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supercells 0.0.4

pip install supercells

Copy PIP instructions

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Released: Jun 20, 2023

Easily assess quality control data across multiple single cell datasets

Navigation

- [Project description](#)
- [Release history](#)
- [Download files](#)

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- [Homepage](#)

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Meta

License: BSD License

Author: [Compugen LTD](#)

Requires: Python >=3.7

Maintainers



[royg_cgen](#)

Classifiers

- License**
 - [OSI Approved :: BSD License](#)
 - Operating System**
 - [OS Independent](#)
 - Programming Language**
 - [Python :: 3](#)
- [Project description](#)
 - [Project details](#)
 - [Release history](#)
 - [Download files](#)

Project description



Easily assess **quality control data across multiple single cell datasets**

Supercells is a tool which generates a single report for multiple 10x cellranger samples - thus saving time and allowing comparative QC analysis.

It is written in Python (tested with v3.7-3.9).

code style

black

pypi

v0.0.4

Follow

Installation

Using PyPI:

```
pip install supercells
```

Clone or download the repository and navigate to the package directory, then invoke:

```
pip install .
```

Usage

Once supercells is installed it is run by invoking:

```
supercells -i <experiment folder>
```

Unless specified otherwise it will generate `supercells_report.html` within the input folder as well as `supercells_report` folder containing summarizing `xlsx` file and `CSV` with the raw data. To specify an output directory use the `-o <output folder>` flag

	Sample1	Sample2	Sample3
Estimated Number of Cells	16491	16475	21597
Mean Reads per Cell	27578	27093	22567
Median Genes per Cell	1987	1976	1447
Number of Reads	4.55E+08	4.46E+08	4.87E+08
Valid Barcodes	84.00%	84.70%	87.10%
Sequencing Saturation	36.10%	35.90%	52.50%
Q30 Bases in Barcode	91.80%	91.30%	92.00%
Q30 Bases in RNA Read	87.30%	89.30%	89.20%
Q30 Bases in UMI	91.90%	91.90%	92.00%
Reads Mapped to Genome	84.00%	82.20%	88.10%
Reads Mapped Confidently to Genome	76.00%	74.50%	81.30%
Reads Mapped Confidently to Intergenic Regions	15.30%	13.90%	11.10%
Reads Mapped Confidently to Intronic Regions	9.90%	9.70%	16.60%
Reads Mapped Confidently to Exonic Regions	50.80%	50.90%	53.70%
Reads Mapped Confidently to Transcriptome	51.40%	51.60%	59.50%
Reads Mapped Antisense to Gene	9.10%	8.80%	10.30%
Fraction Reads in Cells	90.40%	90.40%	86.70%
Total Genes Detected	24464	24407	24046
Median UMI Counts per Cell	5524	5483	3651

Further development

Suggestions for additional features and code contributions are welcomed

Project details

Project links

- [Homepage](#)

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- Forks:**
- Open issues:**
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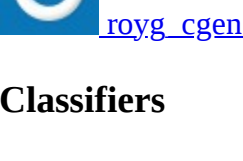
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Release history [Release notifications](#) | [RSS feed](#)

This version



[0.0.4](#)

[Jun 20, 2023](#)



[0.0.3](#)

[Mar 1, 2023](#)



[0.0.2](#)

[Sep 1, 2022](#)



[0.0.1](#)

[Jul 27, 2021](#)

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Source Distributions

No source distribution files available for this release.See tutorial on [generating distribution archives](#).

Built Distribution

[supercells-0.0.4-py3-none-any.whl](#) (11.1 kB [view hashes](#))

Uploaded Jun 20, 2023 py3

[Close](#)

Hashes for supercells-0.0.4-py3-none-any.whl

Hashes for supercells-0.0.4-py3-none-any.whl	
Algorithm	Hash digest
SHA256	320d66ad221f3ed423a75177ef459fd0a1ba617dae724a4e6b2d0af7e65094ca Copy
MD5	f73f6583967475ac59353deb2d08945c Copy
BLAKE2b-256	8a4cc994c479732f06a58c77286e22578d1c1e934f10ba8d53458cd06f4e472a Copy

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- [Uploading packages](#)
- [User guide](#)
- [Project name retention](#)
- [FAQs](#)

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Status: [all systems operational](#)

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