# Package: PTBinteRface (via r-universe)

May 9, 2026

**Title** Interface to the paratuberculosis model contained in the PTBinraeR package

**Version** 0.2.2-1

**Date** 2026-03-10

**Description** This is a wrapper package for INRAE's PTB model. The model can be run using the run_ptb_model function. See the vignette for more information.

**License** GPL (>= 3)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Additional_repositories** https://ku-awdc.github.io/drat/

**Depends** R (>= 4.1.0)

**LinkingTo** Rcpp, PTBinraeR (>= 0.2.0)

**Imports** methods, PTBinraeR, Rcpp, readr, rlang

**Suggests** knitr, spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**Language** en-GB

**SystemRequirements** C++20

**Repository** https://ku-awdc.r-universe.dev

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**RemoteUrl** https://github.com/ku-awdc/PTBinteRface

**RemoteRef** v0.2.2

**RemoteSha** 94e9ca22b96d5393d1a26780e3a0af6b0812a35a

## Contents

`run_ptb_model` *Wrapper function to run the Para TB model*

## Description

This is a wrapper for the INRAE PTB model. Note that (currently) this is a very thin wrapper; all RNG are C++ i.e. set.seed will have no effect. Also there is no checking for interrupt signals...

## Usage

```
run_ptb_model(
  runsNb = 1L,
  calfExposure = 1,
  cullingRateIh = 1/26,
  testSensitivityItIl = 0.15,
  testSensitivityIm = 0.47,
  testSensitivityIh = 0.71,
  testSpecificity = 1,
  startGrazing = 14L,
  endGrazing = 46L,
  ageAtWeaning = 10L,
  ageAtGrazing = 26L,
  ageYoungHeifer = 52L,
  ageHeifer = 91L,
  ageAtFirstCalving = 130L,
  noInfection = FALSE,
  InitialInfection = PTBinraeR::InitialInfection,
  BirthFemaleEvents = PTBinraeR::BirthFemaleEvents,
  CullingRates = PTBinraeR::CullingRates,
  Headcounts = PTBinraeR::Headcounts,
  Network = PTBinraeR::Network,
  seed = sample(.Machine$integer.max, 1)
)
```

## Arguments

| | |
|---|---|
| `runsNb` | number of repetitions (default=1L) |
| `calfExposure` | calf rearing improvement is defined as a reduced exposure to the general environment by varying parameter from 1.0 to 0.35 (default=1.0) |
| `cullingRateIh` | culling rate of detected Ih animals (default=1.0/26.0) |
| `testSensitivityItIl` | test sensitivity of low positive animals. (default=0.15) |
| `testSensitivityIm` | test sensitivity of moderately positive animals. (default=0.47) |
| `testSensitivityIh` | test sensitivity of highly positive animals. (default=0.71) |

`testSpecificity`
: test specificity. (default=1.0)

`startGrazing`
: Grazing start week (from 0 to 51, default=14L, beginning of April)

`endGrazing`
: Grazing end week (from 0 to 51, default=46L, mid November)

`ageAtWeaning`
: From this age, in terms of number of weeks, the animal is weaned (default=10L)

`ageAtGrazing`
: From this age, in terms of number of weeks, the animal can go outside during grazing period (default=26L)

`ageYoungHeifer`
: From this age, in terms of number of weeks, the animal is considered to be a young heifer (default=52L, one year old)

`ageHeifer`
: From this age, in terms of number of weeks, the animal is considered to be a heifer, starts reproduction (default=91L)

`ageAtFirstCalving`
: From this age, in terms of number of weeks, the animal is considered to be a cow, calves for the first time (default=130L)

`noInfection`
: all herds will be initialized without infected animals, so no PTB spread (default=FALSE)

`InitialInfection`
: if not empty, then load initial 'infection' from this DF/tibble: 1 line = 1 infected herd with id, nbInfectedAnimals, prevalence and repetitionNum refering to a line in 'initCondFileName' (tibble/DF, default=0 rows)

`BirthFemaleEvents`
: a tibble/DF - see ?BirthFemaleEvents

`CullingRates`
: a tibble/DF - see ?CullingRates

`Headcounts`
: a tibble/DF - see ?Headcounts

`Network`
: a tibble/DF - see ?Network

`seed`
: the random number seed to use

## Value

a list of tibbles corresponding to the files output by the model

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