Package ‘HTSeedGLM’

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Type Package

Title Hydro Thermal Time Analysis of Seed Germination Using Generalised Linear Model

Description Seed germinates through the physical process of water uptake by dry seed driven by the difference in water potential between the seed and the water. There exists seed-to-seed variability in the base seed water potential. Hence, there is a need for a distribution such that a viable seed with its base seed water potential germinates if and only if the soil water potential is more than the base seed water potential. This package estimates the stress tolerance and uniformity parameters of the seed lot for germination under various temperatures by using the hydro-time model of counts of germinated seeds under various water potentials. The distribution of base seed water potential has been considered to follow Normal, Logistic and Extreme value distribution. The estimated proportion of germinated seeds along with the estimates of stress and uniformity parameters are obtained using a generalised linear model. The significance test of the above parameters for within and between temperatures is also performed in the analysis. Details can be found in Kebreab and Murdoch (1999) <doi:10.1093/jxb/50.334.655> and Bradford (2002) <`https://www.jstor.org/stable/4046371`>.

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Imports stats

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License GPL-3

NeedsCompilation no

RoxygenNote 7.3.2

Repository CRAN

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Contents

`BaseWPDist` *Distribution of base seed water potential*

Description

This function provides the estimates of stress and uniformity parameters along with respective variances using generalised linear model fitted to observed germination percentage of seed. The model can be fitted under logit, probit and cloglog transformations.

Usage

```
BaseWPDist(model)
```

Arguments

`model`	Fitted model

Value

- Degrees of freedom
- p_value: For testing significance of water potential
- stress: Location parameter of the base seed water potential
- uniformity: Scale parameter of the base seed water potential
- var_stress: Variance of estimator of the location parameter
- var_uniformity: Variance of estimator of the scale parameter

References

- Bradford, K. J. (2002). Applications of Hydrothermal Time to Quantifying and Modeling Seed Germination and Dormancy. Weed Science, 50(2), 248–260. http://www.jstor.org/stable/4046371
- Kebreab, E., & Murdoch, A. J. (1999). Modelling the effects of water stress and temperature on germination rate of Orobanche aegyptiaca seeds. Journal of Experimental Botany, 50(334), 655-664. doi:10.1093/jxb/50.334.655
- Dobson, A. J., & Barnett, A. G. (2018). An introduction to generalized linear models. Chapman and Hall/CRC.

Examples

```
X <- c(0,-0.3,-0.6,-0.9) # Various water potentials
y <- c(44,10,10,4) # Number of germinated seeds
n <- c(100,100,100,100) # Total number of viable seeds
n_y <- n-y
sg.mat <- cbind(y,n_y)
res.glm1 <- glm(sg.mat~ X,family=binomial(link=logit)) # Using logit transformation
my.bdl<- BaseWPDist(res.glm1)
res.glm2 <- glm(sg.mat~ X,family=binomial(link=probit)) # Using probit transformation
my.bdp<- BaseWPDist(res.glm2)
res.glm3 <- glm(sg.mat~ X,family=binomial(link=cloglog))# Using cloglog transformation
my.bdcl<- BaseWPDist(res.glm3)
```

`FStat` *F-test between two fitted models*

Description

This function considers two fitted models as inputs. Considering the first model as full model, it performs testing equality of uniformity parameters representing the model under null hypothesis and provides the p-value and degrees of freedom of the test statistic.

Usage

```
FStat(model1, model2)
```

Arguments

`model1`	First fitted model
`model2`	Second fitted model

Value

- Degrees of freedom and p-value

References

- Bradford, K. J. (2002). Applications of Hydrothermal Time to Quantifying and Modeling Seed Germination and Dormancy. Weed Science, 50(2), 248–260. http://www.jstor.org/stable/4046371
- Kebreab, E., & Murdoch, A. J. (1999). Modelling the effects of water stress and temperature on germination rate of Orobanche aegyptiaca seeds. Journal of Experimental Botany, 50(334), 655-664. doi:10.1093/jxb/50.334.655
- Dobson, A. J., & Barnett, A. G. (2018). An introduction to generalized linear models. Chapman and Hall/CRC.

Examples

```
data1 <- data.frame(cbind(sg = c(rep(1, 95), rep(0, 5), rep(1, 87), rep(0, 13),
rep(1, 80), rep(0, 20), rep(1, 59), rep(0, 41),
rep(1, 50), rep(0, 50), rep(1, 79), rep(0, 21),
rep(1, 69), rep(0, 31), rep(1, 72), rep(0, 28),
rep(1, 44), rep(0, 56), rep(1, 14), rep(0, 86)),
v1 = c(rep(1, 500), rep(0, 500)),
v2 = c(rep(0, 500), rep(1, 500)),
wp1 = c(rep(0, 100), rep(-0.3, 100), rep(-0.6, 100),
       rep(-0.9, 100), rep(-1.2, 100), rep(0, 500)),
wp2 = c(rep(0, 600), rep(-0.3, 100), rep(-0.6, 100),
       rep(-0.9, 100), rep(-1.2, 100))))
data2 <- data.frame(cbind(sg = c(rep(1, 95), rep(0, 5), rep(1, 87), rep(0, 13),
rep(1, 80), rep(0, 20), rep(1, 59), rep(0, 41),
rep(1, 50), rep(0, 50), rep(1, 79), rep(0, 21),
rep(1, 69), rep(0, 31), rep(1, 72), rep(0, 28),
rep(1, 44), rep(0, 56), rep(1, 14), rep(0, 86)),
v1 = c(rep(1, 500), rep(0, 500)),
v2 = c(rep(0, 500), rep(1, 500)),
wp = c(rep(0, 100), rep(-0.3, 100), rep(-0.6, 100),
      rep(-0.9, 100), rep(-1.2, 100), rep(0, 100),
      rep(-0.3, 100), rep(-0.6, 100), rep(-0.9, 100),
      rep(-1.2, 100))))
myprobit1 <- glm(sg ~ v1 + v2 + wp1 + wp2 - 1, data = data1, family = binomial(link = probit))
myprobit2 <- glm(sg ~ v1 + v2 + wp - 1, data = data2,
family = binomial(link = probit))
my.f<- FStat(myprobit1, myprobit2)
```

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