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# Kabsch algorithm

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The **Kabsch algorithm**, named after **Wolfgang Kabsch**, is a method for calculating the optimal **rotation matrix** that minimizes the **RMSD** (**root mean squared deviation**) between two paired sets of points. It is useful in graphics, **cheminformatics** to compare molecular structures, and also **bioinformatics** for comparing **protein** structures (in particular, see **root-mean-square deviation (bioinformatics)**).

The algorithm only computes the rotation matrix, but it also requires the computation of a translation vector. When both the translation and rotation are actually performed, the algorithm is sometimes called partial **Procrustes superimposition** (see also **orthogonal Procrustes problem**).

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## Description [\[edit\]](#)

The algorithm starts with two sets of paired points, *P* and *Q*. Each set of points can be represented as an *N*×3 **matrix**. The first row is the coordinates of the first point, the second row is the coordinates of the second point, the *N*th row is the coordinates of the *N*th point.

$$\begin{pmatrix} x_1 & y_1 & z_1 \\ x_2 & y_2 & z_2 \\ \vdots & \vdots & \vdots \\ x_N & y_N & z_N \end{pmatrix}$$

The algorithm works in three steps: a translation, the computation of a covariance matrix, and the computation of the optimal rotation matrix.

### Translation [\[edit\]](#)

Both sets of coordinates must be translated first, so that their **centroid** coincides with the origin of the **coordinate system**. This is done by subtracting from the point coordinates the coordinates of the respective centroid.

### Computation of the covariance matrix [\[edit\]](#)

The second step consist of calculating a **covariance matrix** *A*. In matrix notation,

$$A = P^T Q$$

or, using summation notation,

$$A_{ij} = \sum_{k=1}^N P_{ki} Q_{kj},$$

### Computation of the optimal rotation matrix [\[edit\]](#)

It is possible to calculate the optimal rotation *U* based on the matrix formula  $U = (A^T A)^{1/2} A^{-1}$  but implementing a numerical solution to this formula becomes complicated when all special cases are accounted for (for example, the case of *A* not having an inverse).

If **singular value decomposition** (SVD) routines are available, the optimal rotation, *U*, can be calculated using

the following simple algorithm.

First, calculate the SVD of the covariance matrix *A*.

$$A = VSW^T$$

Next, decide whether we need to correct our rotation matrix to ensure a right-handed coordinate system

$$d = \text{sign}(\det(WV^T))$$

Finally, calculate our optimal rotation matrix, *U*, as

$$U = W \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & d \end{pmatrix} V^T$$

Coutsias, Seok, and Dill<sup>[1]</sup> have found an equivalent method that uses **quaternions**. Expressing the optimal rotation matrix with a **quaternion** goes back to 1999: see appendix in <sup>[2]</sup> and was generalized in 2002 to probability distributions (continuous or not): see appendix A.5 in <sup>[3]</sup>

### Generalizations <sup>[edit]</sup>

The algorithm was described for points in a three-dimensional space. The generalization to *D* dimensions is immediate.

### External links <sup>[edit]</sup>

This SVD algorithm is described in more detail at <http://cnx.org/content/m11608/latest/> <sup>[↗]</sup>

A **Matlab** function is available at <http://www.mathworks.com/matlabcentral/fileexchange/25746-kabsch-algorithm> <sup>[↗]</sup>

A **C++** [implementation](#) <sup>[↗]</sup> (and unit test) using **Eigen**

A **Python** script is available at <https://github.com/charnley/rmsd> <sup>[↗]</sup>

A free **PyMol** plugin easily implementing Kabsch is **Cealign** <sup>[↗]</sup>. **VMD** uses the Kabsch algorithm for its alignment.

### See also <sup>[edit]</sup>

**Wahba's Problem**

### References <sup>[edit]</sup>

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Categories: **Bioinformatics algorithms**

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