	Add the name of the dependent label to the top left of table.
<code>dependent_label_prefix</code>	Add text before dependent label.
<code>dependent_label_suffix</code>	Add text after dependent label.
<code>keep_fit_id</code>	Keep original model output coefficient label (internal).
<code>...</code>	Other arguments to pass to <code>fit2df</code> : <code>estimate_name</code> , <code>digits</code> , <code>confint_type</code> , <code>confint_level</code> , <code>confint</code> .

## Value

Returns a data frame with the final model table.

## Examples

```
library(finalfit)
library(dplyr)

# Summary, univariable and multivariable analyses of the form:
# glm(dependent ~ explanatory, family="binomial")
# lmuni(), lmmulti(), lmmixed(), glmuni(), glmmulti(), glmmixed(), glmmultiboot(),
# coxphuni(), coxphmulti()

data(colon_s) # Modified from survival::colon
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  finalfit(dependent, explanatory)

# Multivariable analysis with subset of explanatory
# variable set used in univariable analysis
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
explanatory_multi = c("age.factor", "obstruct.factor")
dependent = "mort_5yr"
colon_s %>%
  finalfit(dependent, explanatory, explanatory_multi)

# Summary, univariable and multivariable analyses of the form:
```

```

# lme4::glmer(dependent ~ explanatory + (1 | random_effect), family="binomial")

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
explanatory_multi = c("age.factor", "obstruct.factor")
random_effect = "hospital"
dependent = "mort_5yr"
# colon_s %>%
# finalfit(dependent, explanatory, explanatory_multi, random_effect)

# Include model metrics:
colon_s %>%
  finalfit(dependent, explanatory, explanatory_multi, metrics=TRUE)

# Summary, univariable and multivariable analyses of the form:
# survival::coxph(dependent ~ explanatory)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "Surv(time, status)"

colon_s %>%
  finalfit(dependent, explanatory)

# Rather than going all-in-one, any number of subset models can
# be manually added on to a summary_factorlist() table using finalfit.merge().
# This is particularly useful when models take a long-time to run or are complicated.

# Note requirement for fit_id=TRUE.
# `fit2df` is a subfunction extracting most common models to a dataframe.

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  finalfit(dependent, explanatory, metrics=TRUE)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
explanatory_multi = c("age.factor", "obstruct.factor")
random_effect = "hospital"
dependent = 'mort_5yr'

# Separate tables
colon_s %>%
  summary_factorlist(dependent, explanatory, fit_id=TRUE) -> example.summary

colon_s %>%
  glmuni(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (univariable)") -> example.univariable

colon_s %>%
  glmmulti(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (multivariable)") -> example.multivariable

# Edited as CRAN slow to run these
# colon_s %>%

```

```
# glmmixed(dependent, explanatory, random_effect) %>%
# fit2df(estimate_suffix=" (multilevel") -> example.multilevel

# Pipe together
example.summary %>%
  finalfit_merge(example.univariable) %>%
  finalfit_merge(example.multivariable, last_merge = TRUE)
# finalfit_merge(example.multilevel)
```

---

fit2df	<i>Extract model fit results to dataframe (generic): finalfit model extractors</i>
--------	--

---

## Description

Takes output from finalfit model wrappers and extracts to a dataframe, convenient for further processing in preparation for final results table.

fit2df.lm is the model extract method for `lm`.

fit2df.lmlist is the model extract method for `lmuni` and `lmmulti`.

fit2df.glm is the model extract method for standard `glm` models, which have not used finalfit model wrappers.

fit2df.glmboot is the model extract method for `glmmulti_boot` models.

fit2df.glm1ist is the model extract method for `glmuni` and `glmmulti`.

fit2df.svyglm1ist is the model extract method for `svyglmuni` and `svyglmmulti`.

fit2df.lmerMod is the model extract method for standard `lme4::lmer` models and for the `finalfit::lmmixed` model wrapper.

fit2df.glmerMod is the model extract method for standard `lme4::glmer` models and for the `finalfit::glmmixed` model wrapper.

fit2df.coxph is the model extract method for `survival::coxph`.

fit2df.coxph1ist is the model extract method for `coxphuni` and `coxphmulti`.

fit2df.crr is the model extract method for `cmprsk::crr`.

fit2df.coxme is the model extract method for `eoxme::coxme`.

fit2df.crr is the model extract method for `crruni` and `crrmulti`.

fit2df.stanfit is the model extract method for our standard Bayesian hierarchical binomial logistic regression models. These models will be fully documented separately. However this should work for a single or multilevel Bayesian logistic regression done in Stan, as long as the fixed effects are specified in the parameters block as a vector named `beta`, of length `P`, where `P` is the number of fixed effect parameters. e.g. `parameters vector[P] beta;`

fit2df.mipo is the model extract method for the `mipo` object created using `mice::pool`.

**Usage**

```
fit2df(...)  
  
## S3 method for class 'lm'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "Coefficient", estimate_suffix = "", p_name = "p",  
  digits = c(2, 2, 3), confint_level = 0.95, confint_sep = " to ",  
  ...)  
  
## S3 method for class 'lmlist'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "Coefficient", estimate_suffix = "", p_name = "p",  
  digits = c(2, 2, 3), confint_level = 0.95, confint_sep = " to ",  
  ...)  
  
## S3 method for class 'glm'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "OR", estimate_suffix = "", p_name = "p",  
  digits = c(2, 2, 3), exp = TRUE, confint_type = "profile",  
  confint_level = 0.95, confint_sep = "-", ...)  
  
## S3 method for class 'glmboot'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "OR", estimate_suffix = "", p_name = "p",  
  digits = c(2, 2, 3), exp = TRUE, confint_sep = "-", ...)  
  
## S3 method for class 'glmmlist'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "OR", estimate_suffix = "", p_name = "p",  
  digits = c(2, 2, 3), exp = TRUE, confint_type = "profile",  
  confint_level = 0.95, confint_sep = "-", ...)  
  
## S3 method for class 'svyglmmlist'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "Coefficient", estimate_suffix = "", p_name = "p",  
  digits = c(2, 2, 3), exp = FALSE, confint_type = "profile",  
  confint_level = 0.95, confint_sep = "-", ...)  
  
## S3 method for class 'lmerMod'  
fit2df(.data, condense = TRUE, metrics = FALSE,  
  remove_intercept = TRUE, explanatory_name = "explanatory",  
  estimate_name = "Coefficient", estimate_suffix = "", p_name = "p",
```

```
digits = c(2, 2, 3), confint_type = "Wald", confint_level = 0.95,
confint_sep = "-", ...)
```

```
## S3 method for class 'glmerMod'
fit2df(.data, condense = TRUE, metrics = FALSE,
  remove_intercept = TRUE, explanatory_name = "explanatory",
  estimate_name = "OR", estimate_suffix = "", p_name = "p",
  digits = c(2, 2, 3), exp = TRUE, confint_type = "Wald",
  confint_level = 0.95, confint_sep = "-", ...)
```

```
## S3 method for class 'coxph'
fit2df(.data, condense = TRUE, metrics = FALSE,
  explanatory_name = "explanatory", estimate_name = "HR",
  estimate_suffix = "", p_name = "p", digits = c(2, 2, 3),
  confint_sep = "-", ...)
```

```
## S3 method for class 'coxphlist'
fit2df(.data, condense = TRUE, metrics = FALSE,
  explanatory_name = "explanatory", estimate_name = "HR",
  estimate_suffix = "", p_name = "p", digits = c(2, 2, 3),
  confint_sep = "-", ...)
```

```
## S3 method for class 'crr'
fit2df(.data, condense = TRUE, metrics = FALSE,
  explanatory_name = "explanatory", estimate_name = "HR",
  estimate_suffix = "", p_name = "p", digits = c(2, 2, 3),
  confint_sep = "-", ...)
```

```
## S3 method for class 'coxme'
fit2df(.data, condense = TRUE, metrics = FALSE,
  explanatory_name = "explanatory", estimate_name = "HR",
  estimate_suffix = "", p_name = "p", digits = c(2, 2, 3),
  confint_sep = "-", ...)
```

```
## S3 method for class 'crrlist'
fit2df(.data, condense = TRUE, metrics = FALSE,
  explanatory_name = "explanatory", estimate_name = "HR",
  estimate_suffix = "", p_name = "p", digits = c(2, 2, 3),
  confint_sep = "-", ...)
```

```
## S3 method for class 'stanfit'
fit2df(.data, condense = TRUE, metrics = FALSE,
  remove_intercept = TRUE, explanatory_name = "explanatory",
  estimate_name = "OR", estimate_suffix = "", p_name = "p",
  digits = c(2, 2, 3), confint_sep = "-", ...)
```

```
## S3 method for class 'mipo'
fit2df(.data, condense = TRUE, metrics = FALSE,
```



```
remove_intercept = TRUE, explanatory_name = "explanatory",
estimate_name = "Coefficient", estimate_suffix = "", p_name = "p",
digits = c(2, 2, 3), exp = FALSE, confint_level = 0.95,
confint_sep = "-", ...)
```

## Arguments

...	Other arguments: X: Design matrix from stanfit modelling. Details documented else where.
.data	Output from finalfit model wrappers.
condense	Logical: when true, effect estimates, confidence intervals and p-values are pasted conveniently together in single cell.
metrics	Logical: when true, useful model metrics are extracted.
remove_intercept	Logical: remove the results for the intercept term.
explanatory_name	Name for this column in output
estimate_name	Name for this column in output
estimate_suffix	Appended to estimate name
p_name	Name given to p-value estimate
digits	Number of digits to round to (1) estimate, (2) confidence interval limits, (3) p-value.
confint_level	The confidence level required.
confint_sep	String to separate confidence intervals, typically "-" or " to ".
exp	Currently GLM only. Exponentiate coefficients and confidence intervals. Defaults to TRUE.
confint_type	One of c("profile", "default") for GLM models ( <a href="#">confint.glm</a> ) or c("profile", "Wald", "boot") for glmer/lmer models ( <a href="#">confint.merMod</a> ). Not implemented for lm, coxph or coxphlist.

## Details

fit2df is a generic (S3) function for model extract.

## Value

A dataframe of model parameters. When metrics=TRUE output is a list of two dataframes, one is model parameters, one is model metrics. length two

## Examples

```
library(finalfit)
library(dplyr)
library(survival)
# glm
```

```

fit = glm(mort_5yr ~ age.factor + sex.factor + obstruct.factor + perfor.factor,
  data=colon_s, family="binomial")
fit %>%
  fit2df(estimate_suffix=" (multivariable)")

# glmlist
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
colon_s %>%
  glmulti(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (univariable)")

# glmerMod
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
random_effect = "hospital"
dependent = "mort_5yr"
colon_s %>%
  glmmixed(dependent, explanatory, random_effect) %>%
  fit2df(estimate_suffix=" (multilevel)")

# glmboot
## Note number of draws set to 100 just for speed in this example
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
colon_s %>%
  glmulti_boot(dependent, explanatory, R = 100) %>%
  fit2df(estimate_suffix=" (multivariable (BS CIs))")

# lm
fit = lm(nodes ~ age.factor + sex.factor + obstruct.factor + perfor.factor,
  data=colon_s)
fit %>%
  fit2df(estimate_suffix=" (multivariable)")

# lmerMod
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
random_effect = "hospital"
dependent = "nodes"

colon_s %>%
  lmmixed(dependent, explanatory, random_effect) %>%
  fit2df(estimate_suffix=" (multilevel)")

# coxphlist
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "Surv(time, status)"

colon_s %>%
  coxphuni(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (univariable)")

colon_s %>%
  coxphmulti(dependent, explanatory) %>%

```

```

fit2df(estimate_suffix=" (multivariable)")

# coxph
fit = coxph(Surv(time, status) ~ age.factor + sex.factor + obstruct.factor + perfor.factor,
  data = colon_s)

fit %>%
  fit2df(estimate_suffix=" (multivariable)")

# crr: competing risks
melanoma = boot::melanoma
melanoma = melanoma %>%
  mutate(
    status_crr = ifelse(status == 2, 0, # "still alive"
      ifelse(status == 1, 1, # "died of melanoma"
        2)), # "died of other causes"
    sex = factor(sex),
    ulcer = factor(ulcer)
  )

dependent = c("Surv(time, status_crr)")
explanatory = c("sex", "age", "ulcer")
melanoma %>%
  summary_factorlist(dependent, explanatory, column = TRUE, fit_id = TRUE) %>%
  ff_merge(
    melanoma %>%
      crrmulti(dependent, explanatory) %>%
      fit2df(estimate_suffix = " (competing risks)")
  ) %>%
  select(-fit_id, -index) %>%
  dependent_label(melanoma, dependent)

```

---

format_n_percent	<i>Format n and percent as a character</i>
------------------	--

---

## Description

Internal, function, not called directly

## Usage

```
format_n_percent(n, percent, digits)
```

## Arguments

n	Value
percent	Value
digits	Value

---

glmmixed	<i>Mixed effects binomial logistic regression models: finalfit model wrapper</i>
----------	--

---

## Description

Using `finalfit` conventions, produces mixed effects binomial logistic regression models for a set of explanatory variables against a binary dependent.

## Usage

```
glmmixed(.data, dependent, explanatory, random_effect, ...)
```

## Arguments

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1, name of dependent variable (must have 2 levels).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>random_effect</code>	Character vector of length 1, either, (1) name of random intercept variable, e.g. "var1", (automatically converted to "(1   var1)"); or, (2) the full lme4 specification, e.g. "(var1   var2)". Note parenthesis MUST be included in (2) but NOT included in (1).
<code>...</code>	Other arguments to pass to <code>lme4::glmer</code> .

## Details

Uses `lme4::glmer` with `finalfit` modelling conventions. Output can be passed to `fit2df`. This is only currently set-up to take a single random effect as a random intercept. Can be updated in future to allow multiple random intercepts, random gradients and interactions on random effects if there is a need

## Value

A list of multivariable `lme4::glmer` fitted model outputs. Output is of class `glmerMod`.

## See Also

`fit2df`, `finalfit_merge`

Other `finalfit` model wrappers: `coxphmulti`, `coxphuni`, `crrmulti`, `crruni`, `glmmulti_boot`, `glmmulti`, `glmuni`, `lmmixed`, `lmmulti`, `lmuni`, `svyglmmulti`, `svyglmuni`

**Examples**

```
library(finalfit)
library(dplyr)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
random_effect = "hospital"
dependent = "mort_5yr"

colon_s %>%
  glmmixed(dependent, explanatory, random_effect) %>%
  fit2df(estimate_suffix=" (multilevel)")
```

---

glmmulti	<i>Binomial logistic regression multivariable models: finalfit model wrapper</i>
----------	--

---

**Description**

Using `finalfit` conventions, produces a multivariable binomial logistic regression model for a set of explanatory variables against a binary dependent.

**Usage**

```
glmmulti(.data, dependent, explanatory, family = "binomial", ...)
```

**Arguments**

<code>.data</code>	Data frame.
<code>dependent</code>	Character vector of length 1: name of dependent variable (must have 2 levels).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>family</code>	Character vector quoted or unquoted of the error distribution and link function to be used in the model, see <a href="#">glm</a> .
<code>...</code>	Other arguments to pass to <a href="#">glm</a> .

**Details**

Uses [glm](#) with `finalfit` modelling conventions. Output can be passed to [fit2df](#).

**Value**

A multivariable [glm](#) fitted model.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other `finalfit` model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```
library(finalfit)
library(dplyr)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"

colon_s %>%
  glmmulti(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (univariable)")
```

---

glmmulti_boot	<i>Binomial logistic regression multivariable models with bootstrapped confidence intervals: finalfit model wrapper</i>
---------------	---

---

**Description**

Using finalfit conventions, produces a multivariable binomial logistic regression models for a set of explanatory variables against a binary dependent.

**Usage**

```
glmmulti_boot(.data, dependent, explanatory, R = 1000)
```

**Arguments**

.data	Dataframe.
dependent	Character vector length 1: name of dependent variable (must have 2 levels).
explanatory	Character vector of any length: name(s) of explanatory variables.
R	Number of draws.

**Details**

Uses `glm` with finalfit modelling conventions. `boot::boot` is used to draw bootstrapped confidence intervals on fixed effect model coefficients. Output can be passed to `fit2df`.

**Value**

A multivariable `glm` fitted model with bootstrapped confidence intervals. Output is of class `glmboot`.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other finalfit model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

## Examples

```
library(finalfit)
library(dplyr)
## Note number of draws set to 100 just for speed in this example
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"

colon_s %>%
  glmmulti_boot(dependent, explanatory, R=100) %>%
  fit2df(estimate_suffix="(multivariable (BS CIs))")
```

---

glmuni	<i>Binomial logistic regression univariable models: finalfit model wrapper</i>
--------	--

---

## Description

Using `finalfit` conventions, produces multiple univariable binomial logistic regression models for a set of explanatory variables against a binary dependent.

## Usage

```
glmuni(.data, dependent, explanatory, family = "binomial", ...)
```

## Arguments

<code>.data</code>	Data frame.
<code>dependent</code>	Character vector of length 1: name of dependent variable (must have 2 levels).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>family</code>	Character vector quoted or unquoted of the error distribution and link function to be used in the model, see <code>glm</code> .
<code>...</code>	Other arguments to pass to <code>glm</code> .

## Details

Uses `glm` with `finalfit` modelling conventions. Output can be passed to `fit2df`.

## Value

A list of univariable `glm` fitted model outputs. Output is of class `glm` list.

## See Also

[fit2df](#), [finalfit\\_merge](#)

Other `finalfit` model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```

library(finalfit)
library(dplyr)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"

colon_s %>%
  glmuni(dependent, explanatory) %>%
  fit2df(estimate_suffix=" (univariable)")

```

---

**hr\_plot***Produce a hazard ratio table and plot*

---

**Description**

Produce hazard ratio table and plot from a Cox Proportional Hazards analysis, `survival::coxph()`.

**Usage**

```

hr_plot(.data, dependent, explanatory, factorlist = NULL,
  coxfit = NULL, remove_ref = FALSE, breaks = NULL,
  column_space = c(-0.5, 0, 0.5), dependent_label = "Survival",
  prefix = "", suffix = ": HR (95% CI, p-value)",
  table_text_size = 5, title_text_size = 18, plot_opts = NULL,
  table_opts = NULL, ...)

```

**Arguments**

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1: name of survival object in form <code>Surv(time, status)</code> .
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>factorlist</code>	Option to provide output directly from <code>summary_factorlist()</code> .
<code>coxfit</code>	Option to provide output directly from <code>coxphmulti()</code> .
<code>remove_ref</code>	Logical. Remove reference level for factors.
<code>breaks</code>	Manually specify x-axis breaks in format <code>c(0.1, 1, 10)</code> .
<code>column_space</code>	Adjust table column spacing.
<code>dependent_label</code>	Main label for plot.
<code>prefix</code>	Plots are titled by default with the dependent variable. This adds text before that label.
<code>suffix</code>	Plots are titled with the dependent variable. This adds text after that label.
<code>table_text_size</code>	Alter font size of table text.



```

title_text_size      Alter font size of title text.
plot_opts            A list of arguments to be appended to the ggplot call by "+".
table_opts           A list of arguments to be appended to the ggplot table call by "+".
...                 Other parameters passed to fit2df().

```

**Value**

Returns a table and plot produced in ggplot2.

**See Also**

Other finalfit plot functions: [coefficient\\_plot](#), [ff\\_plot](#), [or\\_plot](#), [surv\\_plot](#)

**Examples**

```

# HR plot
library(finalfit)
library(dplyr)
library(ggplot2)

data(colon_s)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "Surv(time, status)"
colon_s %>%
  hr_plot(dependent, explanatory, dependent_label = "Survival")

colon_s %>%
  hr_plot(dependent, explanatory, dependent_label = "Survival",
          table_text_size=4, title_text_size=14,
          plot_opts=list(xlab("HR, 95% CI"), theme(axis.title = element_text(size=12))))

```

---

labels_to_column	<i>Labels to column names</i>
------------------	-------------------------------

---

**Description**

Labels to column names

**Usage**

```
labels_to_column(.data)
```

**Arguments**

.data            Data frame or tibble.

**Value**

Data frame or tibble

**Examples**

```
library(dplyr)
colon_s %>%
  select(sex.factor) %>%
  labels_to_column()
```

---

labels_to_level	<i>Labels to level</i>
-----------------	------------------------

---

**Description**

For use with `forcats::fct_relabel`.

**Usage**

```
labels_to_level(.data, .labels)
```

**Arguments**

`.data` Data frame or tibble.  
`.labels` Output from `extract_variable_label`.

**Value**

Data frame or tibble

**Examples**

```
library(dplyr)
vlabels = extract_variable_label(colon_s)
colon_s %>%
  select(sex.factor, obstruct.factor) %>%
  tidyr::gather() %>%
  mutate(
    key = forcats::fct_relabel(key, labels_to_level, vlabels)
  )
```

---

lmmixed

*Mixed effects linear regression models: finalfit model wrapper*


---

## Description

Using `finalfit` conventions, produces mixed effects linear regression models for a set of explanatory variables against a continuous dependent.

## Usage

```
lmmixed(.data, dependent, explanatory, random_effect, ...)
```

## Arguments

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1, name of dependent variable (must be continuous vector).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>random_effect</code>	Character vector of length 1, either, (1) name of random intercept variable, e.g. "var1", (automatically converted to "(1   var1)"); or, (2) the full lme4 specification, e.g. "(var1   var2)". Note parenthesis MUST be included in (2) but NOT included in (1).
<code>...</code>	Other arguments to pass to <code>lme4::lmer</code> .

## Details

Uses `lme4::lmer` with `finalfit` modelling conventions. Output can be passed to `fit2df`. This is only currently set-up to take a single random effect as a random intercept. Can be updated in future to allow multiple random intercepts, random gradients and interactions on random effects if there is a need.

## Value

A list of multivariable `lme4::lmer` fitted model outputs. Output is of class `lmerMod`.

## See Also

[fit2df](#)

Other `finalfit` model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```
library(finalfit)
library(dplyr)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
random_effect = "hospital"
dependent = "nodes"

colon_s %>%
  lmmixed(dependent, explanatory, random_effect) %>%
  fit2df(estimate_suffix=" (multilevel)")
```

---

lmmulti

---

*Linear regression multivariable models: finalfit model wrapper*


---

**Description**

Using `finalfit` conventions, produces a multivariable linear regression model for a set of explanatory variables against a continuous dependent.

**Usage**

```
lmmulti(.data, dependent, explanatory, ...)
```

**Arguments**

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1: name of dependent variable (must a continuous vector).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>...</code>	Other arguments to pass to <code>lm</code> .

**Details**

Uses `lm` with `finalfit` modelling conventions. Output can be passed to `fit2df`.

**Value**

A multivariable `lm` fitted model.

**See Also**

[fit2df](#)

Other `finalfit` model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmuni](#), [svyglmmulti](#), [svyglmuni](#)

**Examples**

```
library(finalfit)
library(dplyr)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "nodes"

colon_s %>%
  lmmulti(dependent, explanatory) %>%
  fit2df()
```

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 Imuni

---

*Linear regression univariable models: finalfit model wrapper*


---

**Description**

Using `finalfit` conventions, produces multiple univariable linear regression models for a set of explanatory variables against a continuous dependent.

**Usage**

```
lmuni(.data, dependent, explanatory, ...)
```

**Arguments**

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1, name of dependent variable (must be continuous vector).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>...</code>	Other arguments to pass to <code>lm</code> .

**Details**

Uses `lm` with `finalfit` modelling conventions. Output can be passed to `fit2df`.

**Value**

A list of multivariable `lm` fitted model outputs. Output is of class `lm` list.

**See Also**

[fit2df](#)

Other `finalfit` model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glm](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [svyglm](#), [svyglmuni](#)

**Examples**

```
library(finalfit)
library(dplyr)

explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "nodes"

colon_s %>%
  lmuni(dependent, explanatory) %>%
  fit2df()
```

---

metrics_hoslem	<i>Hosmer-Lemeshow goodness of fit test</i>
----------------	---

---

**Description**

Internal, not usually called directly

**Usage**

```
metrics_hoslem(y, yhat, g = 10, digits = c(2, 3))
```

**Arguments**

y	Observed y, usually of the form <code>fit\$y</code> .
yhat	Predicted <code>y_hat</code> , usually for the form <code>fit\$fitted</code>
g	Number of bins to calculate quantiles.
digits	Number of decimal places of form <code>c(2, 3)</code> , where <code>digits[1]</code> is for chi-sq estimate and <code>digits[2]</code> is for p-value.

**Value**

Character string of chi-sq result, df, and p-value. Significant p-value suggests poor fit.

**Author(s)**

Adapted from Peter Solymos.

**Source**

<https://github.com/psolymos/ResourceSelection/blob/master/R/hoslem.test.R>

**Examples**

```
fit = glm(mort_5yr~age.factor+extent.factor, data=colon_s, family="binomial")
metrics_hoslem(fit$y, fit$fitted)
```

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missing_compare	<i>Compare missing data</i>
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---

## Description

Compare missing data

## Usage

```
missing_compare(.data, dependent, explanatory, na_include = FALSE, ...)
```

## Arguments

.data	Dataframe.
dependent	Variable to test missingness against other variables with.
explanatory	Variables to have missingness tested against.
na_include	Include missing data in explanatory variables as a factor level.
...	Other arguments to <a href="#">summary_factorlist()</a> .

## Value

A dataframe comparing missing data in the dependent variable across explanatory variables. Continuous data are compared with a Kruskal Wallis test. Discrete data are compared with a chi-squared test.

## Examples

```
library(finalfit)

explanatory = c("age", "age.factor", "extent.factor", "perfor.factor")
dependent = "mort_5yr"

colon_s %>%
  ff_glimpse(dependent, explanatory)

colon_s %>%
  missing_pattern(dependent, explanatory)

colon_s %>%
  missing_compare(dependent, explanatory)
```

---

missing_glimpse	<i>Summary of missing values</i>
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---

**Description**

Summary of missing values

**Usage**

```
missing_glimpse(.data, dependent = NULL, explanatory = NULL,
  digits = 1)
```

**Arguments**

.data	Data frame.
dependent	Optional character vector: name(s) of dependent variable(s).
explanatory	Optional character vector: name(s) of explanatory variable(s).
digits	Number of decimal places to show for percentage missing.

**Value**

Data frame.

**Examples**

```
colon_s %>%
  missing_glimpse()
```

---

missing_pairs	<i>Missing values pairs plot</i>
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---

**Description**

Compare the occurrence of missing values in all variables by each other. Suggest limit the number of variables to a maximum of around six. Dependent and explanatory are for convenience of variable selection, are optional, and have no other specific function.

**Usage**

```
missing_pairs(.data, dependent = NULL, explanatory = NULL,
  use_labels = TRUE, title = NULL, position = "stack",
  showXAxisPlotLabels = TRUE, showYAxisPlotLabels = FALSE)
```



**Arguments**

.data	Data frame.
dependent	Character vector. Optional name of dependent variable.
explanatory	Character vector. Optional name(s) of explanatory variables.
use_labels	Use variable label names in plot labelling.
title	Character vector. Optional title for plot.
position	For discrete variables, choose "stack" or "fill" to show counts or proportions.
showXAxisPlotLabels	Show x-axis plot labels.
showYAxisPlotLabels	Show y-axis plot labels.

**Value**

A plot matrix comparing missing values in all variables against each other.

**Examples**

```
## Not run:
explanatory = c("age", "nodes", "age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = 'mort_5yr'
colon_s %>%
  missing_pairs(dependent, explanatory)

## End(Not run)
```

---

missing_pattern	<i>Characterise missing data for finalfit models</i>
-----------------	--

---

**Description**

Using finalfit conventions, produces a missing data matrix using [md.pattern](#).

**Usage**

```
missing_pattern(.data, dependent = NULL, explanatory = NULL,
  rotate.names = TRUE, ...)
```

**Arguments**

.data	Data frame. Missing values must be coded NA.
dependent	Character vector usually of length 1, name of dependent variable.
explanatory	Character vector of any length: name(s) of explanatory variables.
rotate.names	Logical. Should the orientation of variable names on plot should be vertical.
...	pass other arguments such as plot = TRUE to <a href="#">md.pattern</a> .

**Value**

A matrix with  $\text{ncol}(x)+1$  columns, in which each row corresponds to a missing data pattern (1=observed, 0=missing). Rows and columns are sorted in increasing amounts of missing information. The last column and row contain row and column counts, respectively.

**Examples**

```
library(finalfit)
library(dplyr)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"

colon_s %>%
  missing_pattern(dependent, explanatory)
```

---

missing_plot	<i>Missing values occurrence plot</i>
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**Description**

Create a plot of missing values by observations on the x-axis and variable on the y-axis. Dependent and explanatory are for convenience and are optional.

**Usage**

```
missing_plot(.data, dependent = NULL, explanatory = NULL,
  use_labels = TRUE, title = NULL, plot_opts = NULL)
```

**Arguments**

.data	Data frame.
dependent	Character vector. Optional name of dependent variable.
explanatory	Character vector. Optional name(s) of explanatory variables.
use_labels	Use variable label names in plot labelling.
title	Character vector. Optional title for plot.
plot_opts	A list of arguments to be appended to the ggplot call by "+".

**Value**

Heat map of missing values in dataset.

**Examples**

```
colon_s %>%
  missing_plot()
```

---

`missing_predictorMatrix`*Create predictorMatrix for use with mice*

---

**Description**

Create predictorMatrix for use with mice

**Usage**

```
missing_predictorMatrix(.data, drop_from_imputed = NULL,  
  drop_from_imputer = NULL)
```

**Arguments**

<code>.data</code>	Data frame.
<code>drop_from_imputed</code>	Quoted names of variables not to impute.
<code>drop_from_imputer</code>	Quoted names of variables not to use in imputation algorithm.

**Value**

Matrix formatted for predictorMatrix argument in mice.

**Examples**

```
library(mice)  
library(dplyr)  
  
# Create some extra missing data  
## Smoking missing completely at random  
set.seed(1)  
colon_s$smoking_mcar =  
  sample(c("Smoker", "Non-smoker", NA),  
    dim(colon_s)[1], replace=TRUE,  
    prob = c(0.2, 0.7, 0.1)) %>%  
  factor() %>%  
  ff_label("Smoking (MCAR)")  
  
## Make smoking missing conditional on patient sex  
colon_s$smoking_mar[colon_s$sex.factor == "Female"] =  
  sample(c("Smoker", "Non-smoker", NA),  
    sum(colon_s$sex.factor == "Female"),  
    replace = TRUE, prob = c(0.1, 0.5, 0.4))  
  
colon_s$smoking_mar[colon_s$sex.factor == "Male"] =  
  sample(c("Smoker", "Non-smoker", NA),  
    sum(colon_s$sex.factor == "Male"),
```

```

replace=TRUE, prob = c(0.15, 0.75, 0.1))
colon_s$smoking_mar = factor(colon_s$smoking_mar)%>%
  ff_label("Smoking (MAR)")

explanatory = c("age", "sex.factor",
  "nodes", "obstruct.factor", "smoking_mar")
dependent = "mort_5yr"

colon_s %>%
  select(dependent, explanatory) %>%
  missing_predictorMatrix(drop_from_imputed =
    c("obstruct.factor", "mort_5yr")) -> predM

colon_s %>%
  select(dependent, explanatory) %>%
  mice(m = 2, predictorMatrix = predM) %>% # e.g. m=10 when for real
  # Run logistic regression on each imputed set
  with(glm(formula(ff_formula(dependent, explanatory)),
    family="binomial")) %>%
  pool() %>%
  summary(conf.int = TRUE, exponentiate = TRUE) %>%
  # Jiggle into finalfit format
  mutate(explanatory_name = rownames(.)) %>%
  select(explanatory_name, estimate, `2.5 %`, `97.5 %`, p.value) %>%
  condense_fit(estimate_suffix = " (multiple imputation)") %>%
  remove_intercept() -> fit_imputed

```

---

or\_plot

---

*Produce an odds ratio table and plot*


---

## Description

Produce an odds ratio table and plot from a `glm()` or `lme4::glmer()` model.

## Usage

```

or_plot(.data, dependent, explanatory, random_effect = NULL,
  factorlist = NULL, glmfit = NULL, confint_type = NULL,
  remove_ref = FALSE, breaks = NULL, column_space = c(-0.5, 0, 0.5),
  dependent_label = NULL, prefix = "",
  suffix = ": OR (95% CI, p-value)", table_text_size = 5,
  title_text_size = 18, plot_opts = NULL, table_opts = NULL, ...)

```

## Arguments

<code>.data</code>	Data frame.
<code>dependent</code>	Character vector of length 1: name of dependent variable (must have 2 levels).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.

random_effect	Character vector of length 1, name of random effect variable.
factorlist	Option to provide output directly from <code>summary_factorlist()</code> .
glmfit	Option to provide output directly from <code>glmmulti()</code> and <code>glmmixed()</code> .
confint_type	One of <code>c("profile", "default")</code> for GLM models or <code>c("default", "Wald", "profile", "boot")</code> for glmer models. Note "default" == "Wald".
remove_ref	Logical. Remove reference level for factors.
breaks	Manually specify x-axis breaks in format <code>c(0.1, 1, 10)</code> .
column_space	Adjust table column spacing.
dependent_label	Main label for plot.
prefix	Plots are titled by default with the dependent variable. This adds text before that label.
suffix	Plots are titled with the dependent variable. This adds text after that label.
table_text_size	Alter font size of table text.
title_text_size	Alter font size of title text.
plot_opts	A list of arguments to be appended to the <code>ggplot</code> call by "+".
table_opts	A list of arguments to be appended to the <code>ggplot</code> table call by "+".
...	Other parameters.

**Value**

Returns a table and plot produced in `ggplot2`.

**See Also**

Other finalfit plot functions: [coefficient\\_plot](#), [ff\\_plot](#), [hr\\_plot](#), [surv\\_plot](#)

**Examples**

```
library(finalfit)
library(dplyr)
library(ggplot2)

# OR plot
data(colon_s)
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
colon_s %>%
  or_plot(dependent, explanatory)

colon_s %>%
  or_plot(dependent, explanatory, table_text_size=4, title_text_size=14,
    plot_opts=list(xlab("OR, 95% CI"), theme(axis.title = element_text(size=12))))
```

---

p\_tidy *Round p-values but keep trailing zeros*

---

### Description

Internal function, not called directly

### Usage

```
p_tidy(x, digits, prefix = "=")
```

### Arguments

x                    Numeric vector of values to round  
 digits              Integer of length one: value to round to.  
 prefix              Appended in front of values for use with condense\_fit.

### Details

e.g. for 3 decimal places I want 0.100, not 0.1. Note this function with convert 0.000 to <0.001. All other values are prefixed with "=" by default

### Value

Vector of strings.

---

rm\_duplicates *Remove duplicates and replace*

---

### Description

Remove duplicates and replace

### Usage

```
rm_duplicates(.var, fromLast = FALSE, replacement = "")
```

### Arguments

.var                Vector.  
 fromLast           Logical. Consider duplication from last to first.  
 replacement        Character for what to replace duplicate with.

### Value

Character vector.

---

round_tidy	<i>Round values but keep trailing zeros</i>
------------	---

---

**Description**

e.g. for 3 decimal places I want 1.200, not 1.2.

**Usage**

```
round_tidy(x, digits)
```

**Arguments**

x	Numeric vector of values to round
digits	Integer of length one: value to round to.

**Value**

Vector of strings.

**Examples**

```
round_tidy(0.01023, 3)
```

---

summary_factorlist	<i>Summarise a set of factors (or continuous variables) by a dependent variable</i>
--------------------	---

---

**Description**

A function that takes a single dependent variable with a vector of explanatory variable names (continuous or categorical variables) to produce a summary table.

**Usage**

```
summary_factorlist(.data, dependent = NULL, explanatory, cont = "mean",
  cont_nonpara = NULL, cont_cut = 5, cont_range = FALSE, p = FALSE,
  p_cont_para = "aov", p_cat = "chisq", column = TRUE,
  total_col = FALSE, orderbytotal = FALSE, digits = c(1, 1, 3, 1),
  na_include = FALSE, na_include_dependent = FALSE,
  na_complete_cases = FALSE, na_to_p = FALSE, fit_id = FALSE,
  add_dependent_label = FALSE, dependent_label_prefix = "Dependent: ",
  dependent_label_suffix = "", add_col_totals = FALSE,
  include_col_totals_percent = TRUE, col_totals_rowname = NULL,
  col_totals_prefix = "", add_row_totals = FALSE,
  include_row_missing_col = TRUE, row_totals_colname = "Total N",
  row_missing_colname = "Missing N", catTest = NULL)
```

**Arguments**

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1: name of dependent variable (2 to 5 factor levels).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>cont</code>	Summary for continuous explanatory variables: "mean" (standard deviation) or "median" (interquartile range). If "median" then non-parametric hypothesis test performed (see below).
<code>cont_nonpara</code>	Numeric vector of form e.g. <code>c(1, 2)</code> . Specify which variables to perform non-parametric hypothesis tests on and summarise with "median".
<code>cont_cut</code>	Numeric: number of unique values in continuous variable at which to consider it a factor.
<code>cont_range</code>	Logical. Median is show with 1st and 3rd quartiles.
<code>p</code>	Logical: Include null hypothesis statistical test.
<code>p_cont_para</code>	Character. Continuous variable parametric test. One of either "aov" (analysis of variance) or "t.test" for Welch two sample t-test. Note continuous non-parametric test is always Kruskal Wallis ( <code>kruskal.test</code> ) which in two-group setting is equivalent to Mann-Whitney U /Wilcoxon rank sum test. For continous dependent and continuous explanatory, the parametric test p-value returned is for the Pearson correlation coefficient. The non-parametric equivalent is for the p-value for the Spearman correlation coefficient.
<code>p_cat</code>	Character. Categorical variable test. One of either "chisq" or "fisher".
<code>column</code>	Logical: Compute margins by column rather than row.
<code>total_col</code>	Logical: include a total column summing across factor levels.
<code>orderbytotal</code>	Logical: order final table by total column high to low.
<code>digits</code>	Number of digits to round to (1) mean/median, (2) standard deviation / interquartile range, (3) p-value, (4) count percentage.
<code>na_include</code>	Logical: make explanatory variables missing data explicit (NA).
<code>na_include_dependent</code>	Logical: make dependent variable missing data explicit.
<code>na_complete_cases</code>	Logical: include only rows with complete data.
<code>na_to_p</code>	Logical: include missing as group in statistical test.
<code>fit_id</code>	Logical: allows merging via <code>finalfit_merge</code> .
<code>add_dependent_label</code>	Add the name of the dependent label to the top left of table.
<code>dependent_label_prefix</code>	Add text before dependent label.
<code>dependent_label_suffix</code>	Add text after dependent label.
<code>add_col_totals</code>	Logical. Include column total n.
<code>include_col_totals_percent</code>	Include column percentage of total.



col_totals_rowname	Logical. Row name for column totals.
col_totals_prefix	Character. Prefix to column totals, e.g. "N=".
add_row_totals	Logical. Include row totals. Note this differs from total_col above particularly for continuous explanatory variables.
include_row_missing_col	Logical. Include missing data total for each row. Only used when add_row_totals is TRUE.
row_totals_colname	Character. Column name for row totals.
row_missing_colname	Character. Column name for missing data totals for each row.
catTest	Deprecated. See p_cat above.

## Details

This function aims to produce publication-ready summary tables for categorical or continuous dependent variables. It usually takes a categorical dependent variable to produce a cross table of counts and proportions expressed as percentages or summarised continuous explanatory variables. However, it will take a continuous dependent variable to produce mean (standard deviation) or median (interquartile range) for use with linear regression models.

## Value

Returns a factorlist dataframe.

## See Also

[fit2df](#) [ff\\_column\\_totals](#) [ff\\_row\\_totals](#) [ff\\_label](#) [ff\\_glimpse](#) [ff\\_percent\\_only](#)

## Examples

```
library(finalfit)
library(dplyr)
# Load example dataset, modified version of survival::colon
data(colon_s)

# Table 1 - Patient demographics ----
explanatory = c("age", "age.factor", "sex.factor", "obstruct.factor")
dependent = "perfor.factor"
colon_s %>%
  summary_factorlist(dependent, explanatory, p=TRUE)

# summary_factorlist() is also commonly used to summarise any number of
# variables by an outcome variable (say dead yes/no).

# Table 2 - 5 yr mortality ----
explanatory = c("age.factor", "sex.factor", "obstruct.factor", "perfor.factor")
dependent = "mort_5yr"
```

```
colon_s %>%
  summary_factorlist(dependent, explanatory)
```

---

surv_plot	<i>Plot survival curves with number-at-risk table</i>
-----------	---

---

## Description

Produce a survival curve plot and number-at-risk table using `survminer::ggsurvplot` and `finalfit` conventions.

## Usage

```
surv_plot(.data, dependent, explanatory, ...)
```

## Arguments

<code>.data</code>	Dataframe.
<code>dependent</code>	Character vector of length 1: Survival object of the form <code>Surv(time, status)</code> .
<code>explanatory</code>	Character vector of max length 2: quoted name(s) of explanatory variables.
<code>...</code>	Arguments passed to <code>ggsurvplot</code> .

## Value

Returns a table and plot produced in `ggplot2`.

## See Also

Other `finalfit` plot functions: [coefficient\\_plot](#), [ff\\_plot](#), [hr\\_plot](#), [or\\_plot](#)

## Examples

```
library(finalfit)
library(dplyr)

# Survival plot
data(colon_s)
explanatory = c("perfor.factor")
dependent = "Surv(time, status)"
colon_s %>%
  surv_plot(dependent, explanatory, xlab="Time (days)", pval=TRUE, legend="none")
```

---

`svyglmmulti`*Multivariable survey-weighted generalised linear models*

---

**Description**

Wrapper for `svyglm`. Fit a generalised linear model to data from a complex survey design, with inverse-probability weighting and design-based standard errors.

**Usage**

```
svyglmmulti(design, dependent, explanatory, ...)
```

**Arguments**

<code>design</code>	Survey design.
<code>dependent</code>	Character vector of length 1: name of dependent variable (must have 2 levels).
<code>explanatory</code>	Character vector of any length: name(s) of explanatory variables.
<code>...</code>	Other arguments to be passed to <code>svyglm</code> .

**Value**

A list of univariable fitted model outputs. Output is of class `svyglm`.

**See Also**

[fit2df](#), [finalfit\\_merge](#)

Other finalfit model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glm](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmuni](#)

**Examples**

```
# Examples taken from survey::svyglm() help page.

library(survey)
library(dplyr)

data(api)
dependent = "api00"
explanatory = c("ell", "meals", "mobility")

library(survey)
library(dplyr)

data(api)

apistrat = apistrat %>%
  mutate(
    api00 = ff_label(api00, "API in 2000 (api00)"),
```

```

ell = ff_label(ell, "English language learners (percent)(ell)",
meals = ff_label(meals, "Meals eligible (percent)(meals)",
mobility = ff_label(mobility, "First year at the school (percent)(mobility)",
sch.wide = ff_label(sch.wide, "School-wide target met (sch.wide)")
)

# Linear example
dependent = "api00"
explanatory = c("ell", "meals", "mobility")

# Stratified design
dstrat = svydesign(id=~1, strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)

# Univariable fit
fit_uni = dstrat %>%
  svyglmuni(dependent, explanatory) %>%
  fit2df(estimate_suffix = " (univariable)")

# Multivariable fit
fit_multi = dstrat %>%
  svyglmulti(dependent, explanatory) %>%
  fit2df(estimate_suffix = " (multivariable)")

# Pipe together
apistrat %>%
  summary_factorlist(dependent, explanatory, fit_id = TRUE) %>%
  ff_merge(fit_uni) %>%
  ff_merge(fit_multi) %>%
  select(-fit_id, -index) %>%
  dependent_label(apistrat, dependent)

# Binomial example
## Note model family needs specified and exponentiation if desired

dependent = "sch.wide"
explanatory = c("ell", "meals", "mobility")

# Univariable fit
fit_uni = dstrat %>%
  svyglmuni(dependent, explanatory, family = "quasibinomial") %>%
  fit2df(exp = TRUE, estimate_name = "OR", estimate_suffix = " (univariable)")

# Multivariable fit
fit_multi = dstrat %>%
  svyglmulti(dependent, explanatory, family = "quasibinomial") %>%
  fit2df(exp = TRUE, estimate_name = "OR", estimate_suffix = " (multivariable)")

# Pipe together
apistrat %>%
  summary_factorlist(dependent, explanatory, fit_id = TRUE) %>%
  ff_merge(fit_uni) %>%
  ff_merge(fit_multi) %>%
  select(-fit_id, -index) %>%

```

```
dependent_label(apistrat, dependent)
```

---

 svyglmuni

*Univariable survey-weighted generalised linear models*


---

## Description

Wrapper for [svyglm](#). Fit a generalised linear model to data from a complex survey design, with inverse-probability weighting and design-based standard errors.

## Usage

```
svyglmuni(design, dependent, explanatory, ...)
```

## Arguments

design	Survey design.
dependent	Character vector of length 1: name of dependent variable (must have 2 levels).
explanatory	Character vector of any length: name(s) of explanatory variables.
...	Other arguments to be passed to <a href="#">svyglm</a> .

## Value

A list of univariable fitted model outputs. Output is of class `svyglm1list`.

## See Also

[fit2df](#), [finalfit\\_merge](#)

Other finalfit model wrappers: [coxphmulti](#), [coxphuni](#), [crrmulti](#), [crruni](#), [glmmixed](#), [glmmulti\\_boot](#), [glmmulti](#), [glmuni](#), [lmmixed](#), [lmmulti](#), [lmuni](#), [svyglmmulti](#)

## Examples

```
# Examples taken from survey::svyglm() help page.
```

```
library(survey)
library(dplyr)
```

```
data(api)
dependent = "api00"
explanatory = c("ell", "meals", "mobility")
```

```
library(survey)
library(dplyr)
```

```
data(api)
```

```
apistrat = apistrat %>%
```

```

mutate(
  api00 = ff_label(api00, "API in 2000 (api00)"),
  ell = ff_label(ell, "English language learners (percent)(ell)"),
  meals = ff_label(meals, "Meals eligible (percent)(meals)"),
  mobility = ff_label(mobility, "First year at the school (percent)(mobility)"),
  sch.wide = ff_label(sch.wide, "School-wide target met (sch.wide)")
)

# Linear example
dependent = "api00"
explanatory = c("ell", "meals", "mobility")

# Stratified design
dstrat = svydesign(id=~1, strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)

# Univariable fit
fit_uni = dstrat %>%
  svyglmuni(dependent, explanatory) %>%
  fit2df(estimate_suffix = " (univariable)")

# Multivariable fit
fit_multi = dstrat %>%
  svyglmulti(dependent, explanatory) %>%
  fit2df(estimate_suffix = " (multivariable)")

# Pipe together
apistrat %>%
  summary_factorlist(dependent, explanatory, fit_id = TRUE) %>%
  ff_merge(fit_uni) %>%
  ff_merge(fit_multi) %>%
  select(-fit_id, -index) %>%
  dependent_label(apistrat, dependent)

# Binomial example
## Note model family needs specified and exponentiation if desired

dependent = "sch.wide"
explanatory = c("ell", "meals", "mobility")

# Univariable fit
fit_uni = dstrat %>%
  svyglmuni(dependent, explanatory, family = "quasibinomial") %>%
  fit2df(exp = TRUE, estimate_name = "OR", estimate_suffix = " (univariable)")

# Multivariable fit
fit_multi = dstrat %>%
  svyglmulti(dependent, explanatory, family = "quasibinomial") %>%
  fit2df(exp = TRUE, estimate_name = "OR", estimate_suffix = " (multivariable)")

# Pipe together
apistrat %>%
  summary_factorlist(dependent, explanatory, fit_id = TRUE) %>%
  ff_merge(fit_uni) %>%

```

```
ff_merge(fit_multi) %>%
select(-fit_id, -index) %>%
dependent_label(apistrat, dependent)
```

---

wcfgs

*Western Collaborative Group Study*


---

## Description

3154 healthy young men aged 39-59 from the San Francisco area were assessed for their personality type. All were free from coronary heart disease at the start of the research. Eight and a half years later change in this situation was recorded.

## Usage

```
data(wcfgs)
```

## Format

A data frame with 3154 observations on the following 13 variables.

- id Subject ID
- age Age: age in years
- height Height: height in inches
- weight Weight: weight in pounds
- sbp Systolic blood pressure: mmHg
- dbp Diastolic blood pressure: mmHg
- chol Cholesterol: mg/100 ml
- personality Personality type/Behavior pattern: a factor with levels A1, A2, B3, B4
- personality\_2L Dichotomous personality type / behavior pattern: A = aggressive; B = passive
- ncigs0 Smoking: Cigarettes/day
- smoking Smoking: No, Yes
- arcus0 Corneal arcus: No, Yes
- chd Coronary heart disease event: No Yes
- typechd coronary heart disease is a factor with levels No, MI\_SD (MI or sudden death), Silent\_MI, Angina
- timechd Observation (follow up) time: Days

**Details**

The WCGS began in 1960 with 3,524 male volunteers who were employed by 11 California companies. Subjects were 39 to 59 years old and free of heart disease as determined by electrocardiogram. After the initial screening, the study population dropped to 3,154 and the number of companies to 10 because of various exclusions. The cohort comprised both blue- and white-collar employees. At baseline the following information was collected: socio-demographic including age, education, marital status, income, occupation; physical and physiological including height, weight, blood pressure, electrocardiogram, and corneal arcus; biochemical including cholesterol and lipoprotein fractions; medical and family history and use of medications; behavioral data including Type A interview, smoking, exercise, and alcohol use. Later surveys added data on anthropometry, triglycerides, Jenkins Activity Survey, and caffeine use. Average follow-up continued for 8.5 years with repeat examinations

**Source**

Statistics for Epidemiology by N. Jewell (2004)

**References**

Coronary Heart Disease in the Western Collaborative Group Study Final Follow-up Experience of 8 1/2 Years Ray H. Rosenman, MD; Richard J. Brand, PhD; C. David Jenkins, PhD; Meyer Friedman, MD; Reuben Straus, MD; Moses Wurm, MD JAMA. 1975;233(8):872-877. doi:10.1001/jama.1975.03260080034016.



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