



## **fastcluster: Fast Hierarchical, Agglomerative Clustering Routines for R and Python**

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### **Abstract**

The **fastcluster** package is a C++ library for hierarchical, agglomerative clustering. It provides a fast implementation of the most efficient, current algorithms when the input is a dissimilarity index. Moreover, it features memory-saving routines for hierarchical clustering of vector data. It improves both asymptotic time complexity (in most cases) and practical performance (in all cases) compared to the existing implementations in standard software: several R packages, MATLAB, Mathematica, Python with **SciPy**.

The **fastcluster** package presently has interfaces to R and Python. Part of the functionality is designed as a drop-in replacement for the methods `hclust` and `flashClust` in R and `scipy.cluster.hierarchy.linkage` in Python, so that existing programs can be effortlessly adapted for improved performance.

*Keywords:* clustering, algorithm, hierarchical, agglomerative, linkage, single, complete, average, UPGMA, weighted, WPGMA, McQuitty, Ward, centroid, UPGMC, median, WPGMC, MATLAB, Mathematica, Python, **SciPy**, C++.

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## **1. Introduction**

Hierarchical clustering is an important, well-established technique in unsupervised machine learning. The common hierarchical, agglomerative clustering methods share the same algorithmic definition but differ in the way in which inter-cluster distances are updated after each clustering step (Anderberg 1973, page 133). The seven common clustering schemes are called single, complete, average (UPGMA), weighted (WPGMA, McQuitty), Ward, centroid (UPGMC) and median (WPGMC) linkage (Everitt, Landau, Leese, and Stahl 2011, Table 4.1)

A variety of algorithms has been developed in the past decades to improve performance compared to the primitive algorithmic setup, in particular Anderberg (1973, page 135), Rohlf (1973), Sibson (1973), Day and Edelsbrunner (1984, Table 5), Murtagh (1984), Eppstein

(2000), Cardinal and Eppstein (2004). Also, hierarchical clustering methods have been implemented in standard scientific software such as R (R Core Team 2011), MATLAB (The MathWorks, Inc. 2011), Mathematica (Wolfram Research, Inc. 2010) and the **SciPy** library for the programming language Python (Jones, Oliphant, Peterson *et al.* 2001; van Rossum *et al.* 2011). Specifically, there are the following functions:

- `hclust` in R's **stats** package (R Core Team 2011),
- `flashClust` in R's **flashClust** package (Langfelder 2011),
- `agnes` in R's **cluster** package (Mächler, Rousseeuw, Struyf, Hubert, and Hornik 2011),
- `linkage` in MATLAB's **statistics** toolbox (The MathWorks, Inc. 2011),
- `Agglomerate` and `DirectAgglomerate` in Mathematica (Wolfram Research, Inc. 2010),
- `linkage` in the Python module `scipy.cluster.hierarchy` (Eads 2008).

We found that all these implementations do not give satisfactory performance because—insofar as this can be checked only for open-source software—they use inferior algorithms. The **fastcluster** package, which is available from the Comprehensive R Archive Network at <http://CRAN.R-project.org/package=fastcluster>, builds upon the author's work (Müllner 2011), where we identified three algorithms, including a new one by the author, as the most efficient current algorithms for the seven clustering schemes above, when the input is given by pairwise dissimilarities between elements. The **fastcluster** package also has memory-saving algorithms for some of the clustering schemes when the input is given as vector data. It provides a fast C++ implementation of each algorithm and currently offers interfaces to R and Python. We improve both the asymptotic worst-case time complexity (in those cases where this can be determined due to open source) and the practical performance (in all cases) of the existing implementations listed above.

The paper is structured as follows: In Section 2, we briefly introduce the clustering methods which our package provides in order to establish the technical context. The presentation is selective and focuses on the aspects which are important for this paper. For a general introduction to the well-known hierarchical clustering methods, we refer to textbooks, e.g., Anderberg (1973) or Everitt *et al.* (2011). Section 3 contains information about the algorithms and the implementation. Section 4 compares the performance of the package with existing software, both in a theoretical, asymptotic complexity analysis in Section 4.1 and by use case performance experiments in Sections 4.2 and 4.3. In Section 5, we explain how to use the **fastcluster** package and point to differences between the interfaces. This part is independent of the two preceding sections. A detailed user's manual is available in the package distribution. The paper finishes with a short conclusion in Section 6.

## 2. SAHN clustering methods

The clustering methods in this paper have been characterized by the acronym SAHN (sequential, agglomerative, hierarchic, nonoverlapping methods) by Sneath and Sokal (1973, Sections 5.4 and 5.5). The input to the methods is a *dissimilarity index* on a finite set (see Hansen

and Jaumard 1997, Section 2.1). For a set  $S$ , this is by definition a map  $d : S \times S \rightarrow [0, \infty)$  which is reflexive and symmetric, i.e., we have  $d(x, x) = 0$  and  $d(x, y) = d(y, x)$  for all  $x, y \in S$ . A metric on  $S$  is certainly a dissimilarity index. The dissimilarity index can be given directly to a clustering algorithm as the  $\binom{N}{2}$  pairwise dissimilarities. This is the *stored matrix approach* (Anderberg 1973, Section 6.2). Alternatively, the input points can be specified in a different manner, e.g., as points in a normed vector space, where the dissimilarity information is given implicitly by the metric on the ambient space. This input format is called the *stored data approach* (Anderberg 1973, Section 6.3).

The first option has input size  $\Theta(N^2)$  for  $N$  elements, and the second option  $\Theta(ND)$  for  $N$  points in a  $D$ -dimensional vector space. We call an algorithm *memory-saving* in this paper if it accepts vector data and the required memory is of class  $O(ND)$ .

The common procedural definition for all clustering methods in this paper is as follows (cf. Anderberg 1973, Section 6.1):

1. Let  $S$  be the current set of nodes, with implicit or explicit dissimilarity information. Determine a pair of mutually closest points  $(a, b)$ .
2. Join  $a$  and  $b$  into a new node  $n$ . Delete  $a$  and  $b$  from the set of nodes and add  $n$  to it.
3. Output the node labels  $a$  and  $b$  and their dissimilarity  $d(a, b)$ .
4. Update the dissimilarity information by specifying the distance from  $n$  to all other nodes. This can be done explicitly by specifying the distances, or by defining a cluster representative in the *stored data approach*.
5. Repeat steps 1–4 until there is a single node left, which contains all the initial nodes.

The clustering schemes differ in the update formula for cluster dissimilarities in step 4. Table 1 lists the formulas for the seven common clustering schemes.

The output of the clustering procedure is a list of  $N - 1$  triples  $(a_i, b_i, \delta_i)$ , which encodes a *stepwise dendrogram* (see Müllner 2011, Section 2.2, for the difference to non-stepwise variants): The  $i$ -th triple contains the information which nodes are joined into a new node in the  $i$ -th step, and what was the cluster dissimilarity between  $a_i$  and  $b_i$ . This is sufficient information to draw the usual representation of the dendrogram as a rooted tree, where the leaves are the initial nodes, and a branching point at a given height  $\delta_i$  represents the joining of nodes  $a_i, b_i$  with mutual distance  $\delta_i := d(a_i, b_i)$ .

Note that the output of the clustering procedure above is not unique: if more than one pair of nodes realizes the current minimal distance in step 1, any of them might be chosen, and this influences later steps. The algorithms in the **fastcluster** package are correct in the sense that they always return one of the possible outputs of the procedure above, and hence resolve ties in one of possibly several correct ways. For detailed information on why the handling of ties is a non-trivial matter and how it influences the choice of algorithms in the **fastcluster** package, see Müllner (2011, Sections 3 and 5).

The procedural definition of the clustering scheme above already constitutes a primitive algorithm. This algorithm has a time complexity of  $\Theta(N^3)$  for  $N$  input points, since in the  $i$ -th iteration a pair of closest nodes is searched among  $N - i + 1$  nodes in step 1, which requires  $\Theta((N - i)^2)$  comparisons by an exhaustive search. The **fastcluster** package reduces the time

Name	Distance update formula for $d(I \cup J, K)$	Cluster dissimilarity between clusters $A$ and $B$
Single	$\min(d(I, K), d(J, K))$	$\min_{a \in A, b \in B} d[a, b]$
Complete	$\max(d(I, K), d(J, K))$	$\max_{a \in A, b \in B} d[a, b]$
Average	$\frac{n_I d(I, K) + n_J d(J, K)}{n_I + n_J}$	$\frac{1}{ A  B } \sum_{a \in A} \sum_{b \in B} d[a, b]$
Weighted/McQuitty	$\frac{d(I, K) + d(J, K)}{2}$	
Ward	$\sqrt{\frac{(n_I + n_K)d(I, K)^2 + (n_J + n_K)d(J, K)^2 - n_K d(I, J)^2}{n_I + n_J + n_K}}$	$\sqrt{\frac{2 A  B }{ A  +  B }} \cdot \ \vec{c}_A - \vec{c}_B\ _2$
Centroid	$\sqrt{\frac{n_I d(I, K)^2 + n_J d(J, K)^2}{n_I + n_J} - \frac{n_I n_J d(I, J)^2}{(n_I + n_J)^2}}$	$\ \vec{c}_A - \vec{c}_B\ _2$
Median	$\sqrt{\frac{d(I, K)^2}{2} + \frac{d(J, K)^2}{2} - \frac{d(I, J)^2}{4}}$	$\ \vec{w}_A - \vec{w}_B\ _2$

Table 1: Agglomerative clustering schemes. Let  $I, J$  be two clusters joined into a new cluster, and let  $K$  be any other cluster. Denote by  $n_I, n_J$  and  $n_K$  the sizes of (i.e., number of elements in) clusters  $I, J, K$ , respectively.

The update formulas for the “Ward”, “Centroid” and “Median” methods assume that the input points are given as vectors in Euclidean space with the Euclidean distance as dissimilarity measure. The expression  $\vec{c}_X$  denotes the centroid of a cluster  $X$ . The point  $\vec{w}_X$  is defined iteratively and depends on the order of clustering steps: If the cluster  $L$  is formed by joining  $I$  and  $J$ , we define  $\vec{w}_L$  as the midpoint  $\frac{1}{2}(\vec{w}_I + \vec{w}_J)$ .

References: [Lance and Williams \(1967\)](#), [Kaufman and Rousseeuw \(1990, Section 5.5.1\)](#).

complexity from cubic to quadratic: as a theoretically guaranteed worst-case complexity for five of the seven methods, and as a heuristic behavior in all observed cases for the “centroid” and “median” distance update formulas.

The formulas in Table 1 show that inter-cluster distances can be conveniently defined and computed in constant time from (weighted or unweighted) cluster centroids in Euclidean space for the “Ward”, “centroid” and “median” methods. Hence, these clustering schemes are predestined for a memory-saving clustering algorithm where not all distance values are stored but distances are computed as they are needed. Moreover, there are algorithms for single linkage clustering (including the one which is used in the **fastcluster** package) which read in every pairwise dissimilarity value between initial nodes exactly once, and otherwise need only  $O(N)$  temporary memory. Hence, also single linkage clustering can be implemented in a memory-saving manner. The **fastcluster** package contains memory-saving algorithms for these four methods. It assumes Euclidean distances between input vectors for the “Ward”, “centroid” and “median” methods and provides a variety of metrics for the “single” method.

### 3. Algorithms and implementation

The efficient algorithms which are used in the **fastcluster** package were described in detail by the author in Müllner (2011). In that paper, the author introduced an algorithm which works with any distance formula, proved the correctness of two existing algorithms by Rohlf and Murtagh and identified the most efficient algorithms. The **fastcluster** package builds upon this knowledge and implements the most efficient algorithms. There are three algorithms in total: For single linkage clustering, an algorithm by Rohlf (1973) is used. It links Prim’s algorithm for the minimum spanning tree of a graph (see Cormen, Leiserson, Rivest, and Stein 2009, Section 23.2) with the observation that a single linkage dendrogram can be obtained from the minimum spanning tree of a graph. More precisely, this graph is the weighted, complete graph whose adjacency matrix is the dissimilarity index (Gower and Ross 1969).

The “complete”, “average”, “weighted” and “Ward” (for dissimilarity input) methods use the nearest-neighbor chain algorithm by Murtagh (1984, page 86). This algorithm exploits the fact that pairs of mutually closest points can be merged in any order, if the distance update formula fulfills certain criteria (see also Müllner 2011, Theorem 3). The “centroid”, “median” and “Ward” (vector input) methods use the author’s algorithm (Müllner 2011, Section 3.1), which delays repeated searches for nearest neighbors as long as possible.

The algorithms are fairly optimized for speed. For example, there are two variants of the author’s algorithm, which differ by the indexing of intermediate results and how the list of nearest neighbors for all nodes is organized. These two variants perform different enough to make the distinction worthwhile. The final choice which algorithm to use for which method was then made according to performance on test datasets.

All algorithms in the **fastcluster** package are implemented in a C++ library. The core code is the same for both interfaces. It is accompanied by language-specific wrappers, which handle the input and output in the interface-specific array data structures and also handle the different indexing conventions and extra output (like the `order` field in the R interface). The interface code in the interpreted languages R and Python is very short so that the overhead is low. The C++ code extensively uses template programming to avoid code duplication among the seven methods. Also the data types are flexible through template programming. The current setup always uses double precision for floating-point numbers since this is the default in Python and R. The indices to the data points are represented by at least 32 bit wide signed integers, and indices to the dissimilarity array of size  $\binom{N}{2}$  are represented by signed 64-bit integers. This is in theory sufficient to handle  $2^{29} - 1$  data points, hence does not pose an actual obstruction.

### 4. Performance

In this section, we compare the performance of the **fastcluster** package with the other implementations in standard software. In Section 4.1, we analyze the asymptotic time complexity of the algorithms whose source code is available, both in the worst and in the best case. We then compare the performance of all implementations experimentally on a range of test datasets. Section 4.2 deals with the case when the input is a dissimilarity index, and Section 4.3 covers the memory-saving routines for vector input.

#### 4.1. Asymptotic run-time complexity

The asymptotic worst-case time complexity of the methods in open-source packages (**agnes** in **cluster**, **flashClust** in **flashClust**, **hclust** in **stats** and **linkage** in **SciPy**) is  $\Theta(N^3)$  throughout. These bounds were determined by careful inspection of the source code and constructing series of worst-case examples. The **fastcluster** package improves performance to  $\Theta(N^2)$  worst-case time complexity for the “single”, “complete”, “average”, “weighted” and “Ward” (dissimilarity input case only) methods. For the “centroid”, “median” and “Ward” (vector input) methods, we still use  $O(N^3)$  algorithms due to their better performance in practice, even though quadratic run-time algorithms are available (Eppstein 2000).

Regarding the best-case complexity, only the **fastcluster** and **flashClust** packages achieve the theoretically optimal bound of  $\Theta(N^2)$ . **SciPy**, **agnes** and **hclust** have a best-case complexity of only  $\Theta(N^3)$ .

#### 4.2. Use case performance: Dissimilarity methods

As indicated by the asymptotic best-case complexity, the various algorithms indeed perform differently (quadratic vs. cubic time) in test cases. The diagrams in Figure 1 show the performance on a range of test datasets for all seven methods. The **fastcluster** package consistently outperforms all other packages, and by rather significant factors in the majority of cases. Also, the performance on very small datasets is very good, due to a low overhead. To be fair, the measurements for small datasets depend on the software environment in addition to the clustering algorithms, so, e.g., the R **fastcluster** package can only be directly compared to the other three R packages: here it has the lowest overhead. The other graphs were generated by different interpreters (Python, MATLAB, Mathematica). **fastcluster**’s Python interface has even lower overhead than the R version and gives otherwise similar timings.

In summary, the **fastcluster** package not only improves the theoretical, asymptotic bounds of the clustering algorithms, but it also significantly improves the run-time performance of the existing implementations.

The test sets were synthetic datasets: i.i.d. samples from a mixture of multivariate Gaussian distributions in Euclidean space with standard covariance. For each number of input points  $N$ , we generated 12 test sets by varying the following parameters:

- Dimension of the Euclidean space: 2, 3, 10, 200.
- Number of centers of Gaussian distributions: 1, 5,  $\text{round}(\sqrt{N})$ . The centers are also distributed according to a Gaussian distribution.

Moreover, for the methods for which it makes sense (single, complete, average, weighted: the “combinatorial” methods), we also generated 10 test sets per number of input points with a uniform distribution of dissimilarities.

The timings were obtained on a PC with an Intel dual-core CPU T7500 with 2.2 GHz clock speed and 4GB of RAM and no swap space. The operating system was Ubuntu 11.04 64-bit. R version: 2.13.0, **fastcluster** version: 1.1.5, **flashClust** version: 1.01, **cluster** version: 1.13.3, **stats** version: 2.13.0, Python version: 2.7.1, **NumPy** version: 1.5.1, **SciPy** version: 0.8.0.



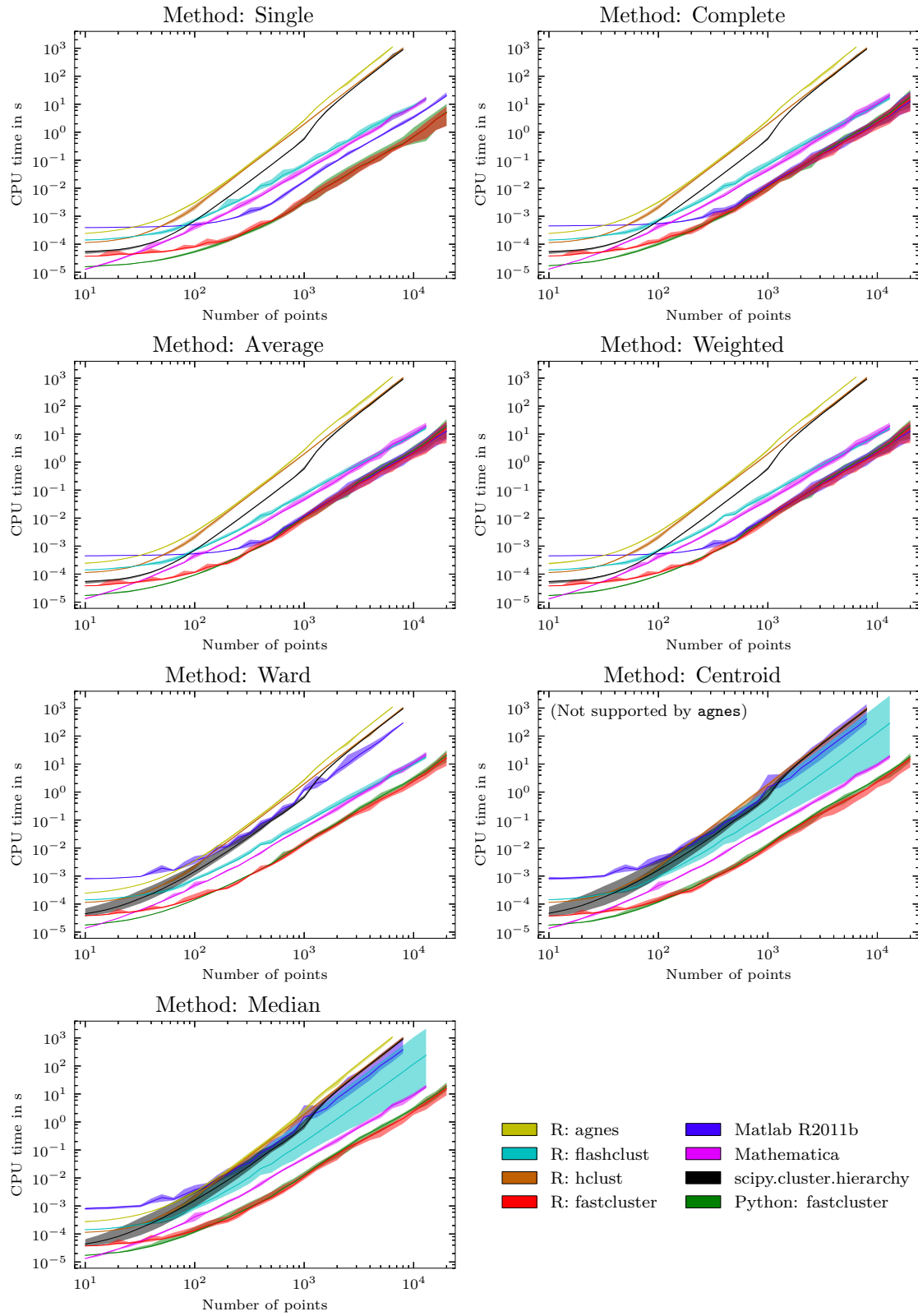


Figure 1: Performance comparison for dissimilarity matrix input. Lightly colored bands: Min-max range. Solid curves: Mean values.

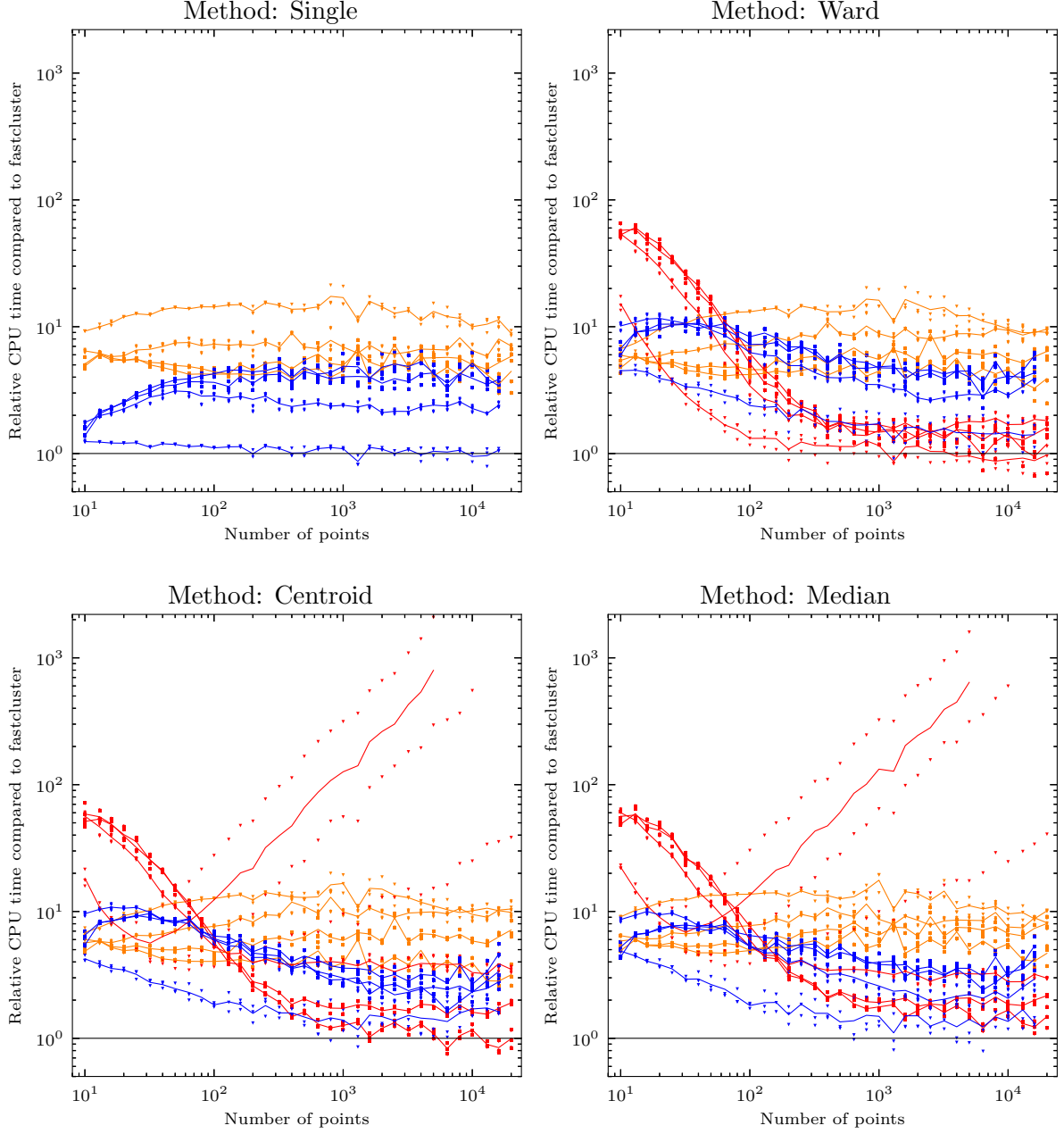


Figure 2: Performance comparison for vector input. Legend:

- Mathematica vs. `fastcluster` (Python interface),
- MATLAB Release 2011b vs. `fastcluster` (Python interface),
- `fastcluster` (R interface) vs. `fastcluster` (Python interface).



Only one core of the two available CPU cores was used in all cases except the “Ward”, “centroid” and “median” methods in MATLAB.<sup>1</sup>

The memory requirements of all these algorithms are similar: they all keep the input array of  $\binom{N}{2}$  floating-point numbers in memory plus a working copy (hence  $8N(N-1)$  bytes in total with double-precision floating point numbers). The only exception is **fastcluster**’s single linkage algorithm, which uses less memory. Apart from the distance array, the **fastcluster** algorithms only needs  $O(N)$  memory for intermediate storage and the output. Although no extensive memory analysis was done, the **fastcluster** package can process as large datasets and sometimes even larger datasets than its competitors at a given memory size.

### 4.3. Performance of the vector methods

Three packages offer memory-saving clustering when the input consists of vector data: **fastcluster**, **Mathematica** and **MATLAB**. **MATLAB** has routines for “Ward”, “centroid” and “median” linkage; **fastcluster** and **Mathematica** additionally offer single linkage.

The asymptotic time complexity of the **fastcluster** package is  $\Theta(N^2D)$  for  $N$  points in  $\mathbb{R}^D$  in the best case. The worst-case complexity is also  $\Theta(N^2D)$  for the “single” method and  $O(N^3D)$  for the “Ward”, “centroid” and “median” methods. For the commercial software, the complexity cannot be determined exactly since the source code is not available. From our use case experiments it seems that **MATLAB** and **Mathematica** also have a best-case complexity of  $\Theta(N^2D)$ , and **MATLAB** has a worst-case complexity of  $\Omega(N^3D)$ .

We tested the performance of the three packages on the same datasets as in the previous Section 4.2. Since the run time depends heavily on the dimensionality of the dataset, it makes no sense to put the absolute timings into a common diagram. Instead, Figure 2 shows the relative run time of the commercial software versus the **fastcluster** package with the Python interface (blue and red graphs). Four average curves are plotted, one for each dimensionality (2, 3, 10, 200). We only tested Euclidean distances although a variety of distance measures is possible for the single linkage method. The curves clearly show that our Python module consistently outperforms **MATLAB** and **Mathematica** in this task. **MATLAB**’s run times show cubic asymptotic behavior for the high-dimensional datasets. **Mathematica** aborted on two different machines with a segmentation fault at 20000 input points, so the output of **Mathematica**’s vector clustering methods should be double-checked independently for critical data. For this reason we did not continue the test after 20000 input points even though the **fastcluster** package is able to handle larger data.

The orange graph in Figure 2 shows the timings of **fastcluster**’s R interface versus the Python interface. The R interface is slower by high factors ranging from 2.6 to 21, but for a good reason: The R distance function checks every coordinate whether it is marked as missing data (a NA value in R syntax), so that  $2D$  extra comparisons (and therefore conditional

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<sup>1</sup>In fact, **MATLAB** seems to use only one core for the actual clustering step, like the other packages. However, for the three “geometric” methods “Ward”, “centroid”, and “median”, **MATLAB** carries out an additional precheck, which tests whether the  $\binom{N}{2}$  pairwise distances can be generated from a configuration of  $N$  points in Euclidean space. This involves checking whether a dense, symmetric  $N \times N$  matrix is positive semidefinite, for which **MATLAB** apparently uses a parallelized eigenvalue algorithm. Moreover, for double-centering of a matrix, **MATLAB** unnecessarily carries out matrix multiplication, which has time complexity  $\Theta(N^3)$  in its straightforward implementation. Hence the precheck requires much more time than the actual clustering task. This is reflected in Figure 1, where **MATLAB** is much slower for the “geometric” methods than for the other four “combinatorial” methods.

branch instructions on machine code level) are needed to compute the distance between any two points. By doing so, the **fastcluster** R package follows exactly the internal formulas of the `dist` method in the R core **stats** package to handle missing data. However, this makes the process considerably slower than the straightforward calculation in the Python module. MATLAB and Mathematica are compared to the Python module since neither handles missing data automatically.

## 5. Usage of the **fastcluster** package

The **fastcluster** package features interfaces to R and Python. These interfaces can be used as drop-in replacements for the `linkage` function in the Python module **scipy.cluster.hierarchy**, for the `hclust` function in R's **stats** package, and for `hclust` alias `flashClust` in R's **flashClust** package. The replacements share the same syntax and output specifications but are faster.

The **fastcluster** package can be downloaded from the Comprehensive R Archive Network at <http://CRAN.R-project.org/package=fastcluster>. Installation instructions for both R and Python are included in the package documentation. The Python part is additionally available at PyPI (<http://pypi.python.org/pypi/fastcluster>) from where it can be easily installed with Python's **setuptools**.

Nothing in the source code is specific to a certain operating system, so it should be possible to install the **fastcluster** package on a wide variety of hardware architectures and operating systems.

### 5.1. The R interface

In R, the package is loaded as usual with the command:

```
R> library("fastcluster")
```

The **fastcluster** package overwrites the function `hclust` from the **stats** package, in the same way as the **flashClust** package does. It is recommended to remove references to the **flashClust** package when the **fastcluster** package is used to not accidentally overwrite the `hclust` function with the **flashClust** version.

If needed, or in order to prevent confusion, all three functions can be specified unambiguously by their namespace:

```
stats::hclust(...)
fastcluster::hclust(...)
flashClust::hclust(...)
```

All three `hclust` functions have exactly the same calling conventions and output format. A user may simply load the package and immediately and effortlessly enjoy the performance improvements to the `hclust` function. The function `flashClust` in the **flashClust** package is an alias for `flashClust::hclust`, so the `flashClust` function may be replaced as well.

The `agnes` function from the **cluster** package has a slightly different input and output format, but in many cases it should be possible with little effort to use the faster alternative in the **fastcluster** package.

An exact and detailed specification of the methods is given in the user's manual in the **fastcluster** distribution.<sup>2</sup> As a short description, the method

```
hclust(d, method = "complete", members = NULL)
```

performs agglomerative clustering on the compressed distance matrix **d**. The array **d** is a one-dimensional array which contains the upper triangular part of the symmetric matrix of dissimilarities, as it is produced e.g., by R's **dist** function.

The parameter **method** is a string which specifies the dissimilarity update formula from Table 1. It must be one of "single", "complete", "average", "mcquitty", "ward", "centroid", "median" or an unambiguous abbreviation thereof.

The optional parameter **members** may contain a vector which specifies weights for the initial nodes. This can be used, e.g., to start or re-start the hierarchical clustering process when partial clusters have been formed beforehand, so that nodes have cardinalities different from 1.

The output of the **hclust** method is an object of class "hclust" which mainly encodes a stepwise dendrogram. It can be processed by the existing methods in R, in particular there is a specific **plot** method for the output which draws the dendrogram.

The new method

```
hclust.vector(X, method = "single", members = NULL, metric = "euclidean",
  p = NULL)
```

is a memory-saving option if the input to the clustering algorithm is given as vector data. Instead of keeping the entire matrix of dissimilarities in memory, the vector method computes distances on-the-fly from vectors, with the metric which is specified by the "metric" parameter. This is currently possible for the "single", "ward", "centroid" and "median" methods.

In short, the call

```
R> hclust.vector(X, method = "single", metric = [...])
```

gives the same result as

```
R> hclust(dist(X, metric = [...]), method = "single")
```

but uses less memory and is equally fast, if not faster. The parameter **p** is used for the "minkowski" metrics only and specifies the exponent for this family of metrics. The output is again a stepwise dendrogram.

If **method** is one of "centroid", "median", or "ward", clustering is performed with respect to Euclidean distances. In this case, the parameter **metric** must be "euclidean". Notice that **hclust.vector** operates on Euclidean distances for compatibility with the **dist** method, while **hclust** assumes *squared* Euclidean distances for compatibility with the **stats::hclust** method. Hence, the call

```
R> hc <- hclust.vector(X, method = "ward")
```

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<sup>2</sup>This is stored as a vignette, i.e., the file `inst/doc/fastcluster.pdf` in the source distribution, and can be accessed in R using `vignette("fastcluster", package = "fastcluster")`.

is, aside from the lesser memory requirements, equivalent to:

```
R> d <- dist(X)
R> hc <- hclust(d^2, method = "ward")
R> hc$height <- sqrt(hc$height)
```

(1)

The same applies to the "centroid" and "median" methods. Differences may arise only from rounding errors due to squaring and taking the square root (which may, however, in extreme cases affect the entire clustering result due to the inherently unstable nature of the clustering schemes).

The same issue, that the R interface for the **fastcluster** package sometimes interprets input values as ordinary and sometimes as squared Euclidean distances, accounts also for the biggest difference between the R and the Python interface. See the next Section 5.2 for details. Even though this might seem to provoke complications unnecessarily, these differences were in fact designed intentionally, in order for the **fastcluster** package to comply best with the varying conventions in existing packages.

## 5.2. Caveat

R and MATLAB/SciPy use different conventions for the "Ward", "centroid" and "median" methods, if the input is a dissimilarity matrix. R assumes that the data consists of *squared* Euclidean distances, while MATLAB and SciPy expect *non-squared* Euclidean distances. The **fastcluster** package respects these conventions and uses different formulas in the two interfaces.

Let **d** be a compressed array of pairwise distances, as it is used by all three programs MATLAB, SciPy and R. In order to obtain the same results in all programs, the R method must be given the entry-wise square of the distance array, **d**<sup>2</sup>, for the "Ward", "centroid" and "median" methods, compared to the other software. After the calculation, the square root of the **height** field in the dendrogram may be taken. For the "average" and "weighted" alias "McQuitty" methods, the same distance array **d** must be used in all programs for identical results. The "single" and "complete" methods only depend on the relative order of the distances, hence it does not make a difference whether one uses the distances or the squared distances.

Therefore, the R code example (1) above, where the dissimilarity matrix entries are squared, gives the same result as the following Python code:

```
>>> d = scipy.spatial.distance.pdist(X)
>>> hc = fastcluster.hclust(d, method = "ward")
```

## 5.3. The Python interface

The **fastcluster** package is imported as usual by:

```
>>> import fastcluster
```

It provides the following functions:

```
linkage(X, method = "single", metric = "euclidean", preserve_input = True)
single(X)
```

```

complete(X)
average(X)
weighted(X)
ward(X)
centroid(X)
median(X)
linkage_vector(X, method = "single", metric = "euclidean", extraarg = None)

```

The function `linkage` can process both dissimilarity and vector input as the first argument `X`. The input is preferably a **NumPy** array (Oliphant *et al.* 2011) with double-precision floating point entries. Any other data format will be converted before it is processed.

If `X` is a one-dimensional array, it is considered a condensed matrix of pairwise dissimilarities, in the same format as is returned by the function `scipy.spatial.distance.pdist` in the **SciPy** software for computing pairwise distances between row vectors of a matrix. If the input array is two-dimensional, it is regarded as vector data and is converted to a dissimilarity index with the method `scipy.spatial.distance.pdist` with the `metric` parameter first.

The `method` parameter specifies the distance update formula and must be one of "single", "complete", "average", "weighted", "ward", "centroid" or "median". The parameter `preserve_input` specifies whether a working copy of the input array is made or not. This can save approximately half the memory if the dissimilarity array is created for the clustering only and is not needed afterward.

The functions `single`, `complete`, `average`, `weighted`, `ward`, `centroid` and `median` are aliases for the `linkage` function with the corresponding `method` parameter and are mainly there for compatibility with the **scipy.cluster.hierarchy** package.

The function `linkage_vector` provides the memory-saving clustering routines for the methods "single", "ward", "centroid" and "median". The input array is interpreted as  $N$  data points in  $\mathbb{R}^D$ , i.e., as an  $(N \times D)$  array, in the same way as the two-dimensional input for the `linkage` function.

The “Ward”, “centroid” and “median” methods require the Euclidean metric, while single linkage clustering accepts the same wide variety of `metric` parameters for floating-point and Boolean matrices as the function `scipy.spatial.distance.pdist`. The exact formulas for the pairwise distances and the documentation differ in some cases from **SciPy**’s `pdist` method since the author modified/corrected a few details. Therefore, we refer to the user’s manual in the **fastcluster** package for authoritative details and specifications of all metrics. The `extraarg` parameter is used by some metrics for additional parameters.

#### 5.4. A Python example

We present a short but complete example of a cluster analysis in **Python** which includes plotting the results. An example for **R**, which was taken from the original **stats** package, can be obtained from the **R** command line by:

```
R> example(hclust)
```

The source code of the following **Python** example is contained in the supplements to this paper. From version 1.1.8 on, the **fastcluster** package will support both **Python** 2 and 3.

First, import the necessary packages:

```
>>> import fastcluster
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy.cluster.hierarchy import dendrogram
>>> from scipy.spatial.distance import pdist
```

We analyze the well-known iris dataset ([Fisher 1936](#)). This is loaded from a publicly available source. The first few lines of code make the example work with both Python 2 and Python 3.

```
>>> import sys
>>> if sys.hexversion < 0x03000000:
>>>     from urllib2 import urlopen
>>> else:
>>>     from urllib.request import urlopen
>>> f = urlopen('http://scipy-cluster.googlecode.com/svn/trunk/hcluster'
...             '/tests/iris.txt')
>>> X = np.loadtxt(f)
>>> f.close()
>>> N = len(X)
```

The iris dataset consists of 150 observations in 4 variables. The features are measurements of sepal length and width, and petal length and width from 150 iris flowers of three species. There are 50 observations from each of *I. setosa*, *I. versicolor* and *I. virginica* in this order in the dataset. We record the classification by color codes for later plotting.

```
>>> classes = ['g'] * 50 + ['r'] * 50 + ['c'] * 50
```

For demonstration purposes, we want to compare clustering results with the known classification. We define a dedicated function for this. To plot a simple dendrogram, calling the function `scipy.cluster.hierarchy.dendrogram` as in the first two lines of the function would be enough.

```
>>> def plot_with_labels(Z, num_clust):
...     threshold = Z[-num_clust + 1, 2]
...     dg = dendrogram(Z, no_labels = True, color_threshold = threshold)
...
...     color = [classes[k] for k in dg['leaves']]
...     b = .1 * Z[-1, 2]
...     plt.bar(np.arange(N) * 10, np.ones(N) * b, bottom = -b, width = 10,
...             color = color, edgecolor = 'none')
...     plt.gca().set_ylim((-b, None))
...     plt.show()
```

When the data is clustered with single linkage and the Euclidean metric, *I. setosa* is clearly separated from the other two species but *I. versicolor* and *I. virginica* are not distinguished (see Figure 3). The so-called chaining effect is clearly visible in the dendrogram, as many single points and small clusters points join the main clusters in late stages of the clustering process.

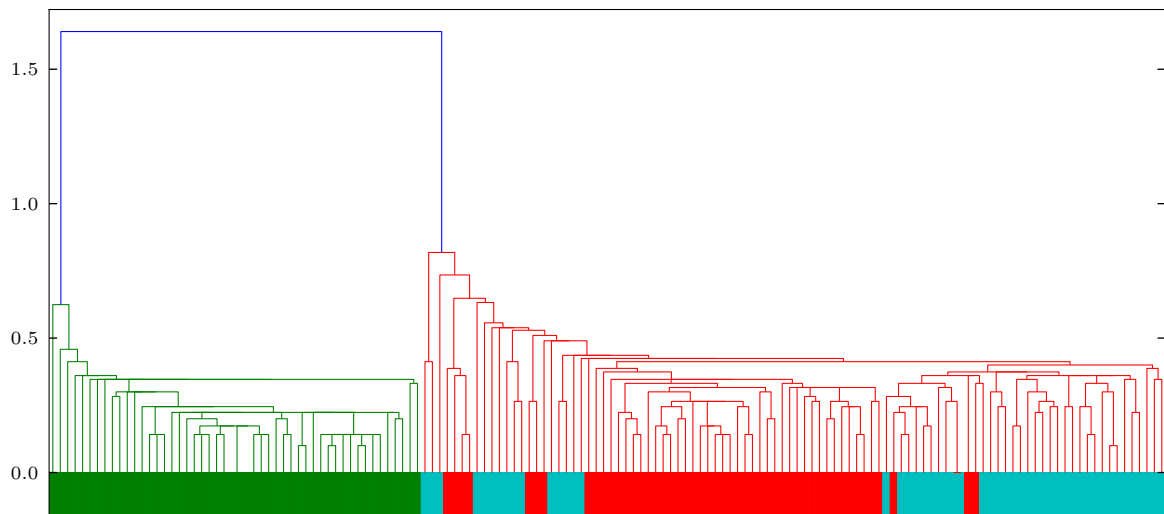


Figure 3: Python example, single linkage dendrogram.

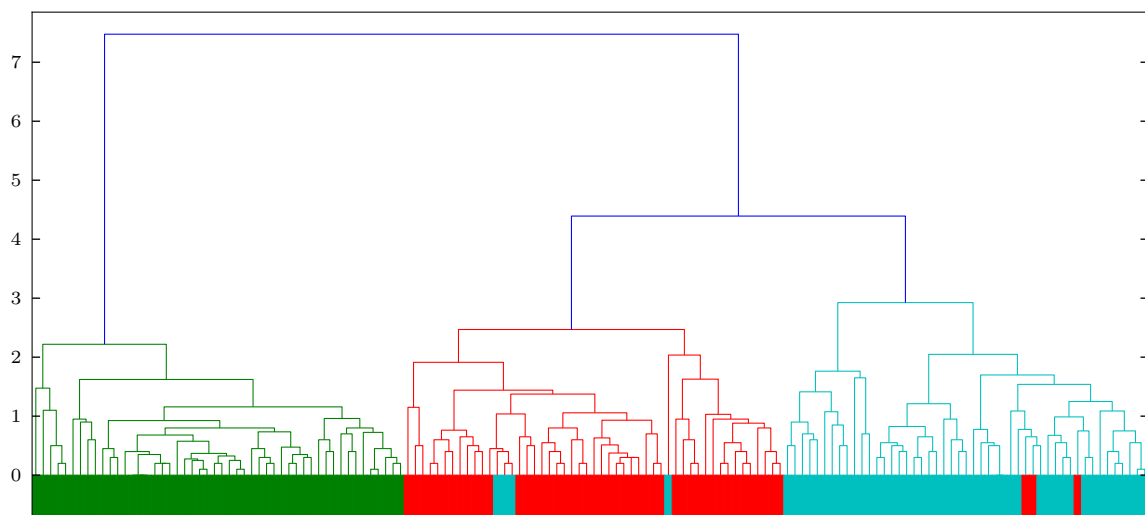


Figure 4: Python example, dendrogram for “weighted” linkage.

```
>>> Z = fastcluster.linkage(X, method = 'single')
>>> plot_with_labels(Z, 2)
```

However, when we try the “weighted” clustering scheme on the dataset with  $L_1$  distances, clustering identifies three clusters which correspond up to a small error (7 misclassifications out of 150) to the three species. For a change, we generate pairwise distances explicitly and feed the distance array into the clustering routine. See Figure 4 for the dendrogram.

```
>>> D = pdist(X, metric = 'cityblock')
>>> Z = fastcluster.linkage(D, method = 'weighted')
>>> plot_with_labels(Z, 3)
```



## 6. Conclusion

The **fastcluster** package currently offers the fastest implementation of the widely used agglomerative, hierarchical clustering methods in standard software. It complements the theoretical work by the author (Müllner 2011) with a fast C++ library of the most efficient algorithms. The dual interface to R and Python makes it versatile, and the syntactic compatibility with existing packages also allows effortless performance improvements for existing software.

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