### k-Means has Polynomial Smoothed Complexity

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# Data Clustering — Further Examples

### Second Example: Color Reduction



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0	1	2	3	4	5	6	7

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#### Third Example: Protein Clustering



----WIGLAVITIKKIAKWKYDEWAELTEK KATHKTITIAN EGEPADKLHEIGKKING ----WRIMAVITQERKIAKWKIEEVKELEGKLREWHIIIAN EGEPADKLHEIGKKING ----WRIMIALAKQRKYASUKLEEKKELTETIKNSNTILIGN HEGEPADKLHEIKKKINK MSVVSJVGQMYKKEKPIPEMKILMIRELEELSKNYVIFADLTGTPTFVGRVKKKINK -MHIATGKRAVVERGYDARVKIVESKATELIQKVVYVFEDDHISSRILHEIKKINK

### Outline

#### Main Questions

- Data Clustering What is the k-means method?
- Smoothed Analysis What can we do when worst case analysis is too pessimistic?
- Smoothed Analysis of the k-Means Method What is the smoothed complexity of the k-means method?
- Extensions and Conclusions

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- **Theory:** The problem is NP-hard, but a PTAS exists. (running time is exponential in k)
- Practice: *k*-Means Method.

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"by far the most popular clustering algorithm used in scientific and industrial applications" (Berkhin 2002)

"in practice the number of iterations is generally much less than the number of points" (Duda et al. 2001)

#### **Running Time**

Upper Bound: At most  $(k^2n)^{kd}$  iterations. No clustering can occur twice. Lower Bound: At least  $2^{\Omega(k)}$  iterations for  $d \ge 2$ . [Andrea Vattani (SoCG'09)]

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 $\Rightarrow$  Huge discrepancy between theory and practice. (Focus of this talk: running time.)

#### Main Questions

- Data Clustering What is the k-means method?
- Smoothed Analysis
  What can we do when worst case analysis is too pessimistic?
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- models, e.g., measurement errors or numerical imprecision
- Smoothed compl. low  $\Rightarrow$  bad performance unlikely in practice





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**Model:** Every point is perturbed by independent *d*-dimensional Gaussian with standard deviation  $\sigma$ .

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#### Our Result (FOCS 2009)

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#### Lemma

For  $d \ge 2$ , for every  $X \subseteq [0, 1]^d$ , in the model of smoothed analysis:

$$\mathbf{E}\left[\frac{1}{\Delta}\right] = \operatorname{poly}(n, 1/\sigma) \,.$$

 $\Rightarrow \max_{X,|X|=n} \mathbf{E}(\# \text{Iterations}(\text{per}_{\sigma}(X))) = \text{poly}(n, 1/\sigma).$ 

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- Goal: Show that in every iteration
  - either a center moves significantly
  - or a reassigned point is significantly far from bisector.

Configuration C is  $\varepsilon$ -bad if  $\Phi(C) - \Phi(\operatorname{succ}(C)) \leq \varepsilon$ . Naive approach: Union Bound over all configurations.

$$\Pr\left[\exists \mathsf{Configuration} \ \mathcal{C} \colon \mathcal{C} \text{ is } \varepsilon\text{-bad}\right] \leq \sum_{\mathsf{Configuration} \ \mathcal{C}} \Pr\left[\mathcal{C} \text{ is } \varepsilon\text{-bad}\right]$$

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- Third glance: Enough information!

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small potential drop  $\Rightarrow$  cm(C) must be close to approx(A, B)

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-bad blueprint]  $\leq (k^2 n)^m \cdot (\varepsilon/\sigma)^m$ 

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**Technical Difficulties:** Data points are not independent from approx. bisectors, approximate centers not defined for balanced clusters, blueprints must have enough edges, ...

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#### Extensions and Conclusions

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#### Kullback-Leibler divergence (relative entropy):

$$\mathrm{KLD}(p,q) = \sum_{i=1}^{d} p_i \log\left(\frac{p_i}{q_i}\right)$$

- = number of bits to encode p with Huffman code for q
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### **Bregman Divergences**

**Bregman divergences** are distance measures that generalize squared Euclidean distances and the Kullback-Leibler divergence.

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For any well-behaved Bregman divergence:

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- poly $(n^{\sqrt{k}}, 1/\sigma)$
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Polynomial bound does not extend as it uses special properties of Gaussian perturbations.

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#### **Future Research:**

- improve exponents for *k*-means (currently  $\approx n^{30}$ ) better understanding of dynamics seems necessary for this
- explanation for good approximation ratio
- better analysis of Bregman divergences
- more systematic theory of smoothed local search
- Are all local search problems in PLS easy in smoothed analysis?

# Thank you for your attention!



## **Questions?**