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| **FastQC Report Generator** |

FastQC Report Generator is a lightweight command-line tool for creating report files and visualisations from FastQC text files.

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| **System Requirements** |

* Python 3.4+ is required to run FastQC Report Generator.
* FastQC Report Generator requires the following scientific libraries: **Matplotlib**, **Seaborn**, **NumPy**, **Pandas**, **SciPy**, which can be installed using pip or conda.

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| **Installation** |

FastQC Report Generator does not require an installation procedure, simply open the terminal in Linux / MacOS or the Command Prompt in Windows, navigate to the fastqc\_report directory and run fastqc\_report.py (see below) using Python from the command-line.

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| **Usage** |

To generate reports for specific FastQC modules (e.g., *Per base sequence quality* (module 2) and *K-mer Content* (module 12) parsed from an input file (fastqc.txt) in output directory (outdir), type the following in the command-line:

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| python fastqc\_report.py fastqc.txt outdir m2 m12 m1 |

To generate reports and graphs for **all** modules, type:

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| python fastqc\_report.py fastqc.txt outdir m1 -all |

Alternatively, all reports can be generated in the Python console by typing:

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| runfile(“fastqc\_report.py”, args=”fastqc.txt outdir m1 -all”) |

For additional help, add the **–h** or **--help** flag:

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| python fastqc\_report.py -h |