# clustur: An R package for clustering features using sparse distances matrices

**Running title:** clustur

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**Software Announcement**

## Abstract (needs to be under 50 words)

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## Announcement (needs to be around 500 words, currently 595)

* Problem definition
  + Taxonomic classification of 16S rRNA gene sequences is not great
  + Methods have been developed for de novo clustering of sequences
  + Heuristic methods that have been developed
  + Methods have been developed for reference-based clustering of sequences
  + These are available within mothur
* What does clustur do to solve problem
  + Package bundles together mothur’s functionality
  + Hopes to help spurn further innovation in clustering by making functions accessible via R
  + Will make functionality available to other types of analysis beyond 16S rRNA gene sequences
* Design of clustur
  + Makes use of Rcpp
* How to install and use clustur
  + Users can install via CRAN or through the devtools package’s install\_github function
  + Users provide different inputs depending on desired function, output is a long shared file with columns indicating the sample, OTU, and count

(1–7)

## Data availability

clustur is available through CRAN and developmental versions are available through the project’s GitHub website (https://github.com/schlosslab/clustur). The package is available under the MIT open source license.

## Acknowledgements

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## References

1. **Schloss PD**, **Handelsman J**. 2005. Introducing DOTUR, a computer program for defining operational taxonomic units and estimating species richness. Applied and Environmental Microbiology **71**:1501–1506. doi:[10.1128/aem.71.3.1501-1506.2005](https://doi.org/10.1128/aem.71.3.1501-1506.2005).

2. **Schloss PD**, **Westcott SL**, **Ryabin T**, **Hall JR**, **Hartmann M**, **Hollister EB**, **Lesniewski RA**, **Oakley BB**, **Parks DH**, **Robinson CJ**, **Sahl JW**, **Stres B**, **Thallinger GG**, **Van Horn DJ**, **Weber CF**. 2009. Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. Applied and Environmental Microbiology **75**:7537–7541. doi:[10.1128/aem.01541-09](https://doi.org/10.1128/aem.01541-09).

3. **Schloss PD**, **Westcott SL**. 2011. Assessing and improving methods used in operational taxonomic unit-based approaches for 16S rRNA gene sequence analysis. Applied and Environmental Microbiology **77**:3219–3226. doi:[10.1128/aem.02810-10](https://doi.org/10.1128/aem.02810-10).

4. **Schloss PD**. 2016. Application of a database-independent approach to assess the quality of operational taxonomic unit picking methods. mSystems **1**. doi:[10.1128/msystems.00027-16](https://doi.org/10.1128/msystems.00027-16).

5. **Sovacool KL**, **Westcott SL**, **Mumphrey MB**, **Dotson GA**, **Schloss PD**. 2022. OptiFit: An improved method for fitting amplicon sequences to existing OTUs. mSphere **7**. doi:[10.1128/msphere.00916-21](https://doi.org/10.1128/msphere.00916-21).

6. **Westcott SL**, **Schloss PD**. 2015. De novo clustering methods outperform reference-based methods for assigning 16S rRNA gene sequences to operational taxonomic units. PeerJ **3**:e1487. doi:[10.7717/peerj.1487](https://doi.org/10.7717/peerj.1487).

7. **Westcott SL**, **Schloss PD**. 2017. OptiClust, an improved method for assigning amplicon-based sequence data to operational taxonomic units. mSphere **2**. doi:[10.1128/mspheredirect.00073-17](https://doi.org/10.1128/mspheredirect.00073-17).