BaseTools License agreement

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1. Software

The available BaseTools are:

SSPACE (standard) SSPACE-LongRead GapFiller

For each BaseTool the Software is defined as the main perl script and the related documentation.

For SSPACE (standard) the main perl script is: SSPACE_[version].pl

For SSPACE (LongRead) the main perl script is: SSPACE-LongRead_[version].pl

For GapFiller the main perl script is: GapFiller_[version].pl

2. Authors

The Authors of the Software are Marten Boetzer and Walter Pirovano.

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SSPACE (standard):

Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W (2011), Scaffolding pre-assembled contigs using SSPACE, Bioinformatics, 27(4):578-9.

SSPACE-LongRead:

Boetzer M, Pirovano W (2014), SSPACE-LongRead: Finishing bacterial draft genomes using long read sequence information, submitted for publication.

GapFiller:

Boetzer M, Pirovano W (2012), Toward almost closed genomes with GapFiller, Genome Biology, 13(6).

7. Third party Software

Third party Software (such as the Bowtie alignment program) does not fall within this agreement. You understand that third party products are subject to terms and conditions and/or license agreements from the applicable third party. All third party Software is provided "as is", without modifications and without any warranty from BaseClear B.V. BaseClear B.V. does not respond to any problem or liability that arises from a third party product.

8. Support

All questions related to the Software needs to be by email at basetools@baseclear.com. Based on the complexity of the request and the amount of time needed to solve the issue, BaseClear B.V. may apply a consultancy fee. Applicable consultancy costs will in all cases be notified to You in advance and before any further action is taken. Only upon Your written acceptance of the applicable costs the request will be addressed. BaseClear B.V. reserves the right to stop providing support for it's tools at any time and without prior notice.

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