

# The **texonomy** package\*

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## 1 Introduction

texonomy is an independent L<sup>A</sup>T<sub>E</sub>X package for taxonomic writing. It typesets (plant) taxa in elegant ways. After some simple and natural preparation, one can write taxonomic works without being besieged by font styles, author citation, and genus abbreviation of scientific names — just embrace the scientific names in verticle bar (|, U+7C) pairs, and texonomy will cope with them.

## 2 Defining a taxon

Before a taxon is typeset, it should be defined. The definition of a taxon consists of 4 aspects: rank, local name, scientific name (in Latin), and author citation, in the following format:

$\langle rank \rangle \rightarrow \langle local\ name \rangle \rightarrow \langle scientific\ name \rangle \rightarrow \langle author\ citation \rangle$

In the formula above,  $\langle rank \rangle$  is a macro named by a certain rank in Latin, while  $\langle local\ name \rangle$ ,  $\langle scientific\ name \rangle$ , and  $\langle author\ citation \rangle$  are all token lists to be grabbed as parameters. These components are separated by tabs.

$\langle rank \rangle$  24 ranks based on the *International Code of Nomenclature for algae, fungi, and plants* have been defined as macros, namely, `\regnum`, `\subregnum`, `\phylum`, `\subphylum`, `\classis`, `\subclassis`, `\ordo`, `\subordo`, `\familia`, `\subfamilia`, `\tribus`, `\subtribus`, `\genus`, `\subgenus`, `\sectio`, `\subsectio`, `\series`, `\subseries`, `\species`, `\subspecies`, `\varietas`, `\subvarietas`, `\forma`, and `\subforma`.

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\*Github repository: <https://github.com/Mikumikunisiteageru/texonomy>

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`<local name>` a parameter never typeset unless called by `\zh` (see Section 4) or in non-Latin context (see Section 6). May be left empty or used as comment field.

`<scientific name>` a non-empty parameter able to be fully expanded to unexpanded character tokens. `<scientific name>` of `<rank>` lower than genus should contain more than one word and begin with the genus name. However, `<scientific name>` of a genus or higher rank should be a single word. When the `<rank>` is `\subgenus`, `\sectio`, `\subspecies`, etc., `<scientific name>` should contain `subg.`, `sect.`, `subsp.`, etc., respectively. E.g., `Allium subg. Allium` is a good `<scientific name>`, while `subg. Allium` or `Allium subgenus Allium` is not.

`<author citation>` should not be empty unless taxon is an autonym.

Take garlic as an example: the plant called “garlic” in English is a “species” with scientific name “*Allium sativum*”, whose author is to be cited as “L.”, short for Carolus Linnaeus. To define such a taxon, one should write:

```
\species → garlic → Allium_ sativum → L.
```

where the symbol `→` stands for a tab (U+09), and `_` a space (U+20). Such a definition should occupy a single line *without* comment symbols (by default %), but it can be indented by spaces or tabs.

### 3 Storing Taxon Definitions Outside

When a document involves a large number of taxa, it is suggested to write their definitions in a separate file, and then input into the main source file through `\taxonlist{<file name>}`. This does not only keep the main source neat, but also makes the definition list reusable easily, as the way we store bibliography.

When there are multiple `\taxonlist`’s, files and definitions inside are read in order. If a scientific name is defined for multiple times, only the last time counts.

It is possible to set a common path for files to be input by `\taxonlist` in the rest of the document, through `\taxonlistpath{<path>}`.

### 4 Usage

The typical way to typeset a taxon is to wrap its scientific name in a pair of vertical bars, i.e., `|<scientific name>|`. The author citation of a taxon

occurs only at the first time the taxon is typeset. For taxa lower than genus, their genus part is abbreviated if the last taxon typeset is or belongs to that genus. For example, given

```
\familia → → Amaryllidaceae → J. St.-Hil.
\genus → → Allium → L.
\subgenus → → Allium subg. Allium →
\species → garlic → Allium sativum → L.
```

then the paragraph

```
|Allium| is a genus in |Amaryllidaceae|.
The type species of |Allium| is |Allium sativum|,
in the type subgenus |Allium subg. Allium|.
```

outputs

*Allium* L. is a genus in Amaryllidaceae J. St.-Hil.. The type species of *Allium* is *A. sativum* L., in the type subgenus *A. subg. Allium*.

Tokens wrapped in vertical bars should have been defined literally as scientific name of a taxon. When a pair of vertical bars contains undefined content, the `\content` is typeset in a box to express warning. Note: such warnings will *not* be printed on the console or into the log file.

Apart from using `|\langle scientific name \rangle|` directly, 6 shorthands are defined, including:

`\la|\langle scientific name \rangle|` typesets the scientific name in style according to its rank: `\la|Allium subg. Allium|` outputs *Allium subg. Allium*.

`\au|\langle scientific name \rangle|` typesets the author citation: `\au|Amaryllidaceae|` outputs J. St.-Hil..

`\ge|\langle scientific name \rangle|` typesets the genus part: `\ge|Allium sativum|` outputs *Allium*.

`\ab|\langle scientific name \rangle|` typesets the abbreviated form for taxon lower than genus: `\ab|Allium sativum|` outputs *A. sativum*.

`\fu|\langle scientific name \rangle|` typesets the full form as if typeset for the first time: `\fu|Allium sativum|` outputs *Allium sativum* L..

`\zh|\langle scientific name \rangle|` typesets the local name: `\zh|Allium sativum|` outputs garlic.

## 5 Resetting

For a taxon, `|⟨scientific name⟩|` behaves differently between the first time and the rest of the document. To typeset the full form again, apart from using `\ful⟨scientific name⟩|`, one can also use `\taxonreset[⟨scientific name⟩]` before `|⟨scientific name⟩|` to wipe its presence from the memory. More generally, `\taxonreset` has three usages:

`\taxonreset[⟨scientific name⟩]` resets the memory for a single taxon.

`\taxonreset[⟨scientific name⟩1, ..., ⟨scientific name⟩n]` resets the memory for a list of  $n$  taxa.

`\taxonreset` resets the memory for all taxa.

## 6 Non-Latin Mode

In taxonomic works of some languages, it is preferred to denote a taxon by its local name instead of the scientific name, and the scientific name occurs only at the first time the taxon is mentioned. If so, one should write

```
\usepackage[nonlatin]{texonomy}
```

in the preamble instead of `\usepackage{texonomy}` to load the package in non-Latin mode.

Suppose the non-Latin mode has been on. Given the definitions

```
\familia → 石蒜科 → Amaryllidaceae → J. St.-Hil.
```

```
\genus → 葱属 → Allium → L.
```

```
\species → 蒜 → Allium sativum → L.
```

then the paragraph

```
|Allium| 是 |Amaryllidaceae| 的一个属。
```

```
|Allium| 的模式种为 |Allium sativum|。
```

results in the output

葱属 *Allium* L. 是石蒜科 *Amaryllidaceae* J. St.-Hil. 的一个属。葱属的模式种为蒜 *A. sativum* L.。

## 7 The Predefined Hook

`\tx@hook` is a macro with an argument (`⟨scientific name⟩`) predefined empty. Every time a taxon is typeset (in typical way or by shorthands), the hook macro is executed. This feature may be useful when one wants to make an index with package like glossaries.

## 8 History

**ver. 1.00 (2019.12.25)** First release on Github.

**ver. 1.01 (2019.12.27)** Macro `\tx@expr` rewritten.

## 9 To-do List

- Handle taxa with hybrid sign ( $\times$ ) engine-independently.
- Include my other taxonomic tools (e.g. phylotree drawing) in the package.