# Package 'RSYC'

November 3, 2026

**Title** Remote Sensing-Derived Yield Curves for Canada

**Version** 0.2.0

**Description** Provides published remote sensing-based yield curves for aboveground biomass and total volume across Canada, as described in Tompalski et al. (2024) <doi:10.1016/j.foreco.2024.121894> and Tompalski et al. (2025) <doi:10.1093/forestry/cpaf067>. Models are available for 150 km tiles and four levels of Canada's ecological land classification. Functions help users find curves by species and area, estimate yield at a given stand age, calibrate curves to local observations, and build spatial yield-curve datasets.

**License** GPL (>= 3)

**Encoding** UTF-8

**Depends** R (>= 4.1.0)

**LazyData** true

**Imports** digest, glue, lifecycle, magrittr, tibble

**Suggests** dplyr, purrr, sf, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**URL** https://ptompalski.github.io/RSYC/, https://github.com/ptompalski/RSYC

**BugReports** https://github.com/ptompalski/RSYC/issues

**Config/Needs/website** rmarkdown, knitr, ggplot2, DT, tidyr, jsonlite, scales, ggtext, yardstick, ptompalski/scatter

**Config/roxygen2/version** 8.1.1

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2026-11-03 15:50:24 UTC

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---

`available_rsyc_models` *List Published RSYC Models*

---

## Description

List the published Canada-wide curves that match a forest measure, species, type of area, or area name. Leave a choice as `NULL` to include all of its available values.

## Usage

```
available_rsyc_models(
  response = NULL,
  species = NULL,
  strata_level = NULL,
  strata_id = NULL
)
```

## Arguments

| | |
|---|---|
| `response` | One or both forest measures: `"agb"` for aboveground biomass and `"volume"` for total volume. The default includes both. |
| `species` | One or more species codes or broad groups. Uppercase and lowercase letters are treated the same. The default includes all species. Unknown species codes produce a warning. |
| `strata_level` | One or more types of area: `"tile"`, `"ecozone"`, `"ecoprovince"`, `"ecoregion"`, or `"ecodistrict"`. The default includes all types. |
| `strata_id` | One or more tile IDs, ecological area names or paths, or ecological codes. Tile IDs, names, and paths are matched ignoring case. Numeric values and numeric-looking character values are interpreted as codes when no name or path matches. Code searches require exactly one ecological `strata_level`. Quote ecoprovince codes such as `"10.1"`. Values that match no published curve produce a warning. The default includes all areas. |

## Details

Character `strata_id` values are matched as names or paths before numeric-looking values are interpreted as ecological codes. Ecozone codes 5 and 6 return both published named subdivisions. Ecozone code 10 is also ambiguous, but currently has no published national model rows.

## Value

A table with one row for each published curve that matches the choices. `strata_code` is the canonical character code for ecological rows and `NA` for tiles.

## Examples

```
available_rsyc_models(
  response = "volume", species = "PICE.MAR", strata_level = "tile"
)
available_rsyc_models(
  response = "agb", strata_level = "ecoprovince", strata_id = "7.1"
)
```

---

# `build_rsyc_dataset` *Build an RSYC Spatial Yield-Curve Dataset*

---

## Description

Estimate yield for one or more species across a set of tiles or ecological areas. The boundary map is kept separate from the curve table so that each area shape is stored only once.

## Usage

```
build_rsyc_dataset(
  response,
  species,
  age = 1:150,
  strata_level = "tile",
  strata_id = NULL,
  output = NULL,
  overwrite = FALSE,
  cache_dir = tools::R_user_dir("RSYC", "data"),
  quiet = TRUE
)
```

## Arguments

| | |
|---|---|
| `response` | Forest measure to estimate: `"agb"` for aboveground biomass or `"volume"` for total volume. |

| | |
|---|---|
| species | One or more species codes or broad groups. Uppercase and lowercase letters are treated the same. Requested species without a published curve for the selected response and areas are omitted with a warning. |
| age | One or more stand ages in years. |
| strata_level | Type of area: "tile", "ecozone", "ecoprovince", "ecoregion", or "ecodistrict". |
| strata_id | One or more tile IDs, ecological area names or paths, or ecological codes. Tile IDs, names, and paths are matched ignoring case. Numeric values and numeric-looking character values are interpreted as codes when no name or path matches. Quote ecoprovince codes such as "10.1". By default, every area with a matching published curve is included. If an area name occurs in several places, the function asks for the full sequence of area names. |
| output | Location of an optional GeoPackage file. When supplied, the file contains a boundary map named spatial, a yield table named curves, and a summary table named metadata. |
| overwrite | Replace an existing GeoPackage at output? |
| cache_dir | Folder in which to save the GeoPackage. By default, RSYC uses its standard user data folder, returned by tools::R_user_dir(). |
| quiet | Hide download progress? |

## Details

The function currently uses only curves fitted across Canada. It does not substitute a curve from another type of area or from a regional fit. Ecological boundaries must first be downloaded with download_rsyc_boundaries(); tile boundaries are included with RSYC. Ecozone codes 5, 6, and 10 are ambiguous and must instead be supplied as a subdivision name or path.

## Value

Three named results: spatial, an sf boundary map; curves, a table of yield estimates containing canonical character strata_code values (NA for tiles); and metadata, a one-row summary of the data and choices used. Ecological spatial results contain strata_code plus the hierarchy names and source ID fields through the requested level. Tile spatial results contain strata_id and geometry.

## Examples

```
tile_dataset <- build_rsyc_dataset(
  response = "agb",
  species = c("PICE.MAR", "POPU.TRE"),
  age = c(50, 100, 150),
  strata_level = "tile",
  strata_id = c("H14", "F31")
)
tile_dataset$spatial
tile_dataset$curves
```

`calibrate_rsyc` *Calibrate an RSYC Yield Curve with Local Observations*

## Description

**[Experimental]**

Adjust a published RSYC curve to local field data using a best linear unbiased predictor (BLUP) of the local level. Given one or more observed values (aboveground biomass or total volume) at known stand ages, the function estimates a shrinkage-based local level adjustment and applies it as a multiplicative ratio to the selected national curve.

## Usage

```
calibrate_rsyc(
  response,
  species,
  strata_level,
  strata_id,
  obs_age,
  obs_response,
  predict_age = NULL,
  apply_limits = TRUE,
  random_effect_limit_sd = 3,
  ratio_limit = 5,
  value_limit = 1000
)
```

## Arguments

| | |
|---|---|
| `response` | Forest measure to estimate: `"agb"` for aboveground biomass or `"volume"` for total volume. |
| `species` | A species code or broad group such as `"coniferous"`. Uppercase and lowercase letters are treated the same. |
| `strata_level` | Type of area: `"tile"`, `"ecozone"`, `"ecoprovince"`, `"ecoregion"`, or `"ecodistrict"`. |
| `strata_id` | Tile ID, ecological area name or path, or ecological code. Tile IDs, names, and paths are matched ignoring case. A single area name can be used when it occurs only once. If the name occurs in several places, use the full sequence of area names shown by `rsyc_strata()`. Numeric values are interpreted as codes for the selected ecological `strata_level`; quote ecoprovince codes such as `"10.1"`. |
| `obs_age` | Stand ages, in years, of the local observations. |
| `obs_response` | Observed non-negative values at `obs_age`. Aboveground biomass in Mg/ha or total volume in m3/ha, matching `response`. Must be the same length as `obs_age`. |

`predict_age` One or more stand ages at which to return calibrated predictions. Defaults to the sorted unique `obs_age`.

`apply_limits` When `TRUE` (the default), apply the safeguards that protect against implausible local adjustments: the random effect is constrained to `random_effect_limit_sd` standard deviations, an adjustment ratio above `ratio_limit` is discarded in favour of the bare curve, and any calibrated value above `value_limit` falls back to the bare curve. When `FALSE`, the raw shrunk BLUP adjustment is returned uncapped.

`random_effect_limit_sd` Number of standard deviations of the local random-effect distribution at which the estimate is constrained. The default of `3` corresponds to the central 99.7% of that distribution. Only used when `apply_limits` is `TRUE`.

`ratio_limit` Largest allowed calibration ratio before the adjustment is discarded. Only used when `apply_limits` is `TRUE`.

`value_limit` Largest allowed calibrated value before the prediction falls back to the bare curve. Only used when `apply_limits` is `TRUE`.

## Details

The RSYC models are nonlinear mixed-effects models in which the tile- and pixel-level random effects act on $\beta_1$, the parameter associated with the maximum biomass (or volume) potential (the asymptote parameter):

$$AGB_{ijk} = (\beta_1 + b_i + b_{ij})\, g(age_{ijk}) + \epsilon_{ijk}$$

where $i$ indexes the tile, $j$ the pixel nested within the tile, $k$ the age, and $g(age) = e^{-\beta_4 age}(1 - e^{-\beta_2 age})^{\beta_3}$ is the age-related modifier. The random effects and residual errors are assumed to be independent and normally distributed with mean zero. Hats denote estimated values. The `b1` coefficient published in RSYC_models is the tile-level asymptote parameter, already equal to $\hat{\beta}_1 + \hat{b}_i$, so the yield curve based on the tile-level conditional prediction is $\texttt{b1} \cdot \hat{g}(age)$.

Local calibration estimates the pixel-level random effect $b_{ij}$ of the calibration plot (assumed to coincide with pixel $j$ within tile $i$) conditional on the fitted model. Given observations $y_{ijk}$ at ages $age_{ijk}$, with $m_{ijk} = \hat{g}(age_{ijk})$,

$$\hat{b}_{ij} = \frac{\sum_k m_{ijk}(y_{ijk} - \texttt{b1} \cdot m_{ijk})}{\sum_k m_{ijk}^2 + \hat{\sigma}_\epsilon^2 / \hat{\sigma}_b^2}$$

where $\hat{\sigma}_b^2$ is the estimated pixel-level (nested within tile) random-effect variance and $\hat{\sigma}_\epsilon^2$ is the estimated residual variance. The $\hat{\sigma}_\epsilon^2 / \hat{\sigma}_b^2$ term shrinks weak local evidence toward no adjustment. The calibrated curve substitutes the adjusted asymptote parameter into the same equation,

$$(\texttt{b1} + \hat{b}_{ij})\, \hat{g}(age)$$

which is equivalent to scaling the published curve by $(\texttt{b1} + \hat{b}_{ij})/\texttt{b1}$, reported as `ratio_blup`.

With a single observation this becomes a one-point level anchor. The result should be read as a single-observation BLUP-anchored RSYC curve, not as a local growth trajectory learned from the data.

## Value

A list with the components:

**predictions** A table of `age` and the calibrated `value` at each `predict_age`, together with the bare-curve `value_uncalibrated`.

**ratio_blup** The multiplicative local adjustment applied to the curve.

**b_pixel** The estimated pixel-level random effect $\hat{b}_{ij}$ (capped and shrunk when `apply_limits` is `TRUE`).

**shrinkage_factor** The shrinkage weight in `[0, 1]`; values near 0 mean weak local evidence pulled toward no adjustment.

**n_obs** Number of observations used.

**random_effect_limited, ratio_limited, value_limited** Flags indicating whether each safeguard altered the result.

**model_id** Identifier of the national curve that was calibrated.

## References

Tompalski, P., Hermosilla, T., Baral, S.K., Wulder, M.A., and White, J.C. (2025). National remote sensing-derived aboveground biomass yield curves for Canada. *Forestry: An International Journal of Forest Research*. doi:10.1093/forestry/cpaf067

## Examples

```
# One observation for a tile model selected by tile ID.
calibrate_rsyc(
  "agb", "PICE.MAR", "tile", "H14",
  obs_age = 45,
  obs_response = 65
)

# Two observations for an ecoregion selected by numeric code.
calibrate_rsyc(
  "agb", "PICE.MAR", "ecoregion", 198,
  obs_age = c(45, 70),
  obs_response = c(52, 65)
)

# Four observations for an ecodistrict selected by full hierarchy path.
calibrate_rsyc(
  "agb", "PICE.MAR", "ecodistrict",
  paste(
    "Atlantic Maritime", "Fundy Uplands", "Annapolis-Minas Lowlands",
    "Windsor Lowlands", sep = "/"
  ),
  obs_age = c(30, 50, 70, 90),
  obs_response = c(22, 31, 36, 39)
)
```

`download_rsyc_boundaries` *Download RSYC Ecological Boundaries*

## Description

Download and save the ecological boundary maps used by RSYC. The file is not downloaded when the package is installed or loaded. It contains maps of ecozones, ecoprovinces, ecoregions, and ecodistricts, but no yield curves. Tile boundaries are already included with RSYC.

## Usage

```
download_rsyc_boundaries(
  cache_dir = tools::R_user_dir("RSYC", "data"),
  overwrite = FALSE,
  quiet = FALSE,
  url = getOption("RSYC.ecostrat_url", .rsyc_ecostrat_url)
)
```

## Arguments

| | |
|---|---|
| `cache_dir` | Folder in which to save the GeoPackage. By default, RSYC uses its standard user data folder, returned by `tools::R_user_dir()`. |
| `overwrite` | Replace a previously downloaded file? |
| `quiet` | Hide download progress? |
| `url` | Web address of the boundary file. The default points to the copy published with RSYC. Organizations may instead provide the address of an approved copy. Its contents must match the published file. |

## Value

The full location of the saved GeoPackage. The function returns this location without printing it.

## See Also

`rsyc_boundaries()`

## Examples

```
# Save to a temporary folder here; omit `cache_dir` to use the default.
path <- try(download_rsyc_boundaries(cache_dir = tempdir()))
```

predict_rsyc *Estimate Biomass or Volume from an RSYC Yield Curve*

## Description

Estimate aboveground biomass or total volume at one or more stand ages. The curve is selected by species and area.

## Usage

```
predict_rsyc(response, species, age, strata_level, strata_id)
```

## Arguments

| | |
|---|---|
| response | Forest measure to estimate: "agb" for aboveground biomass or "volume" for total volume. |
| species | A species code or broad group such as "coniferous". Uppercase and lowercase letters are treated the same. |
| age | One or more stand ages in years. |
| strata_level | Type of area: "tile", "ecozone", "ecoprovince", "ecoregion", or "ecodistrict". |
| strata_id | Tile ID, ecological area name or path, or ecological code. Tile IDs, names, and paths are matched ignoring case. A single area name can be used when it occurs only once. If the name occurs in several places, use the full sequence of area names shown by rsyc_strata(). Numeric values are interpreted as codes for the selected ecological strata_level; quote ecoprovince codes such as "10.1". |

## Details

This function currently uses curves fitted across Canada. The curves were fitted for stand ages 1 through 150 years. The function warns when asked to estimate outside this age range; age 0 is also allowed as the start of a curve. When a full ecological area sequence is needed, use / between the ecozone, ecoprovince, ecoregion, and ecodistrict names.

Ecological codes are resolved only within the selected strata_level. Ecozone codes 5, 6, and 10 each identify two named package subdivisions and therefore cannot select a single curve; use the desired subdivision name.

## Value

One estimated value for each stand age. AGB is in Mg/ha and volume is in m3/ha.

## Examples

```
# Select a tile model with its tile ID.
predict_rsyc("agb", "PICE.MAR", c(20, 60, 120), "tile", "H14")

# Select an ecozone model with its unique name.
predict_rsyc(
  response = "volume",
  species = "PICE.MAR",
  age = c(20, 60, 120),
  strata_level = "ecozone",
  strata_id = "Boreal Shield East"
)

# Select an ecoregion model with its numeric ecological code.
predict_rsyc(
  "agb", "PICE.MAR", c(40, 80), "ecoregion", 198
)

# A full hierarchy path is an unambiguous ecological selector.
predict_rsyc(
  "agb", "PICE.MAR", 80, "ecodistrict",
  paste(
    "Atlantic Maritime", "Fundy Uplands", "Annapolis-Minas Lowlands",
    "Windsor Lowlands", sep = "/"
  )
)
```

---

# rsyc_boundaries *Read RSYC Boundary Maps*

---

## Description

Read the tile boundaries or ecological boundaries used for the RSYC yield curves. Tile boundaries are included with the package. Ecological boundaries are read from the file saved by download_rsyc_boundaries(). This function never downloads data on its own.

## Usage

```
rsyc_boundaries(
  strata_level = "tile",
  cache_dir = tools::R_user_dir("RSYC", "data"),
  quiet = TRUE
)
```

## Arguments

| | |
|---|---|
| strata_level | Type of area: "tile", "ecozone", "ecoprovince", "ecoregion", or "ecodistrict". |

| | |
|---|---|
| cache_dir | Folder in which to save the GeoPackage. By default, RSYC uses its standard user data folder, returned by tools::R_user_dir(). |
| quiet | Hide messages produced while the map is read? |

## Value

An sf map in the Canada Atlas Lambert projection (EPSG:3978). Tile maps contain strata_id and geometry. Ecological maps additionally contain canonical character strata_code and the hierarchy names and source ID fields through the requested level.

## Examples

```
if (requireNamespace("sf", quietly = TRUE)) {
  tiles <- rsyc_boundaries("tile")
}

if (requireNamespace("sf", quietly = TRUE)) {
  cache <- tempdir()
  if (!inherits(try(download_rsyc_boundaries(cache_dir = cache)), "try-error")) {
    districts <- rsyc_boundaries("ecodistrict", cache_dir = cache)
  }
}
```

---

# RSYC_models *Published RSYC Yield-Curve Data*

---

## Description

A table containing one row for each published remote sensing-based yield curve. It includes above-ground biomass and total-volume curves fitted across Canada and within individual regions. Curves are available for tiles and four levels of Canada's ecological land classification.

## Usage

```
RSYC_models
```

## Format

A table with 27,208 rows and 42 columns:

**model_id, model_version** Unique name for the curve and the RSYC release in which it was published.

**response, response_units** Forest measure (agb or volume) and its units.

**strata_type, strata_level, strata_id** Type and name of the area represented by the curve.

**ecozone_id, ecoprovince_id, ecoregion_id, ecodistrict_id** Raw identifiers for the four levels of the ecological hierarchy. `ecoprovince_id` is stored as character; the other three are integers. Fields above the row's ecological level, and all four fields for tile rows, may be missing.

**scale, region_id** Whether the curve was fitted across Canada or within a region, and the region name where applicable.

**species, model_group** Species code or broad species group.

**equation, age_min, age_max** Curve equation and age range. Published RSYC curves were fitted for stand ages 1 to 150 years.

**b1, b2, b3, b4** Chapman-Richards curve coefficients.

**b1_se, b2_se, b3_se, b4_se, sigma** Measures of uncertainty around the fitted curve.

**parent_b1_random_effect, parent_b1_var, local_b1_var, residual_var** Variance components and parent effects used by local calibration and retained for model provenance.

**has_cor_struct, has_var_struct, component_ok, component_message** Checks recorded while each curve was fitted.

**n_obs, n_units, converged, singular_or_boundary, fit_ok, publish_ok, model_message** Number of observations and forest units, together with checks used to decide whether the curve was suitable for publication.

## Source

RSYC-Canada model products, version `v20260923`, upstream Git commit `c799aba24b5d99a6a7953a4dcab1dd73b0925c2c`; source RDS SHA-256 `193ebfc1f3279ffc278d84c917d206b4b4bcaeae95f38acf25d9c84a040bd1d5`.

## Examples

```
subset(
  RSYC_models,
  response == "volume" & strata_level == "ecozone" & species == "PICE.MAR"
)
```

---

`rsyc_species` *List Species Available in RSYC Models*

---

## Description

List Species Available in RSYC Models

## Usage

```
rsyc_species(response = NULL, strata_level = NULL, strata_id = NULL)
```

### Arguments

| | |
|---|---|
| response | One or both forest measures: "agb" for aboveground biomass and "volume" for total volume. The default includes both. |
| strata_level | One or more types of area: "tile", "ecozone", "ecoprovince", "ecoregion", or "ecodistrict". The default includes all types. |
| strata_id | One or more tile IDs, ecological area names or paths, or ecological codes. Tile IDs, names, and paths are matched ignoring case. Numeric values and numeric-looking character values are interpreted as codes when no name or path matches. Code searches require exactly one ecological strata_level. Quote ecoprovince codes such as "10.1". Values that match no published curve produce a warning. The default includes all areas. |

### Value

A table giving each species code, common name, and broad model group.

### Examples

```
rsyc_species(response = "agb", strata_level = "ecoregion")
```

---

## rsyc_strata *List Areas Available in RSYC Models*

---

### Description

List Areas Available in RSYC Models

### Usage

```
rsyc_strata(response = NULL, species = NULL, strata_level = NULL)
```

### Arguments

| | |
|---|---|
| response | One or both forest measures: "agb" for aboveground biomass and "volume" for total volume. The default includes both. |
| species | One or more species codes or broad groups. Uppercase and lowercase letters are treated the same. The default includes all species. Unknown species codes produce a warning. |
| strata_level | One or more types of area: "tile", "ecozone", "ecoprovince", "ecoregion", or "ecodistrict". The default includes all types. |

### Value

A table with the short area name (strata_name), its full location within Canada's ecological classification (strata_id), and its canonical character strata_code. Tile rows have NA codes.

## Examples

```
rsyc_strata(
  response = "volume", species = "PICE.MAR", strata_level = "ecozone"
)
```

---

`RSYC_tiles` *RSYC Tile Grid (150 x 150 km)*

---

## Description

A model-aligned GeoPackage containing one polygon or multipolygon for each of the 385 tile IDs used by the v20260923 national RSYC models. The path can be obtained with `system.file("extdata", "RSYC_tiles.gpkg", package = "RSYC")` and read with `sf::st_read()`.

---

`species_codes` *List Available Species Codes and Names*

---

## Description

List the species codes and common names represented in the published RSYC curves. Broad groups are listed first, followed by individual species.

## Usage

```
species_codes(response = NULL, strata_level = NULL)
```

## Arguments

| | |
|---|---|
| `response` | Forest measure to include: `"agb"` for aboveground biomass or `"volume"` for total volume. By default, both are included. |
| `strata_level` | Type of area to include. By default, all types are included. |

## Value

A table with the species code and common name.

## Examples

```
species_codes()
species_codes(response = "volume", strata_level = "ecoregion")
```

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