
mgatk Documentation

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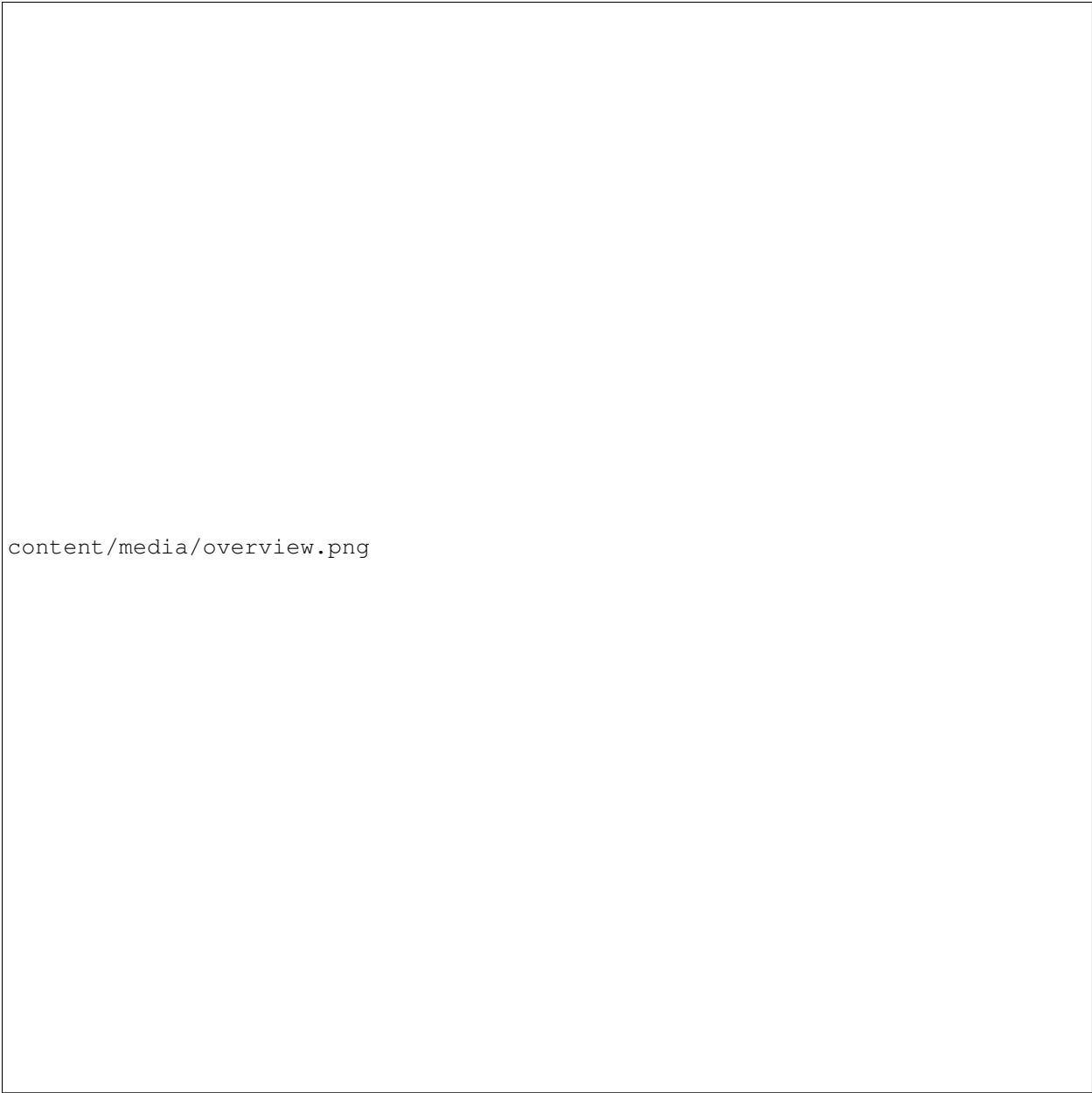
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CHAPTER 1

About

mgatk is a blah blah blah

content/media/overview.png



CHAPTER 2

Installation

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Annotating peaks

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FAQ

Single end reads?

In the current implementation, **proatac** only supports paired-end reads. There's some support on [Biostars](#) that explains what one should do given single-end sequencing data.

I found a bug / error; what do I do?

Please let us know if you find any errors/inconsistencies in the documentation or code by filing a new [GitHub Issue](#).

I ran proatac; now what do I do?

A non-exhaustive list of ideas / resources includes:

- Perform nucleosome calling with [NucleoATAC](#)
- Identify variable transcription factors using [chromVAR](#)
- Compare peaks called from **proatac** to existing datasets. [CistromeDB](#) is a particularly useful resource for this.

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Author

The primary developer is Caleb Lareau in the *Aryee Lab* <<http://aryeelab.org>> and the Buenrostro Lab.

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Citation

If you use **proatac** in your research, please cite our tool at the following URL:

<http://aryeelab.org/mgatk>

CHAPTER 10

Bugs / Errors

Please let us know if you find any errors/inconsistencies in the documentation or code by filing a new [GitHub Issue](#).