

# Package: specio (via r-universe)

August 25, 2024

**Title** Read Spectrum Files

**Version** 0.1.4

**Description** Read data from Spectrum PJNZ file into R consumable format for EPP.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** beers, xml2, yaml

**Remotes** mrc-ide/beers

**Suggests** mockery, testthat, knitr, rmarkdown

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

**Repository** <https://mrc-ide.r-universe.dev>

**RemoteUrl** <https://github.com/mrc-ide/specio>

**RemoteRef** master

**RemoteSha** 11535cf22294071bb6e6b7ed8409823cac2a7ddc

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read_art_pop	<i>Extract ART population data from PJNZ file</i>
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**Description**

Get ART population data separated by year, sex and age. Final age is open ended age group 80+.

**Usage**

```
read_art_pop(pjnz_path, long_format = FALSE)
```

**Arguments**

pjnz_path	Path to PJNZ file to extract the data from.
long_format	If TRUE then data is returned in long format.

**Value**

3D array of ART population data separated by year, sex and age.

**Examples**

```
pjnz_path <- system.file("testdata", "Botswana2017.PJNZ", package = "specio")
art_population <- read_art_pop(pjnz_path)
art_pop_long <- read_art_pop(pjnz_path, TRUE)
```

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read_epp_data	<i>Read EPP fitting surveillance data</i>
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**Description**

Reads the HIV prevalence from sentinel surveillance and household surveillance data from the EPP .xml file within a PJNZ.

**Usage**

```
read_epp_data(pjnz_path)
```

**Arguments**

pjnz_path	Path to Spectrum PJNZ file.
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**Details**

EPP projection sets are identified in the .xml file by searching the XML tree for tag "object", and then selecting objects with "class" attribute equal to "epp2011.core.sets.ProjectionSet".

**Value**

List of data frames containing prevalence and incidence data.

**Examples**

```
pjnz_path <- system.file("testdata", "Botswana2018.PJNZ", package = "specio")
read_epp_data(pjnz_path)
```

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read_epp_subpops	<i>Read EPP subpopulation configuration.</i>
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**Description**

Reads the subpopulation configuration and population sizes from the EPP .xml file within a PJNZ.

**Usage**

```
read_epp_subpops(pjnz_path)
```

**Arguments**

pjnz\_path      file path to Spectrum PJNZ file.

**Details**

EPP projection sets are identified in the .xml file by searching the XML tree for tag "object", and then selecting objects with "class" attribute equal to "epp2011.core.sets.ProjectionSet".

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read_hivproj_param	<i>Read params from DP and PJN file required for HIV model.</i>
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**Description**

Read params from DP and PJN file required for HIV model.

**Usage**

```
read_hivproj_param(pjnz_path)
```

**Arguments**

pjnz\_path      Path to PJNZ zip file containing DP file and PJN file.

**Value**

List of model params.

**Examples**

```
pjnz_path <- system.file("testdata", "Botswana2017.PJNZ", package = "specio")
read_hivproj_param(pjnz_path)
```

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read_hiv_pop	<i>Extract people living with HIV (PLHIV) from PJNZ file</i>
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**Description**

Get HIV population data separated by year, sex and age. Final age is open ended age group 80+.

**Usage**

```
read_hiv_pop(pjnz_path, long_format = FALSE)
```

**Arguments**

pjnz_path	Path to PJNZ file to extract the data from.
long_format	If TRUE then data is returned in long format.

**Value**

3D array of HIV population data separated by year, sex and age.

**Examples**

```
pjnz_path <- system.file("testdata", "Botswana2017.PJNZ", package = "specio")
hiv_population <- read_hiv_pop(pjnz_path)
hiv_pop_long <- read_hiv_pop(pjnz_path, TRUE)
```

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read_pjn_metadata	<i>Get country name, iso3 code and spectrum region code from PJNZ</i>
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**Description**

Get country name, iso3 code and spectrum region code from PJNZ

**Usage**

```
read_pjn_metadata(pjnz)
```

**Arguments**

pjnz	Path to PJNZ file.
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**Value**

The country and region code metadata

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read_spt	<i>Read best fitting HIV incidence and prevalence data from SPT file.</i>
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**Description**

Locates SPT file within the PJNZ file and reads out the best fitting incidence and prevalence data into memory.

**Usage**

```
read_spt(pjnz_path)
```

**Arguments**

`pjnz_path` Path to the PJNZ file.

**Details**

Reads best fitting prevalence and incidence and population data for all regions. The outputs one data frame for each region in the SPT file.

**Value**

List of data frames containing the best fit prevalence and incidence data.

**Examples**

```
pjnz_path <- system.file("testdata", "Botswana2018.PJNZ", package = "specio")
read_spt(pjnz_path)
```

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read_spu	<i>Read EPP uncertainty results from SPU file.</i>
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**Description**

Read EPP uncertainty results from SPU file.

**Usage**

```
read_spu(pjnz_path)
```

**Arguments**

`pjnz_path` Path to the PJNZ file.

**Value**

List containing uncertainty results for prevalence and incidence

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read_total_pop	<i>Extract population data from PJNZ file</i>
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**Description**

Get population data separated by year, sex and age. Final age is open ended age group 80+.

**Usage**

```
read_total_pop(pjnz_path, long_format = FALSE)
```

**Arguments**

pjnz_path	Path to PJNZ file to extract the data from.
long_format	If TRUE then data is returned in long format.

**Value**

3D array of population data separated by year, sex and age.

**Examples**

```
pjnz_path <- system.file("testdata", "Botswana2017.PJNZ", package = "specio")  
population <- read_total_pop(pjnz_path)  
pop_long <- read_total_pop(pjnz_path, TRUE)
```

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