

# Package: multitool (via r-universe)

October 25, 2024

**Title** Run Multiverse Style Analyses

**Version** 0.1.4.9000

**Description** Run the same analysis over a range of arbitrary data processing decisions. 'multitool' provides an interface for creating alternative analysis pipelines and turning them into a grid of all possible pipelines. Using this grid as a blueprint, you can model your data across all possible pipelines and summarize the results.

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**Imports** clipr, correlation, DiagrammeR, dplyr, flextable, ggdist, glue, ggplot2, moments, purrr, rlang, stringr, tibble, tidyr, lme4, parameters, performance, rstudioapi

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**Depends** R (>= 4.1.0)

**LazyData** true

**Repository** <https://ethan-young.r-universe.dev>

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---

add_correlations	<i>Add correlations from the correlation package in easystats</i>
------------------	---

---

## Description

Add correlations from the correlation package in easystats

**Usage**

```
add_correlations(
  .df,
  var_set,
  variables,
  focus_set = NULL,
  method = "auto",
  redundant = TRUE,
  add_matrix = TRUE
)
```

**Arguments**

<code>.df</code>	the original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
<code>var_set</code>	character string. Should be a descriptive name of the correlation matrix.
<code>variables</code>	the variables for which you would like to correlations. These variables will be passed to <code>link[correlation]{correlation}</code> . You can also use <code>tidyselect</code> to select variables.
<code>focus_set</code>	variables to focus one in a table. This produces a table where rows are each focused variables and columns are all other variables
<code>method</code>	a valid method of correlation supplied to <code>link[correlation]{correlation}</code> (e.g., 'pearson' or 'kendall'). Defaults to 'auto'. See <code>link[correlation]{correlation}</code> for more details.
<code>redundant</code>	logical, should the result include repeated correlations? Defaults to TRUE See <code>link[correlation]{correlation}</code> for details.
<code>add_matrix</code>	logical, add a traditional correlation matrix to the output. Defaults to TRUE.

**Value**

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

**Examples**

```
library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
```

```

cov1 = rnorm(500),
cov2 = rnorm(500),
dv1 = rnorm(500),
dv2 = rnorm(500),
include1 = rbinom(500, size = 1, prob = .1),
include2 = sample(1:3, size = 500, replace = TRUE),
include3 = rnorm(500)
)

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_correlations("predictors", matches("iv|mod|cov"), focus_set = c(cov1, cov2))

```

---

add\_filters

*Add filtering/exclusion criteria to a multiverse pipeline*


---

## Description

Add filtering/exclusion criteria to a multiverse pipeline

## Usage

```
add_filters(.df, ...)
```

## Arguments

.df	The original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
...	logical expressions to be used with <code>filter</code> separated by commas. Expressions should not be quoted.

## Value

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

## Examples

```

library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,

```

```

    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5)

```

---

add\_model

*Add a model and formula to a multiverse pipeline*


---

## Description

Add a model and formula to a multiverse pipeline

## Usage

```
add_model(.df, model_desc, code, additional_args = NULL)
```

## Arguments

.df	The original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
model_desc	a human readable name you would like to give the model.
code	literal model syntax you would like to run. You can use glue inside formulas to dynamically generate variable names based on a variable grid. For example, if you make variable grid with two versions of your IVs (e.g., iv1 and iv2), you can write your formula like so: <code>lm(happiness ~ {iv} + control_var)</code> . The only requirement is that the variables written in the formula actually exist in the underlying data. You are also responsible for loading any packages that run a particular model (e.g., lme4 for mixed-models)
additional_args	a list of any additional arguments supplied to parameters::parameters().

## Value

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

**Examples**

```

library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_preprocess("scale_iv", 'mutate({ivs} = scale({ivs}))') |>
  add_model("linear model", lm({dvs} ~ {ivs} * {mods}))

```

---

add\_parameter\_keys      *Add parameter keys names for later use in summarizing model effects*

---

**Description**

Add parameter keys names for later use in summarizing model effects

**Usage**

```
add_parameter_keys(.df, parameter_group, parameter_name)
```

**Arguments**

`.df`                    The original data.frame(e.g., base data set). If part of set of add\_\* decision functions in a pipeline, the base data will be passed along as an attribute.

`parameter_group`      character, a name for the parameter of interest

`parameter_name` quoted or unquoted names of variables involved in a particular parameter of interest. Usually this is just a variable in your model (e.g., a main effect of your iv). However, it could also be an interaction term or some other term. You can use glue syntax to specify an effect that might use alternative versions of the same variable.

### Value

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

### Examples

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear model", lm({dvs} ~ {ivs} * {mods})) |>
  add_parameter_keys("my_interaction", "{ivs}:{mods}") |>
  add_parameter_keys("my_main_effect", {ivs})
```

---

 add\_postprocess

*Add arbitrary postprocessing code to a multiverse pipeline*


---

### Description

Add arbitrary postprocessing code to a multiverse pipeline

**Usage**

```
add_postprocess(.df, postprocess_name, code)
```

**Arguments**

**.df** The original data.frame(e.g., base data set). If part of set of add\_\* decision functions in a pipeline, the base data will be passed along as an attribute.

**postprocess\_name** a character string. A descriptive name for what the postprocessing step accomplishes.

**code** the literal code you would like to execute after each analysis.  
The code should be written to work with pipes (i.e., |> or %>%). Because the post-processing code comes last in each multiverse analysis step, the chosen model object will be passed to the post-processing code.  
For example, if you fit a simple linear model like:  $lm(y \sim x1 + x2)$ , and your post-processing code executes a call to `anova`, you would simply pass `anova()` to `add_postprocess()`. The underlying code would be:  
`data |> filters |> lm(y ~ x1 + x2, data = _) |> anova()`

**Value**

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

**Examples**

```
library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
```



```

add_variables("ivs", iv1, iv2, iv3) |>
add_variables("dvs", dv1, dv2) |>
add_variables("mods", starts_with("mod")) |>
add_preprocess("scale_iv", 'mutate({ivs} = scale({ivs}))') |>
add_model("linear model", lm({dvs} ~ {ivs} * {mods})) |>
add_postprocess("analysis of variance", aov())

```

---

add_preprocess	<i>Add arbitrary preprocessing code to a multiverse analysis pipeline</i>
----------------	---

---

## Description

Add arbitrary preprocessing code to a multiverse analysis pipeline

## Usage

```
add_preprocess(.df, process_name, code)
```

## Arguments

.df	The original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
process_name	a character string. A descriptive name for what the preprocessing step accomplishes.
code	the literal code you would like to execute after data are filtered. <a href="#">glue</a> syntax is allowed. An example might be centering or scaling a predictor after the appropriate filters are applied to the data. The code should be written to work with pipes (i.e.,  > or %>%). Pre-processing code will eventually take the base data along with any filters applied to the data. This means <a href="#">mutate</a> calls are the most natural but other functions that take a data.frame as the first argument should work as well (as long as they also return a data.frame).

## Value

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

## Examples

```

library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),

```

```

    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_preprocess("scale_iv", 'mutate({ivs} = scale({ivs}))')

```

---

add\_reliabilities      *Add item reliabilities to a multiverse pipeline*

---

### Description

Add item reliabilities to a multiverse pipeline

### Usage

```
add_reliabilities(.df, scale_name, items)
```

### Arguments

<code>.df</code>	the original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
<code>scale_name</code>	a character string. Indicates the name of the scale or measure measured by the items or indicators in items.
<code>items</code>	the items (variables) that comprise a scale or measure. These variables will be passed to <code>link[performance]{cronbachs_alpha}</code> , <code>link[performance]{item_intercor}</code> , and <code>link[performance]{item_reliability}</code> . You can also use <code>tidyselect</code> to select variables.

### Value

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

**Examples**

```

library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_reliabilities("unp_scale", c(iv1, iv2, iv3))

```

---

 add\_subgroups

*Add sub groups to the multiverse pipeline*


---

**Description**

Add sub groups to the multiverse pipeline

**Usage**

```
add_subgroups(.df, ..., .only = NULL)
```

**Arguments**

.df	The original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
...	sub group variable(s) in your data whose values specify groupings.
.only	a character vector of sub group values to include. The default includes all sub group values for each sub group variable.

**Value**

a `data.frame` with three columns: `type`, `group`, and `code`. `Type` indicates the decision type, `group` is a decision, and the `code` is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

**Examples**

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500),
    group = sample(1:3, size = 500, replace = TRUE)
  )

the_data |>
  add_subgroups(group)

the_data |>
  add_subgroups(group, .only = c(1,3))
```

---

add_summary_stats	<i>Add a set of descriptive statistics to compute over a set of variables</i>
-------------------	---

---

**Description**

Add a set of descriptive statistics to compute over a set of variables

**Usage**

```
add_summary_stats(.df, var_set, variables, stats)
```

**Arguments**

<code>.df</code>	The original data.frame(e.g., base data set). If part of set of add_* decision functions in a pipeline, the base data will be passed along as an attribute.
<code>var_set</code>	a character string. A name for the set of summary statistics
<code>variables</code>	the variables for which you would like to compute summary statistics. You can also use tidyselect to select variables.
<code>stats</code>	a character vector of stat names (e.g., <code>c("mean", "sd")</code> ). You are responsible for loading any packages that compute your preferred summary statistics. Summary statistic functions must work inside <code>summarize</code> .

**Value**

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

**Examples**

```
library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_preprocess(process_name = "scale_iv", 'mutate({ivs} = scale({ivs}))') |>
  add_preprocess(process_name = "scale_mod", mutate({mods} := scale({mods}))) |>
  add_summary_stats("iv_stats", starts_with("iv"), c("mean", "sd")) |>
  add_summary_stats("dv_stats", starts_with("dv"), c("skewness", "kurtosis"))
```

---

add_variables	<i>Add a set of variable alternatives to a multiverse pipeline</i>
---------------	--

---

## Description

Add a set of variable alternatives to a multiverse pipeline

## Usage

```
add_variables(.df, var_group, ...)
```

## Arguments

<code>.df</code>	The original data.frame(e.g., base data set). If part of set of <code>add_*</code> decision functions in a pipeline, the base data will be passed along as an attribute.
<code>var_group</code>	a character string. Indicates the name of the current set. For example, "primary_iv" could indicate this set are alternatives of the main predictor in an analysis.
<code>...</code>	the bare unquoted names of the variables to include as alternative options for this variable set. You can also use <code>tidyselect</code> to select variables.

## Value

a data.frame with three columns: type, group, and code. Type indicates the decision type, group is a decision, and the code is the actual code that will be executed. If part of a pipe, the current set of decisions will be appended as new rows.

## Examples

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
```

```

      include3 = rnorm(500)
    )

the_data |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod"))

```

---

condense	<i>Summarize multiverse parameters</i>
----------	--

---

## Description

Summarize multiverse parameters

## Usage

```
condense(.unpacked, .what, .how, .group = NULL, list_cols = TRUE)
```

## Arguments

<code>.unpacked</code>	an unpacked (with <a href="#">reveal</a> or <a href="#">unnest</a> ) multiverse dataset.
<code>.what</code>	a specific column to summarize. This could be a model estimate, a summary statistic, correlation, or any other estimate computed over the multiverse.
<code>.how</code>	a named list. The list should contain summary functions (e.g., mean or median) the user would like to compute over the individual estimates from the multiverse
<code>.group</code>	an optional variable to group the results. This argument is passed directly to the <code>.by</code> argument used in <code>dplyr::across</code>
<code>list_cols</code>	logical, whether to create list columns for the raw values of any summarized columns. Useful for creating visualizations and tables. Default is TRUE.

## Value

a summarized tibble containing a column for each summary method from `.how`

## Examples

```

library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id   = 1:500,
    iv1  = rnorm(500),
    iv2  = rnorm(500),
    iv3  = rnorm(500),
    mod1 = rnorm(500),

```

```

    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1  = rnorm(500),
    dv2  = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear_model", lm({dvs} ~ {ivs} * {mods} + cov1))

pipeline_grid <- expand_decisions(full_pipeline)

# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

# Reveal and condense
the_multiverse |>
  reveal_model_parameters() |>
  filter(str_detect(parameter, "iv")) |>
  condense(unstd_coef, list(mean = mean, median = median))

```

---

```
create_blueprint_graph
```

*Create a Analysis Pipeline diagram*

---

## Description

Create a Analysis Pipeline diagram

## Usage

```

create_blueprint_graph(
  .pipeline,
  splines = "line",
  render = TRUE,
  show_code = FALSE,
  ...
)

```



**Arguments**

<code>.pipeline</code>	a <code>data.frame</code> produced by calling a series of <code>add_*</code> functions.
<code>splines</code>	options for how to draw edges (lines) for a <code>grViz</code> diagram
<code>render</code>	whether to render the graph or just output <code>grViz</code> code
<code>show_code</code>	whether to show the code that generated the diagram
<code>...</code>	additional options passed to <code>DiagrammeR::grViz()</code>

**Value**

`grViz` graph of your pipeline

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

create_blueprint_graph(full_pipeline)
```

---

`detect_multiverse_n` *Detect total number of analysis pipelines*

---

**Description**

Detect total number of analysis pipelines

**Usage**

```
detect_multiverse_n(.pipeline, include_models = TRUE)
```

**Arguments**

`.pipeline` a data.frame produced by calling a series of `add_*` functions.

`include_models` Whether to count alternative models if you have more than one `add_model()` call.

**Value**

a numeric, the total number of unique analysis pipelines

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

detect_multiverse_n(full_pipeline)
```

---

detect_n_filters	<i>Detect total number of filtering expressions your pipelines</i>
------------------	--

---

**Description**

Detect total number of filtering expressions your pipelines

**Usage**

```
detect_n_filters(.pipeline)
```

**Arguments**

`.pipeline` a `data.frame` produced by calling a series of `add_*` functions.

**Value**

a numeric, the total number of filtering expressions

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

detect_n_filters(full_pipeline)
```

---

`detect_n_models`*Detect total number of models in your pipelines*

---

**Description**

Detect total number of models in your pipelines

**Usage**

```
detect_n_models(.pipeline)
```

**Arguments**

`.pipeline` a `data.frame` produced by calling a series of `add_*` functions.

**Value**

a numeric, the total number of unique models

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

detect_n_models(full_pipeline)
```

---

`detect_n_subgroups` *Detect total number of subgroups in your pipelines*

---

**Description**

Detect total number of subgroups in your pipelines

**Usage**

```
detect_n_subgroups(.pipeline)
```

**Arguments**

`.pipeline` a data.frame produced by calling a series of `add_*` functions.

**Value**

a numeric, the total number of unique subgroups, including subgroup combinations

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_subgroups(include2) |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

detect_n_variables(full_pipeline)
```

---

`detect_n_variables` *Detect total number of variable sets in your pipelines*

---

**Description**

Detect total number of variable sets in your pipelines

**Usage**

```
detect_n_variables(.pipeline)
```

**Arguments**

`.pipeline` a `data.frame` produced by calling a series of `add_*` functions.

**Value**

a numeric, the total number of unique variable sets

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

detect_n_variables(full_pipeline)
```

---

expand\_decisions

*Expand a set of multiverse decisions into all possible combinations*

---

**Description**

Expand a set of multiverse decisions into all possible combinations

**Usage**

```
expand_decisions(.pipeline)
```

**Arguments**

`.pipeline` a data.frame produced by calling a series of `add_*` functions.

**Value**

a nested data.frame containing all combinations of arbitrary decisions for a multiverse analysis. Decision types will become list columns matching the type of decisions called along the pipeline (e.g., filters, variables, etc.). Any decisions containing `glue` syntax will be populated with the relevant information.

**Examples**

```
library(tidyverse)
library(multitool)

the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, include3 > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_preprocess(process_name = "scale_iv", 'mutate({ivs} = scale({ivs}))') |>
  add_preprocess(process_name = "scale_mod", mutate({mods} := scale({mods}))) |>
  add_summary_stats("iv_stats", starts_with("iv"), c("mean", "sd")) |>
  add_summary_stats("dv_stats", starts_with("dv"), c("skewness", "kurtosis")) |>
  add_correlations("predictors", matches("iv|mod|cov"), focus_set = c(cov1, cov2)) |>
  add_correlations("outcomes", matches("dv|mod"), focus_set = matches("dv")) |>
  add_reliabilities("unp_scale", c(iv1, iv2, iv3)) |>
  add_model("no covariates", lm({dvs} ~ {ivs} * {mods})) |>
  add_model("with covariates", lm({dvs} ~ {ivs} * {mods} + cov1)) |>
```

```
add_postprocess("aov", aov())

pipeline_expanded <- expand_decisions(full_pipeline)
```

---

reveal *Reveal the contents of a multiverse analysis*

---

## Description

Reveal the contents of a multiverse analysis

## Usage

```
reveal(.multi, .what, .which = NULL, .unpack_specs = "no")
```

## Arguments

<code>.multi</code>	a multiverse list-column tibble produced by <code>run_multiverse</code> .
<code>.what</code>	the name of a list-column you would like to unpack
<code>.which</code>	any sub-list columns you would like to unpack
<code>.unpack_specs</code>	character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a <code>decision_set</code> and <code>alternatives</code> columns. This is mainly useful for plotting.

## Value

the unnested part of the multiverse requested. This usually contains the particular estimates or statistics you would like to analyze over the decision grid specified.

## Examples

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
```



```

    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear_model", lm({dvs} ~ {ivs} * {mods} + cov1))

pipeline_grid <- expand_decisions(full_pipeline)

# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

# Reveal results of the linear model
the_multiverse |> reveal(model_fitted, model_parameters)

```

---

 reveal\_corrs

*Reveal a set of multiverse correlations*


---

## Description

Reveal a set of multiverse correlations

## Usage

```
reveal_corrs(.descriptives, .which, .unpack_specs = "no")
```

## Arguments

`.descriptives` a descriptive multiverse list-column tibble produced by [run\\_descriptives](#).

`.which` the specific name of the correlations requested

`.unpack_specs` character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a `decision_set` and `alternatives` columns. This is mainly useful for plotting.

## Value

an unnested set of correlations per decision from the multiverse.

**Examples**

```

library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(
    include1 == 0,
    include2 != 3,
    include2 != 2,
    include3 > -2.5,
    include3 < 2.5,
    between(include3, -2.5, 2.5)
  ) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_correlations("predictors", starts_with("iv")) |>
  add_summary_stats("iv_stats", starts_with("iv"), c("mean", "sd")) |>
  add_reliabilities("vio_scale", starts_with("iv")) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod)) |>
  expand_decisions()

my_descriptives <- run_descriptives(full_pipeline)

my_descriptives |>
  reveal_corrs(predictors_rs)

```

---

reveal\_model\_messages *Reveal any messages about your models during a multiverse analysis*

---

**Description**

Reveal any messages about your models during a multiverse analysis

**Usage**

```
reveal_model_messages(.multi, .unpack_specs = "no")
```

**Arguments**

`.multi` a multiverse list-column tibble produced by `run_multiverse`.

`.unpack_specs` character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a `decision_set` and `alternatives` columns. This is mainly useful for plotting.

**Value**

the unnested model messages captured during analysis.

**Examples**

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear_model", lm({dvs} ~ {ivs} * {mods} + cov1))

pipeline_grid <- expand_decisions(full_pipeline)
```

```
# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

# Reveal results of the linear model
the_multiverse |>
  reveal_model_messages()
```

---

```
reveal_model_parameters
```

*Reveal the model parameters of a multiverse analysis*

---

## Description

Reveal the model parameters of a multiverse analysis

## Usage

```
reveal_model_parameters(.multi, effect_key = NULL, .unpack_specs = "no")
```

## Arguments

<code>.multi</code>	a multiverse list-column tibble produced by <code>run_multiverse</code> .
<code>effect_key</code>	character, if you added parameter keys to your pipeline, you can specify if you would like filter the parameters using one of your parameter keys. This is useful when different variables are being switched out across the multiverse but represent the same effect of interest.
<code>.unpack_specs</code>	character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a <code>decision_set</code> and <code>alternatives</code> columns. This is mainly useful for plotting.

## Value

the unnested model parameters from the multiverse.

## Examples

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id   = 1:500,
    iv1  = rnorm(500),
    iv2  = rnorm(500),
    iv3  = rnorm(500),
```

```

    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear_model", lm({dvs} ~ {ivs} * {mods} + cov1))

pipeline_grid <- expand_decisions(full_pipeline)

# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

# Reveal results of the linear model
the_multiverse |>
  reveal_model_parameters()

```

---

```
reveal_model_performance
```

*Reveal the model performance/fit indices from a multiverse analysis*

---

## Description

Reveal the model performance/fit indices from a multiverse analysis

## Usage

```
reveal_model_performance(.multi, .unpack_specs = "no")
```

## Arguments

<code>.multi</code>	a multiverse list-column tibble produced by <code>run_multiverse</code> .
<code>.unpack_specs</code>	character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a <code>decision_set</code> and <code>alternatives</code> columns. This is mainly useful for plotting.

**Value**

the unnested model performance/fit indices from a multiverse analysis.

**Examples**

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear_model", lm({dvs} ~ {ivs} * {mods} + cov1))

pipeline_grid <- expand_decisions(full_pipeline)

# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

# Reveal results of the linear model
the_multiverse |>
  reveal_model_performance()
```

---

reveal\_model\_warnings *Reveal any warnings about your models during a multiverse analysis*

---

**Description**

Reveal any warnings about your models during a multiverse analysis

**Usage**

```
reveal_model_warnings(.multi, .unpack_specs = "no")
```

**Arguments**

`.multi` a multiverse list-column tibble produced by `run_multiverse`.

`.unpack_specs` character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a `decision_set` and `alternatives` columns. This is mainly useful for plotting.

**Value**

the unnested model warnings captured during analysis

**Examples**

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_model("linear_model", lm({dvs} ~ {ivs} * {mods} + cov1))

pipeline_grid <- expand_decisions(full_pipeline)
```

```
# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

# Reveal results of the linear model
the_multiverse |>
  reveal_model_warnings()
```

---

reveal\_reliabilities *Reveal a set of multiverse cronbach's alpha statistics*

---

## Description

Reveal a set of multiverse cronbach's alpha statistics

## Usage

```
reveal_reliabilities(.descriptives, .which, .unpack_specs = "no")
```

## Arguments

`.descriptives` a descriptive multiverse list-column tibble produced by [run\\_descriptives](#).

`.which` the specific name of the alphas

`.unpack_specs` character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a decision\_set and alternatives columns. This is mainly useful for plotting.

## Value

an unnested set of correlations per decision from the multiverse.

## Examples

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
```



```

      include3 = rnorm(500)
    )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(
    include1 == 0,
    include2 != 3,
    include2 != 2,
    include3 > -2.5,
    include3 < 2.5,
    between(include3, -2.5, 2.5)
  ) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_correlations("predictor correlations", starts_with("iv")) |>
  add_summary_stats("iv_stats", starts_with("iv"), c("mean", "sd")) |>
  add_reliabilities("vio_scale", starts_with("iv")) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod)) |>
  expand_decisions()

my_descriptives <- run_descriptives(full_pipeline)

my_descriptives |>
  reveal_reliabilities(vio_scale_alpha)

```

---

reveal\_summary\_stats *Reveal a set of summary statistics from a multiverse analysis*

---

## Description

Reveal a set of summary statistics from a multiverse analysis

## Usage

```
reveal_summary_stats(.descriptives, .which, .unpack_specs = "no")
```

## Arguments

<code>.descriptives</code>	a descriptive multiverse list-column tibble produced by <a href="#">run_descriptives</a> .
<code>.which</code>	the specific name of the summary statistics
<code>.unpack_specs</code>	character, options are "no", "wide", or "long". "no" (default) keeps specifications in a list column, wide unnests specifications with each specification category as a column. "long" unnests specifications and stacks them into long format, which stacks specifications into a decision_set and alternatives columns. This is mainly useful for plotting.

**Value**

an unnested set of summary statistics per decision from the multiverse.

**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(
    include1 == 0,
    include2 != 3,
    include2 != 2,
    include3 > -2.5,
    include3 < 2.5,
    between(include3, -2.5, 2.5)
  ) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_correlations("predictor correlations", starts_with("iv")) |>
  add_summary_stats("iv_stats", starts_with("iv"), c("mean", "sd")) |>
  add_reliabilities("vio_scale", starts_with("iv")) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod)) |>
  expand_decisions()

my_descriptives <- run_descriptives(full_pipeline)

my_descriptives |>
  reveal_summary_stats(iv_stats)
```

---

run\_descriptives

*Run a multiverse-style descriptive analysis based on a complete decision grid*

---

## Description

Run a multiverse-style descriptive analysis based on a complete decision grid

## Usage

```
run_descriptives(.grid, show_progress = TRUE)
```

## Arguments

`.grid` a tibble produced by [expand\\_decisions](#)  
`show_progress` logical, whether to show a progress bar while running.

## Value

single tibble containing tidied results for all descriptive analyses specified. Because descriptive analyses only change when the underlying cases change, only filtering and/or subgroup decisions will be used and will be internally re-expanded before performing various descriptive analyses.

## Examples

```
library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_summary_stats("iv_stats", starts_with("iv"), c("mean", "sd")) |>
  add_summary_stats("dv_stats", starts_with("dv"), c("skewness", "kurtosis")) |>
```

```

add_correlations("predictors", matches("iv|mod|cov"), focus_set = c(cov1,cov2)) |>
add_correlations("outcomes", matches("dv|mod"), focus_set = matches("dv")) |>
add_reliabilities("unp_scale", c(iv1,iv2,iv3)) |>
add_reliabilities("vio_scale", starts_with("mod")) |>
expand_decisions()

run_descriptives(full_pipeline)

```

---

run_multiverse	<i>Run a multiverse based on a complete decision grid</i>
----------------	---

---

## Description

Run a multiverse based on a complete decision grid

## Usage

```

run_multiverse(
  .grid,
  add_standardized = TRUE,
  save_model = FALSE,
  show_progress = TRUE
)

```

## Arguments

<code>.grid</code>	a tibble produced by <a href="#">expand_decisions</a>
<code>add_standardized</code>	logical. Whether to add standardized coefficients to the model output. Defaults to TRUE.
<code>save_model</code>	logical, indicates whether to save the model object in its entirety. The default is FALSE because model objects are usually large and under the hood, <a href="#">parameters</a> and <a href="#">performance</a> is used to summarize the most useful model information.
<code>show_progress</code>	logical, whether to show a progress bar while running.

## Value

a single tibble containing tidied results for the model and any post-processing tests/tasks. For each unique test (e.g., an `lm` or `aov` called on an `lm`), a list column with the function name is created with [parameters](#) and [performance](#) and any warnings or messages printed while fitting the models. Internally, modeling and post-processing functions are checked to see if there are tidy or glance methods available. If not, `summary` will be called instead.

**Examples**

```

library(tidyverse)
library(multitool)

# Simulate some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod1 = rnorm(500),
    mod2 = rnorm(500),
    mod3 = rnorm(500),
    cov1 = rnorm(500),
    cov2 = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# Decision pipeline
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include2 != 2, scale(include3) > -2.5) |>
  add_variables("ivs", iv1, iv2, iv3) |>
  add_variables("dvs", dv1, dv2) |>
  add_variables("mods", starts_with("mod")) |>
  add_preprocess(process_name = "scale_iv", 'mutate({ivs} = scale({ivs}))') |>
  add_preprocess(process_name = "scale_mod", mutate({mods} := scale({mods}))) |>
  add_model("no covariates", lm({dvs} ~ {ivs} * {mods})) |>
  add_model("covariate", lm({dvs} ~ {ivs} * {mods} + cov1)) |>
  add_postprocess("aov", aov())

pipeline_grid <- expand_decisions(full_pipeline)

# Run the whole multiverse
the_multiverse <- run_multiverse(pipeline_grid[1:10,])

```

---

show\_code\_subgroups    *Show multiverse data code pipelines*

---

**Description**

Each show\_code\* function should be self-explanatory - they indicate where along the multiverse pipeline to extract code. The goal of these functions is to create a window into each multiverse decision set context/results and allow the user to inspect specific decisions straight from the code that produced it.

**Usage**

```
show_code_subgroups(  
  .grid,  
  decision_num,  
  copy = FALSE,  
  console = TRUE,  
  execute = FALSE,  
  ...  
)  
  
show_code_filter(  
  .grid,  
  decision_num,  
  copy = FALSE,  
  console = TRUE,  
  execute = FALSE,  
  ...  
)  
  
show_code_preprocess(  
  .grid,  
  decision_num,  
  copy = FALSE,  
  console = TRUE,  
  execute = FALSE,  
  ...  
)  
  
show_code_model(  
  .grid,  
  decision_num,  
  copy = FALSE,  
  console = TRUE,  
  execute = FALSE,  
  ...  
)  
  
show_code_postprocess(  
  .grid,  
  decision_num,  
  post_step = 1,  
  copy = FALSE,  
  console = TRUE,  
  execute = FALSE,  
  ...  
)  
  
show_code_summary_stats(  
  .grid,  
  decision_num,  
  copy = FALSE,  
  console = TRUE,  
  execute = FALSE,  
  ...  
)
```

```

    .grid,
    decision_num,
    summary_set = 1,
    copy = FALSE,
    console = TRUE,
    execute = FALSE,
    ...
)

show_code_corrs(
  .grid,
  decision_num,
  corr_set = 1,
  copy = FALSE,
  console = TRUE,
  execute = FALSE,
  ...
)

show_code_reliabilities(
  .grid,
  decision_num,
  rel_set = 1,
  copy = FALSE,
  console = TRUE,
  execute = FALSE,
  ...
)

```

### Arguments

<code>.grid</code>	a full decision grid created by <a href="#">expand_decisions</a> .
<code>decision_num</code>	numeric. Indicates which 'universe' in the multiverse to show underlying code.
<code>copy</code>	logical. Whether to copy the pipeline code to the clipboard using <a href="#">write_clip</a> . Defaults to FALSE.
<code>console</code>	logical. Whether to send the code to the console in RStudio. Defaults to TRUE but requires that the code be running in RStudio.
<code>execute</code>	logical. If sending to the console, whether to immediately run the code in the console. Defaults to FALSE.
<code>...</code>	additional arguments passed to <code>rstudioapi::sendToConsole()</code>
<code>post_step</code>	numeric. For <code>show_code_postprocess</code> , Which post-processing step to print. Default is set to the 1.
<code>summary_set</code>	numeric. For <code>show_code_summary_stats</code> , Which set of summary statistics to print. Default is set to the 1.
<code>corr_set</code>	numeric. For <code>show_code_corrs</code> , Which set of correlations to print. Default is set to the 1.

`rel_set` numeric. For `show_code_reliabilities`, Which set of reliabilities to print. Default is set to the 1.

### Value

the code that generated results up to the specified point in an analysis pipeline. The code is printed in the console and can be optionally copied to the clipboard.

### Functions

- `show_code_filter()`: Show the code up to the filtering stage
- `show_code_preprocess()`: Show the code up to the preprocessing stage
- `show_code_model()`: Show the code up to the modeling stage
- `show_code_postprocess()`: Show the code up to the post-processing stage
- `show_code_summary_stats()`: Show the code for computing summary statistics
- `show_code_corrs()`: Show the code for computing correlations
- `show_code_reliabilities()`: Show the code for computing scale reliability

---

`summarize_filter_ns` *Summarize samples sizes for each unique filtering expression*

---

### Description

Summarize samples sizes for each unique filtering expression

### Usage

```
summarize_filter_ns(.pipeline)
```

### Arguments

`.pipeline` a `data.frame` produced by calling a series of `add_*` functions.

### Value

a tibble with each row representing a filtering expression and four columns: `filter_expression`, `variable`, `n_retained`, and `n_excluded`.



**Examples**

```
library(tidyverse)
library(multitool)

# create some data
the_data <-
  data.frame(
    id = 1:500,
    iv1 = rnorm(500),
    iv2 = rnorm(500),
    iv3 = rnorm(500),
    mod = rnorm(500),
    dv1 = rnorm(500),
    dv2 = rnorm(500),
    include1 = rbinom(500, size = 1, prob = .1),
    include2 = sample(1:3, size = 500, replace = TRUE),
    include3 = rnorm(500)
  )

# create a pipeline blueprint
full_pipeline <-
  the_data |>
  add_filters(include1 == 0, include2 != 3, include3 > -2.5) |>
  add_variables(var_group = "ivs", iv1, iv2, iv3) |>
  add_variables(var_group = "dvs", dv1, dv2) |>
  add_model("linear model", lm({dvs} ~ {ivs} * mod))

summarize_filter_ns(full_pipeline)
```

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