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## Dear CCGP PIs and Team Members,

We are excited to announce that we have officially released the R package that we built for the CCGP landscape genomic analysis pipeline! Our goal in designing this package, [\*alga\*](#) ([A Landscape Genomic Analysis Toolkit in R](#)), was to provide an open-access, user-friendly toolkit that includes functions for performing a curated set of core landscape genomics methods on individual-based sampling, tools for generating publication-ready figures from those analysis, and utilities for processing spatial and genomic data.

### Where to find *alga*:

The *alga* package is available for download from [our GitHub repository](#), and our [publication describing \*alga\*](#) is now available from Molecular Ecology Resources. The package also has a [website](#) that displays all the knitted vignettes if you'd like to read through them. To make the *alga* package as accessible as possible, we have also included a series of vignettes and detailed documentation for each analysis.

### Need help?

We have performed a series of validations on all components of the package using a variety of tests, simulations, and preliminary CCGP datasets. We don't anticipate that there are any substantial unknown errors with the package, but there may still be some bugs we haven't discovered. Please reach out to us if you encounter any issues or unexpected behavior from any of the analyses included in the package.

We will not be generating *alga* reports for each of the CCGP projects because of computational limitations and because some analytical decisions should be made specific to each study system. By including detailed walkthroughs and extensive documentation for all of the methods in the package, we believe you should be able to run these analyses for your datasets on your own computer systems even if you haven't worked with these methods previously. We are, of course, happy to respond to any issues that arise with *alga*'s usage for CCGP projects if answers can't be found in the package documentation (you can either submit an issue on GitHub or email [Anne Chambers](#)). We will also be scheduling a limited number of "office hours" on Zoom during which anyone can drop in to ask questions about the package.

### Note for additional or non-CCGP help

If you would like further support in running *alga* on your datasets - for example, if you would like one of us to perform a complete analysis of your data through our pipeline or if you would like to discuss whether we can tailor *alga* to your specific research goals - feel free to reach out to us. In these cases, we would likely request that Anne Chambers or Anusha Bishop, the co-lead authors on the package, be included as a co-author on any resulting publications, given the substantial time commitment and expertise that these activities would require.

We hope that *alga* proves valuable for the overall CCGP and each of your individual projects, and we look forward to hearing from you!

Best Regards,

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**California Conservation Genomics Project**

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