
radcap documentation

Release 1.0.0

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Release v1.0.0. (*Changelog*)

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[radcap](#) is a software package that was developed for analyzing data collected from RADseq loci using the RADcap approach (see [Hoffberg et al. 2016](#) and [References](#) for additional information).

CHAPTER 1

Contributions

`radcap` is open-source (see [License](#)) and we welcome contributions from anyone who is interested. Please make a pull request on [github](#). The issue tracker for `radcap` is also available on [github](#).

CHAPTER 2

Issues

If you have an issue, please ensure that you are experiencing this issue on a supported OS (see *Installation*) using the `conda` installation of `radcap`. If possible, please submit a test case demonstrating the issue and indicate which platform and the git checkout and/or `radcap` version you are using.

3.1 Purpose

3.1.1 Who wrote this?

This documentation was written primarily by Brant Faircloth (<http://faircloth-lab.org>). Brant is also responsible for the development of most of the `radcap` code. Bugs within the code are usually his.

You can find additional authors and contributors in the *Attributions* section.

3.1.2 How do I report bugs?

To report a bug, please post an issue to <https://github.com/faircloth-lab/radcap/issues>. Please also ensure that you are using one of the “supported” platforms:

- Apple OSX 10.9.x
- CentOS 6.x
- Ubuntu 14.04 LTS

and that you have installed `radcap` and dependencies using `conda` as described in the *Installation* section.

3.2 Installation

More soon.

4.1 Citing

If you use the `radcap` code in any form, please cite the following manuscript (which is “in review”):

Please also cite the github repository:

4.1.1 References

4.2 License

4.2.1 Documentation

The documentation for `radcap` is available under a [CC-BY \(2.0\)](#) license. This license gives you permission to copy, distribute, and transmit the work as well as to adapt the work or use this work for commercial purposes, under the condition that you must attribute the work to the author(s).

If you use this documentation or the `radcap` software for your own research, please cite both the software and [Hoffberg et al. 2016](#). See the Citing section for more detail.

4.2.2 Software

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4.3 Changelog

4.3.1 v1.0 (April 2016)

- initial release

4.4 Attributions

A number of people have worked on different aspects of the radcap approach, including creating the laboratory methods to collect the data and the computational methods to analyze the data. Below, we have identified a list of approximately which people/groups did what.

4.4.1 Wrote the code

- [Brant Faircloth](#) (brant at faircloth-lab dot org)

4.4.2 Contributed to the code

- Sandra Hoffberg
- Travis Glenn

4.5 Funding

4.5.1 Primary Sources

The [National Science Foundation \(NSF\)](#) has supported a large portion of our work. The specific programs and proposal identifiers are below:

- NSF DEB-1242260
- NSF DEB-1146440
- NSF PIRE OISE-0730218

4.5.2 Secondary Sources

We have also received funding for computational support from and/or materials from the following organizations:

- MYcroarray
- IDTDNA

4.6 Acknowledgements

We thank the following people, each of whom made contributions ensuring the success of our work. These include:

- Todd Pierson
- Kerin Bentley
- Natalia Bayona

Bibliography

- [SH2016] Hoffberg S, Kieran TJ, Catchen JM, Devault A, Faircloth BC, Mauricio R, Glenn RC. 2016. Adapterama IV: Sequence Capture of Dual-digest RADseq Libraries with Identifiable Duplicates (RADcap). bioRxiv. doi:10.1101/044651.
- [BCF2016] Faircloth BC. RADcap software. <https://github.com/faircloth-lab/radcap>.