

Algorithms for neighborhood searches: The Voronoi diagram approach

Course in Computational Geometry

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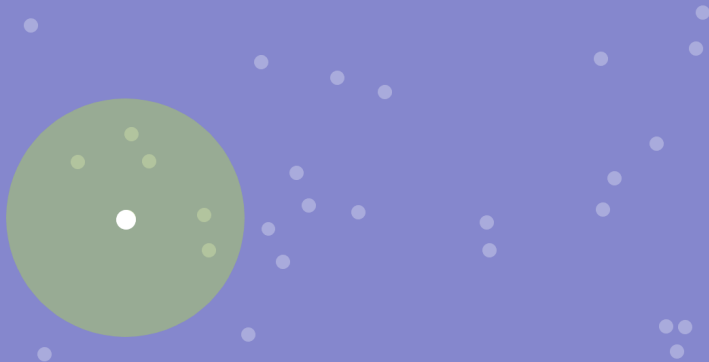
Abstract

In this presentation I consider the neighborhood selection problem which I started to study in my bachelor's thesis and in a previous work¹. I briefly recap the main results which I have already studied, namely, I define the problem in a precise way and I show a straightforward solution, then I review the common algorithmic approaches together with complexity analyses and I show the curse of dimensionality problem. Then I consider the Voronoi diagram approach to solve the neighborhood selection problem. First, I present the algorithm which shows how to properly use the data structure to implement an efficient solution, and second, I compare this method by the previous ones both with theoretical and experimental results.

¹R. Borelli, A. Dovier, and F. Fogolari (2022). "Data Structures and Algorithms for k-th Nearest Neighbours Conformational Entropy Estimation". In: *Biophysica* 2.4, pp. 340–352. DOI: [10.3390/biophysica2040031](https://doi.org/10.3390/biophysica2040031).

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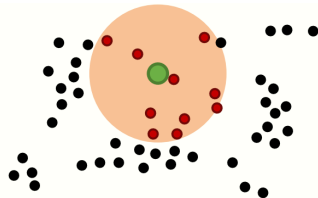
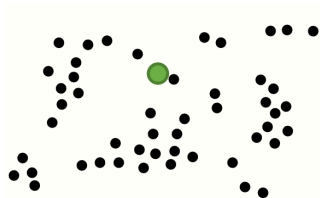
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- 3 Comparison
- 4 Conclusion



Problem overview

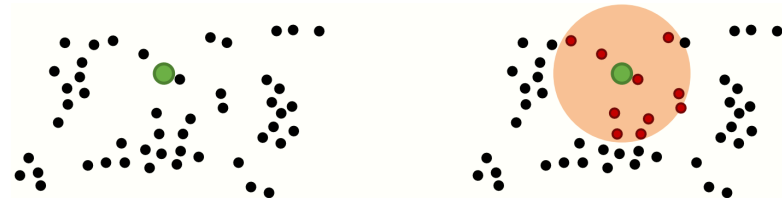
Problem formulation

- ALL-MNN: Given n point in a d dimensional space, find for each point p its m nearest neighbors



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- The problem has a wide range of real applications
 - ▶ Conformational entropy estimation on biomolecular systems
 - ▶ Machine learning

Problem formulation

- I propose a very simple formulation (which I didn't found in the literature) based on integer linear programming
- It evidences the *optimization* nature of the problem
- It's usefull to define precisely the problem
- It doesn't touch the geometry of the problem and it's very inefficient

Problem formulation

Let S be the input set $S = \vec{p}_1, \dots, \vec{p}_n$ and let m be the number of neighbors $0 < m < n$

We call N_1, \dots, N_n the sets of m neighbors for $\vec{p}_1, \dots, \vec{p}_n$.

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We call N_1, \dots, N_n the sets of m neighbors for $\vec{p}_1, \dots, \vec{p}_n$. Let us introduce $n^2 - n$ binary variables of the form $x_{ij}, i \neq j$ with the meaning

$$x_{ij} = \begin{cases} 1 & \text{if } \vec{p}_j \in N_i \\ 0 & \text{otherwise} \end{cases} \quad \forall i, j \in [n], i \neq j \quad (1)$$

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The integer programming model is now the following

$$\min \sum_{i \in [n]} \sum_{j \in [n] \setminus \{i\}} (x_{ij} \text{dist}(\vec{p}_i, \vec{p}_j)) \quad (2)$$

subject to:

$$\sum_{j \in [n] \setminus \{i\}} x_{ij} = m \quad \forall i \in [n] \quad (3)$$

Lower bound

- First lower bound: we have to read the input and print the output:

$$\Omega(nd) + \Omega(nmd) \quad (4)$$

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- I can improve the lower bound by a reduction through
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ELEMENT-UNIQUENESS \preceq CLOSEST-PAIR \preceq ALL-1NN

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 - ➎ To solve the ELEMENT-UNIQUENESS problem, check if $d_j = 0$
- Steps 3 and 4 take linear time
 - Solving the ELEMENT-UNIQUENESS takes $\Omega(n \log n)$ time
 - Solving the ALL-1NN problem in $o(n \log n)$ implies a contradiction

Lower bound

Some details on the reduction:

- Note that `ELEMENT-UNIQUENESS` is a decision problem while the other 2 are functional problems. So we are referring to the more general definition of reduction between functional problems
- One (implicit) key assumption: the `ALL-1NN` takes as input a list (and not a set) of points. Otherwise the reduction doesn't make sense: a set always satisfies the uniqueness property
- In real world situations S is always a set
- By implementing the classical algorithms I observed that the code doesn't change much if we allow or not S to be a list
- To be precise I should also prove that $\text{ALL-1NN}_{\text{lists}} \preceq \text{ALL-1NN}_{\text{sets}}$

The naive approach

- If we consider just one dimension we can easily come up with an optimal algorithm which takes linear space and $\Theta(n \log n + mn)$ time

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- If we consider more dimensions:

NAIVE-ALL-MNN(S)

- 1 For each point p in S , compute the vector \vec{d}_p which contains the distances between p and all the other points
- 2 Order each vector \vec{d}_p
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 - 2 Order each vector \vec{d}_p
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- Ordering (which takes $\Theta(n \log n)$) is not really necessary. After computing \vec{d}_p we could just select (in linear time) the m -th smallest distance
 - So in the general case we have an algorithm which always takes linear space and $O(dn^2)$ time
 - ... which of course is unacceptable

Classical approaches and results

In the literature we can find algorithms based on tree structures (like VP trees, K-D trees, Quad trees, ...) which are made up of the following steps:

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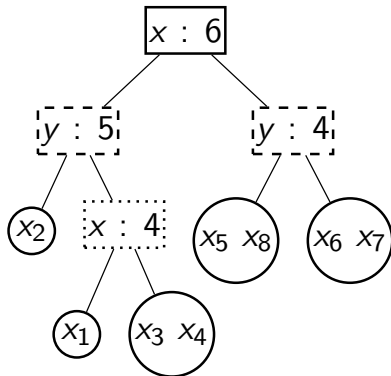
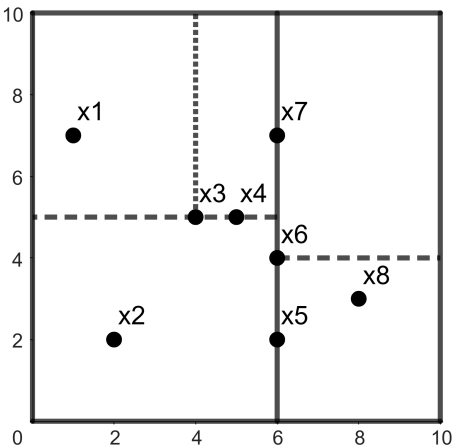
- **Preprocessing:** In this step we prepare a data structure (for example a tree) which tries to partition the space in small regions containing points. For each point in S we then invoke a query algorithm which should take advantage of the structure created.

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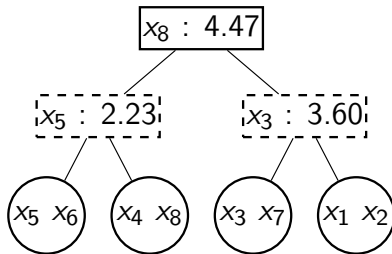
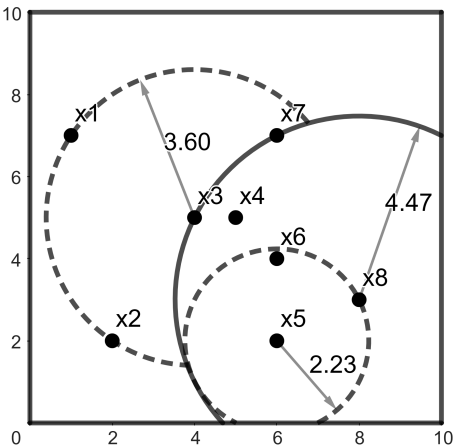
- **Preprocessing:** In this step we prepare a data structure (for example a tree) which tries to partition the space in small regions containing points. For each point in S we then invoke a query algorithm which should take advantage of the structure created.
- **Querying:** Given a point $p \in S$ we visit the data structure (possibly a small part of it) in order to find the m nearest neighbors of p .

Classical approaches and results: The K-D Tree



- Each internal node corresponds to a binary test which involves the projection operation
- At each node the set of points is split into two almost-balanced sets

Classical approaches and results: The VP Tree

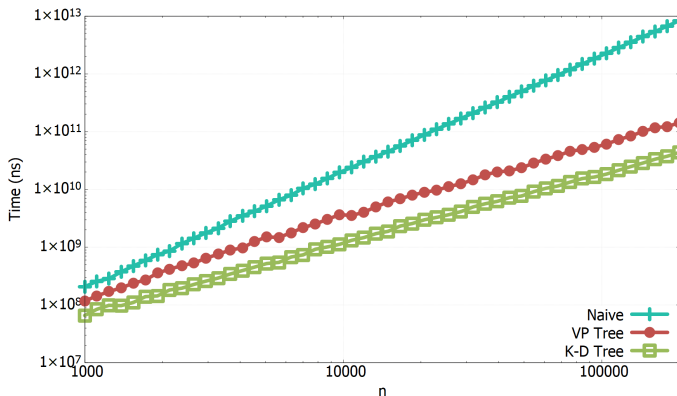


- Similar idea to K-D Trees but more general
- Each internal node is no more associated with a projection but only involves the dicotomy far/near with respect to the vantage point

Classical approaches and results: Costs

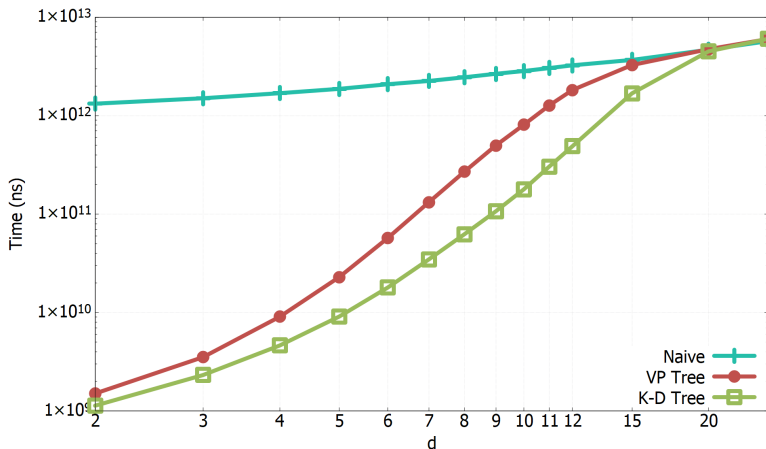
- The preprocessing steps is in some sense *easy* and takes $\Theta(n \log n)$ time
- The query should take $\Theta(\log n)$ time, but with currently-avaible methods this happens only in the avarage case
- We get the worst case when d is sufficiently large. In such case the query algorithm takes linear time (we essentially visit the entire tree structure) and the entire ALL-MNN algorithm degenretes to an exhaustive search which takes quadratic time
- This problem is known in the literature as **curse of dimensionality** and we currently don't know if the problem admits an optimal solution when the number of dimension increases

Classical approaches and results: Comparison



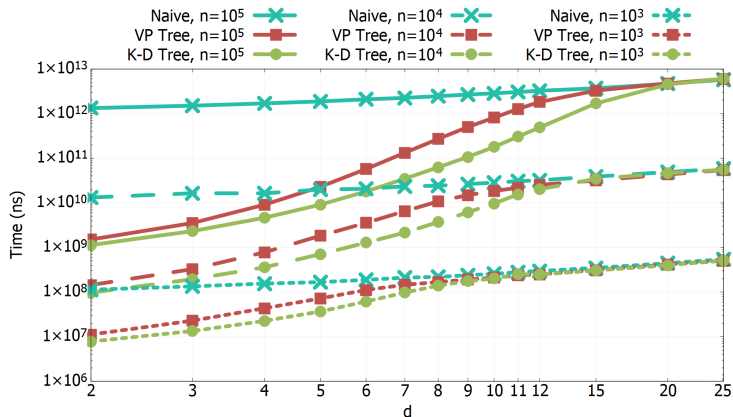
- With $d = 6$ dimensions and $m = 20$ VP Tree and the K-D tree performances are the same expect for a multiplicative constant
- Recall: In double logarithmic scale different lines inclinations means different polinomials

Classical approaches and results: Curse of dimensionality



- While working with $n = 100000$ points and $m = 20$ neighbors per point, advantages of tree-based methods are completely lost at $d = 20$

Classical approaches and results: Curse of dimensionality



- We observed that *curse of dimensionality* tends to attenuate when we increase n
- We also observed that the tree-based approaches degenerate in an exhaustive search when $d \in \Omega(\log n)$



The Voronoi diagram
approach

The Voronoi diagram

Optimal solution to ALL-1NN in 2d

The k -th order Voronoi diagram

Optimal solution to ALL-MNN in 2d



Comparison

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Conclusion

Concluding remarks

Bibliography I



Borelli, R., A. Dovier, and F. Fogolari (2022). “Data Structures and Algorithms for k-th Nearest Neighbours Conformational Entropy Estimation”. In: *Biophysica* 2.4, pp. 340–352. DOI: [10.3390/biophysica2040031](https://doi.org/10.3390/biophysica2040031).



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