As an R package developer, it is important to document functions in a way that aligns with **CRAN** standards (similar to R Oxygen2 documentation) while providing a "Vignette-style" explanation for the end user.

The following documentation is structured as a technical manual for the swimmerplot function and the associated dataset.

Package Documentation: Clinical Swimmer Plots

1. Introduction

The swimmerplot function is designed to visualize individual patient histories in observational studies. It is particularly useful for survival analysis where researchers need to see the timing of an intervention (e.g., surgery) relative to both the start of the study and the patient's birth.

2. Dataset: survdat

The package includes a sample dataset containing 30 patients. This data is derived from the tutorial by Bull and Spiegelhalter (1997).

Variable Descriptions

- **patient**: Unique integer ID for each subject.
- **agepres**: Age at presentation (in days).
- **ageop1**: Age at first operation (in days). NA if no operation occurred.
- **agelast**: Age at death or last follow-up (in days).
- **dead**: Binary indicator (1 = dead, 0 = censored/alive).
- **paanat**: Size of pulmonary arteries at presentation (0 = tiny, 1 = normal).

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3. Function Reference: swimmerplot()

Usage

R

```
swimmerplot(.id, .events, .pre, .dead, data, scaling=TRUE, .sz=TRUE, ...)
```

Arguments

Parameter	Description
.id	Column name for patient identifiers.

Parameter	Description
.events	A character vector of length 3: c("Start", "Intervention", "End").
.pre	Column name for the baseline condition (determines the shape of the entry point).
.dead	Column name for the survival status (binary).
data	The data frame containing the variables.
scaling	Logical. If TRUE, applies a non-linear transform to the X-axis to emphasize early events.
.sz	Logical. If TRUE, "sets to zero" by subtracting the presentation age (plots time since study entry).

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4. Technical Implementation Details

The Scaling Algorithm (scaleX)

In clinical studies, many events (like operations) occur shortly after presentation. A linear scale often masks these details. This function implements a piecewise linear transformation:

- **0 to 2 years:** Occupies the first 50% of the plot area.
- **2 to 18 years:** Occupies the remaining 50%.

$$f(x) = \begin{cases} 0.5 \cdot \frac{x}{2 \cdot 365.24} & x < 2 \text{ yrs} \\ 0.5 + 0.5 \cdot \frac{x - (2 \cdot 365.24)}{18 \cdot 365.24} & x \geq 2 \text{ yrs} \end{cases}$$

Visual Mapping

The function uses specific graphical parameters to represent clinical status:

- **Line Type (lty)**:
    - Solid (1): Observation period before the intervention.
    - Dashed (4): Observation period after the intervention.
- **Point Symbols (pch)**:
    - Diamond (5/18): Presentation (Open = Artery size 0, Filled = Artery size 1).
    - Open Circle (1): Surgical intervention.
    - Cross (3): Terminal event (Death).

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5. Examples

Figure 1: Timeline from Birth

This view is essential for understanding the natural history of a disease relative to the patient's biological age.

R

```
swimmerplot(.id="patient", .events=c("agepres", "ageop1", "agelast"),
               .pre="paanat", .dead="dead", data=survdat, .sz=FALSE,
               xlab="Age in years", main="Histories from Birth")
```

Figure 2: Timeline from Presentation

This view aligns all patients at $T=0$, making it easy to compare the efficacy of treatment and duration of survival post-diagnosis.

R

```
swimmerplot(.id="patient", .events=c("agepres", "ageop1", "agelast"),
               .pre="paanat", .dead="dead", data=survdat, .sz=TRUE,
               xlab="Years after presentation", main="Histories from Presentation")
```

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6. Author and Credits

- **Original Biostatistics Tutorial**: Bull K, Spiegelhalter DJ (1997).
- **R Implementation**: Minato Nakazawa (Kobe University).
- **Documentation**: Built for R package structure.

Would you like me to help you convert this into a formal .Rd file (R Documentation) for inclusion in a package folder?