

SUPPLEMENTARY MATERIAL No.1

HaviStat© v2.2: Application to estimate preference for habitat and resources

HaviStat© v2.2

How to download the software:

- **First option**

1. Access the web page:

<http://miseryukyu.com/MISE%40University_of_the_Ryukyus/Data_sets.html>

2. Click the link indicated by the arrow to download program.

- **Second option**

Directly access the below download link:

http://miseryukyu.com/MISE%40University_of_the_Ryukyus/Data_sets_files/Havistat%20v2,2.zip

- **Third option**

Please send an e-mail to haviStat@gmail.com requesting a copy of the program.



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Zoanthid literature

DATA SETS & SOFTWARE

DNA Alignments
Field Image Archives
Videos

updated 2014.7

HaviStat v2.2 from Montenegro et al. (in review). Free to download in zip format.
Havistat v2,2.zip

Please reference: JA Montenegro, A Acosta, JD Reimer. 2014. HaviStat© v2.2: Application to estimated animal preference for habitat and resources. Universitas Scientiarum (in review).

HaviStat v1.0 from Montenegro & Acosta (2008). Free to download in zip format.
Havistat v1,0.zip

Please reference: JA Montenegro, A Acosta. 2008. HaviStat© v 1.0 Aplicación para evaluar uso y preferencia de hábitat. Pan-American Journal of Aquatic Sciences 3(2): II-IV.

Video presentation for the World Conference of Marine Biodiversity (2011.9, Aberdeen, Scotland).

DNA sequence alignment sets

Click on the different alignment sets below to automatically download them in nexus (.nex) format. Other alignments from our various papers are also available upon request for zoanthids, octocorals, and zooxanthellae (*Symbiodinium*). Please reference the corresponding paper.

Reimer et al. 2012, Contributions to Zoology (note: in fasta format)

1. Brachynermima zoanthid ITS ribosomal DNA alignment.
[SphenolTSv1good.fasta](#)
2. Brachynermima zoanthid 16S ribosomal DNA alignment.
[Sphenopus16Sv2good.fasta](#)