Package: autotracer (via r-universe)

September 12, 2024

Title Probabilistically Identify Clusters in Electronic Medical Records

Version 0.0.1

Description What the package does (one paragraph).

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Imports outbreaker2, data.table, epitrix, distcrete

Depends R (>= 2.10)

Repository https://medewitt.r-universe.dev

RemoteUrl https://github.com/conedatascience/autotracer

RemoteRef HEAD

RemoteSha 5fccabd4b9f663a3a8f5113f5fa25067159d2ca7

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`autotracer_linelist` *Simulated Patient Data Synthetic data that can be used to explore "autotracer"*

Description

Simulated Patient Data Synthetic data that can be used to explore "autotracer"

Usage

```
autotracer_linelist
```

Format

a data.frame with 10500 rows and 9 columns:

x Latitude

y Longitude

Race Race indentifier

patient_id Unique patient indentifier (e.g. MRN)

Age Age of the patient in years

Sex Biological sex of the patient

Language Primary spoken language of the patient

Age10 Age given as a ten year age group

date Date of test or infection identification

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connect_probable_cases

Connect Probable Cases

Description

Probabilistically estimates a likely tranmission chain using EMR derrived data.

Usage

```
connect_probable_cases(
  dat,
  weights_in = NULL,
  threshold = 30,
  exposure_link = NULL
)
```

Arguments

dat	the dataframe of likely connect cases with a column named "date" indicating the onset or positive test date and "patient_id", a unique identifier for the record.
weights_in	the weights to use for the serial interval if available
threshold	integer, the threshold in days at which to discard a connected case (e.g. >30 days from previous case, then discard).
exposure_link	string or column name, how these cases are connected

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