

# StationLengthDist

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StationLengthDist	<i>Station length distribution</i>
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## Description

This function calculates length frequency distribution per SpecCat per serialnumber, either given as percentages, or as counts, possibly normalized by towing distance.

## Usage

```
StationLengthDist(BioticData, LengthDistType = "PercentLengthDist",  
  allowMissingWeight = TRUE, fishstationName = "fishstation",  
  catchsampleName = "catchsample", individualName = "individual", ...)
```

## Arguments

BioticData	The BioticData input, which is a list of data.tables as returned from <a href="#">ReadBioticXML</a> .
LengthDistType	The type of length distribution to use, one of "LengthDist", "NormLengthDist" and "PercentLengthDist" (see 'Details').
allowMissingWeight	Logical: If TRUE and LengthDistType == "PercentLengthDist" accept stations with missing pairs of lengthsampleweight and (total) weight or lengthsample-catch and (total) catch.
fishstationName	The name of the fishstation table in the list BioticData.
catchsampleName	The name of the catchsample table in the list BioticData.
individualName	The name of the individual table in the list BioticData.

## Details

The purpose of function StationLengthDist is to produce a length frequency distribution for each biotic station by species. Three different distributions (LengthDistType) can be generated:

## Value

A data.table is returned with awesome stuff.

**See Also**

StationLengthDist is called by [getBaseline](#).

**Examples**

```
library(Rstox)
# Read biotic data:
dat <- getBaseline("Test_Rstox", input=FALSE, proc="ReadBioticXML", endProcess="ReadBioticXML")
# Convert to data.table, since the current Rstox uses data.frames:
dat <- lapply(dat, data.table::as.data.table)
# Generate the station length distribution using the data.frame names of the current Rstox:
SLD <- StationLengthDist(dat,
  fishstationName = "ReadBioticXML_BioticData_fishstation.txt",
  catchsampleName = "ReadBioticXML_BioticData_catchsample.txt",
  individualName = "ReadBioticXML_BioticData_individual.txt")
str(SLD)
```