Introduction The Boosted DC Algorithm Numerical experiments References

The Boosted Difference of Convex functions Algorithm

Phan Tu Vuong

School of Mathematical Sciences University of Southampton, UK

joint work with Francisco J. Aragón Artacho

Dynamical systems and Semi-algebraic geometry: interactions with Optimization and Deep Learning

Da Lat University, July 17-21, 2023

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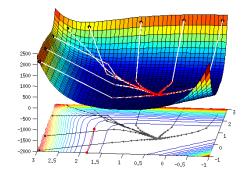
Outline

- Introduction
- The Boosted DC Algorithm
 - The algorithm: Adding a line search step to DCA
 - Convergence under the Kurdyka

 –Łojasiewicz property
- Numerical experiments
 - A DC problem in biochemistry
 - The Minimum Sum-of-Squares Clustering Problem
 - The Multidimensional Scaling Problem
- References

Computational Optimisation





$$\underset{x \in \mathbb{R}^m}{\text{minimise}} \quad \phi(x) + \delta_C(x),$$

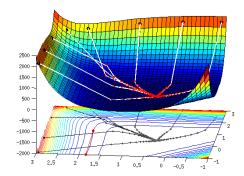
where

$$\delta_{\mathcal{C}}(x) = \begin{cases} 0 & x \in \mathcal{C}, \\ +\infty & \text{otherwise}. \end{cases}$$

Efficient solvers for (strongly) convex cost

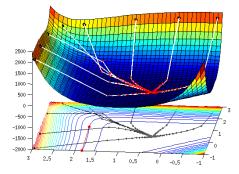
Computational Optimisation

 $\begin{array}{ll}
\text{minimise} & \phi(x) \\
C \subset \mathbb{R}^m
\end{array}$



Computational Optimisation





Algorithm Principles: Given x_k

1. Find a (good) descent direction d_k at x_k (expensive)

$$\phi'(x_k;d_k)<0$$

2. Follow the descent direction as far as possible

We will focus on the nonconvex optimization problem

$$(\mathcal{P})$$
 minimize $g(x) - h(x) =: \phi(x)$,

where $g, h : \mathbb{R}^m \to \mathbb{R} \cup \{+\infty\}$ are convex functions with

$$\inf_{x\in\mathbb{R}^m}\phi(x)>-\infty.$$

The objective function ϕ is a DC function, i.e., a difference of convex functions.

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The following assumptions are made:

• WLOG g and h are strongly convex with modulus $\rho > 0$ (otherwise, take $\widetilde{g}(x) := g(x) + \frac{\rho}{2} ||x||^2$ and $\widetilde{h}(x) := h(x) + \frac{\rho}{2} ||x||^2$).

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- g is continuously differentiable on an open set containing dom h.

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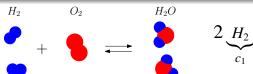
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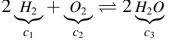
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- g is continuously differentiable on an open set containing dom h.
- h is subdifferentiable at every point in dom h; i.e., $\partial h(x) \neq \emptyset$ for all $x \in \text{dom } h$.

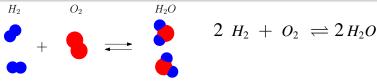
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An example in Biochemistry





An example in Biochemistry



- $(c_1,c_2,c_3)\in\mathbb{R}^3_{>0}$ denotes molecular species concentrations.
- The net reaction rate quantifies the rate of a chemical reaction:

net reaction rate =
$$k_f c_1^2 c_2 - k_r c_3^2$$

 $k_f, k_r \in \mathbb{R}_{\geq 0}$ are the kinetic parameters.

The stoichiometric matrices are defined as

$$F := \left[\begin{array}{c} 2 \\ 1 \\ 0 \end{array} \right] \quad \text{and} \quad R := \left[\begin{array}{c} 0 \\ 0 \\ 2 \end{array} \right]$$

The dynamical equation for time evolution of molecular species is

$$\frac{dc}{dt} = (R - F)(k_f c_1^2 c_2 - k_r c_3^2)$$

A function arising from a biochemical network

Consider a biochemical network with:

- m molecular species, n reversible elementary reactions;
- $F, R \in \mathbb{Z}_{>0}^{m \times n}$ denote the forward and reverse stoichiometric matrices:
- We assume constant non-negative elementary kinetic parameters $k_f, k_r \in \mathbb{R}^n_{>0}$;
- $c \in \mathbb{R}^m_{>0}$ is the vector of molecular species concentrations;
- The dynamical equation of molecular species concentration is

$$\frac{dc}{dt} = (R - F) \left(\exp(\ln(k_f) + F^T \ln(c)) - \exp(\ln(k_r) + R^T \ln(c)) \right);$$

If we transform the right-hand side into logarithmic scale, we get

$$f(x) := [F, R] \exp(p + [F, R]^T x) - [R, F] \exp(p + [F, R]^T x),$$

where $x := \ln(c), p := [\ln(k_f)^T, \ln(k_r)^T]^T$ and $[\cdot, \cdot]$ is the horizontal concatenation operator.

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A simple biochemical network



$$f(x) := ([F, R] - [R, F]) \exp([F, R]^{T}x)$$

A simple biochemical network



$$f(x) := ([F, R] - [R, F]) \exp([F, R]^T x)$$

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$$f(x) := ([F, R] - [R, F]) \exp([F, R]^T x)$$

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Thus, for any $x := (x_1, x_2, x_3)^T \in \mathbb{R}^3$ we have

$$f(x) = \begin{bmatrix} 2e^{x_1} - e^{x_2} - e^{x_3} \\ -e^{x_1} + 2e^{x_2} - e^{x_3} \\ -e^{x_1} - e^{x_2} + 2e^{x_3} \end{bmatrix}.$$

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A DC problem in biochemistry

We are interested in finding zeroes of

$$f(x) := [F, R] \exp(p + [F, R]^T x) - [R, F] \exp(p + [F, R]^T x).$$

Setting

$$p(x) := [F, R] \exp(p + [F, R]^T x)$$
 and $c(x) := [R, F] \exp(p + [F, R]^T x)$

we have an equivalent system of equations

$$p(x) = c(x) \quad x \in \mathbb{R}^m \tag{1}$$

Solving (1) is equivalent to minimising the function

$$||p(x) - c(x)||^2 = 2(||p(x)||^2 + ||c(x)||^2) - ||p(x) + c(x)||^2$$

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$$||p(x) - c(x)||^2 = 2(||p(x)||^2 + ||c(x)||^2) - ||p(x) + c(x)||^2$$

• All the components of p(x) and c(x) are nonnegative convex functions. Hence, $g(x) := 2 (\|p(x)\|^2 + \|c(x)\|^2)$ and $h(x) := \|p(x) + c(x)\|^2$ are nonnegative convex functions.

 (\mathcal{P}) minimize $\phi(x) := g(x) - h(x)$, with g smooth and h convex

Fact (First-order necessary optimality condition)

If $x^* \in dom \phi$ is an optimal solution of $(\mathcal{P}) \Rightarrow \partial h(x^*) = \{\nabla g(x^*)\}$.

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Definition

We say that \bar{x} is a critical point of (P) if $\nabla g(\bar{x}) \in \partial h(\bar{x})$.

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Example

Consider the DC function $\phi:\mathbb{R}^m\to\mathbb{R}$ defined for $x\in\mathbb{R}^m$ by

$$\phi(x) := \left(\|x\|^2 + \sum_{i=1}^m x_i \right) - \left(\sum_{i=1}^m |x_i| \right).$$

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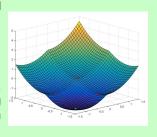
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$$\phi(x) := \left(\|x\|^2 + \sum_{i=1}^m x_i \right) - \left(\sum_{i=1}^m |x_i| \right).$$

Then, ϕ has 2^m critical points (any $x \in \{-1,0\}^m$), and only one point $x^* := (-1,\dots,-1)$ satisfying $\partial h(x^*) = \{\nabla g(x^*)\}$, which is the global minimum of ϕ .



Fukushima-Mine'81

$$(\mathcal{P})$$
 minimize $\phi(x) := g(x) - h(x)$

• In 1981 Fukushima and Mine introduced two algorithms to minimize a composite function g - h, where g is (strictly) convex (possibly nonsmooth) and h is smooth (possibly nonconvex).

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ALGORITHM 1 (FM'81): Fix some parameters $\alpha > 0$ and $0 < \beta < 1$. Let x_0 be any initial point and set k := 0.

• Find the solution y_k of

$$(\mathcal{P}_k)$$
 minimize $g(y) - \langle \nabla h(x_k), y \rangle$.

and set $d_k := y_k - x_k$. If $d_k = 0 \Rightarrow$ stop and return x_k .

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② (Armijo - backtracking) Set $\lambda_k := 1$. while $\phi(x_k + \lambda_k d_k) > \phi(x_k) - \alpha \lambda_k ||d_k||^2$ do $\lambda_k := \beta \lambda_k$.

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- **3** Set $x_{k+1} := x_k + \lambda_k d_k$, k := k+1 and **go to** Step 1.

Le Thi-Pham Dinh-El Bernoussi'86: DC algorithm

$$(\mathcal{P}) \underset{x \in \mathbb{R}^m}{\text{minimize}} \ \phi(x) := g(x) - h(x)$$

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ALGORITHM 2 (DCA): Let x_0 be any initial point and set k := 0.

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 minimize $g(y) - \langle y, u_k \rangle$.

1 If $y_k = x_k \Rightarrow$ stop. Otherwise, set $x_{k+1} := y_k$, k := k+1 and go to Step 1.

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ALGORITHM 2 (DCA): Let x_0 be any initial point and set k := 0.

- ① Choose $u_k \in \partial h(x_k) \Leftrightarrow x_k \in (\partial h)^{-1}(u_k) = \partial h^*(u_k) \Leftrightarrow u_k$ is a solution of (\mathcal{D}_k) minimize $h^*(u) \langle x_k, u \rangle$.
- ② Choose $y_k \in \partial g^*(u_k) \Leftrightarrow u_k \in \partial g(y_k) \Leftrightarrow y_k$ is a solution of (\mathcal{P}_k) minimize $g(y) \langle y, u_k \rangle$.
- **1** If $y_k = x_k \Rightarrow$ **stop**. Otherwise, set $x_{k+1} := y_k$, k := k+1 and **go to** Step 1.

FM'81 and DCA when h is smooth?

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- (Armijo backtracking) Set $\lambda_k := 1$. while $\phi(x_k + \lambda_k d_k) > \phi(x_k) - \alpha \lambda_k ||d_k||^2$ do $\lambda_k := \beta \lambda_k$.
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Proposition

If g and h are strongly convex with constant $\rho > 0$, then

$$\phi(y_k) \le \phi(x_k) - \rho ||d_k||^2 \quad \forall k \in \mathbb{N}.$$

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Proposition

If g and h are strongly convex with constant $\rho > 0$, then $\phi(v_k) < \phi(x_k) - \rho ||d_k||^2 \quad \forall k \in \mathbb{N}.$

 \Rightarrow If $0 < \alpha \leq \rho$, the iterations of FM'81 and DCA coincide.

$$(\mathcal{P}) \underset{x \in \mathbb{R}^m}{\text{minimize}} \ \phi(x) := g(x) - h(x)$$
$$u_k \in \partial h(x_k), y_k \in \partial g^*(u_k)$$

- FM'81 is based on the fact that $d_k := y_k x_k$ is a descent direction at x_k : it holds $\phi'(x_k; d_k) \le -\rho \|d_k\|^2$.
- DCA works thanks to

$$\phi(y_k) = (g - h)(y_k) \le (h^* - g^*)(u_k) - \frac{\rho}{2} ||d_k||^2 \le \phi(x_k) - \rho ||d_k||^2.$$

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Advantages: Simplicity, works well in practice, does not require any line search.

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Drawbacks: It can be very slow.

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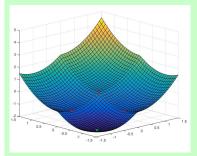
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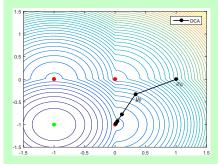
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$$g(x) = \frac{3}{2} \left(x_1^2 + x_2^2 \right) + x_1 + x_2 \quad \text{and} \quad h(x) = |x_1| + |x_2| + \frac{1}{2} \left(x_1^2 + x_2^2 \right).$$



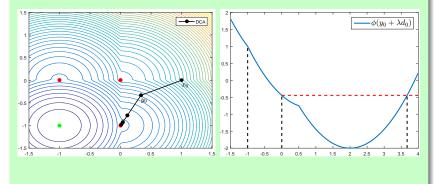
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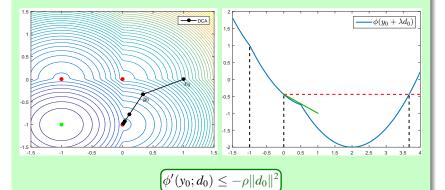
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$$\phi(x) := g(x) - h(x), u_k \in \partial h(x_k), y_k \in \partial g^*(u_k)$$

Proposition

If *g* is differentiable, then $\phi'(y_k; d_k) \leq -\rho ||d_k||^2$.

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Pick any $v \in \partial h(y_k) \neq \emptyset$.

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by convexity of h.

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Since ∂h is strongly monotone with constant ρ and $v \in \partial h(y_k)$,

$$\langle u_k - v, x_k - y_k \rangle \ge \rho ||x_k - y_k||^2 = \rho ||d_k||^2.$$

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Hence

$$\phi'(y_k; d_k) \le \langle \nabla g(y_k) - v, d_k \rangle = \langle u_k - v, y_k - x_k \rangle \le -\rho ||d_k||^2. \quad \blacksquare$$

BDCA (Boosted DC Algorithm)

Fix $\alpha > 0$ and $0 < \beta < 1$. Let x_0 be any initial point and set k := 0.

Select $u_k \in \partial h(x_k)$ and find the unique solution y_k of the problem

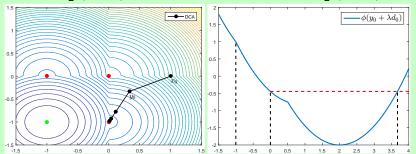
$$(\mathcal{P}_k)$$
 minimize $g(x) - \langle u_k, x \rangle$.

- Set $d_k := y_k x_k$. If $d_k = 0 \Rightarrow$ stop and return x_k .
- Ohoose any $\overline{\lambda}_k \geq 0$. Set $\lambda_k := \overline{\lambda}_k$. while $\phi(y_k + \lambda_k d_k) > \phi(y_k) \alpha \lambda_k^2 \|d_k\|^2$ do $\lambda_k := \beta \lambda_k$.
- **3** Set $x_{k+1} := y_k + \lambda_k d_k, k := k + 1$, and **go to** Step 1.

Example (Revisited)

Consider the DC function $\phi: \mathbb{R}^2 \to \mathbb{R}$ defined as $\phi:=g-h$, where

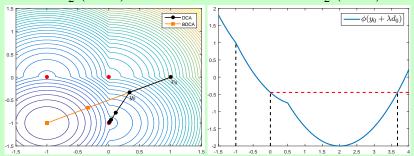
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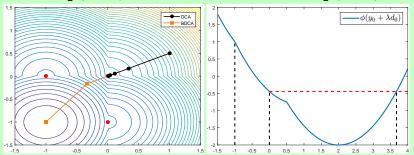
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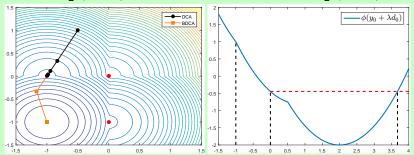
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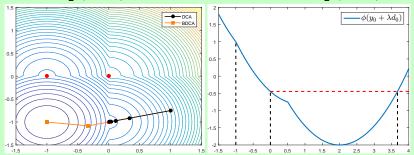
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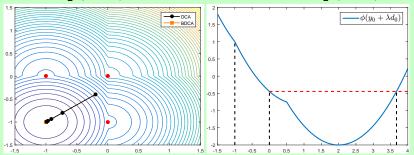
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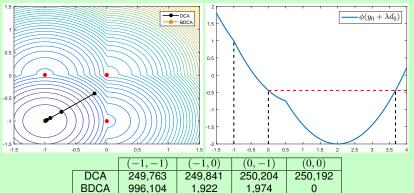


Table: For one million random starting points in $[-1.5, 1.5]^2$, we count the sequences converging to each of the four stationary points.

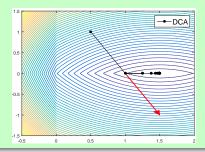
Why to restrict to the case where *g* is differentiable?

Example (Failure of BDCA when g is not differentiable)

Consider the following modification of the previous example

$$g(x) = -\frac{5}{2}x_1 + x_1^2 + x_2^2 + |x_1| + |x_1| \quad \text{and} \quad h(x) = \frac{1}{2}\left(x_1^2 + x_2^2\right),$$

so h is differentiable but g is not. Let $x_0=(0.5,1)$. The point generated by DCA is $y_0=(1,0)$ and $d_0=y_0-x_0=(0.5,-1)$ is not a descent direction for ϕ at y_0 :



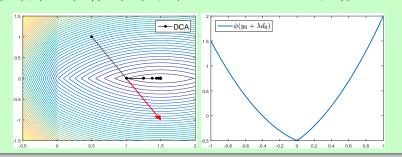
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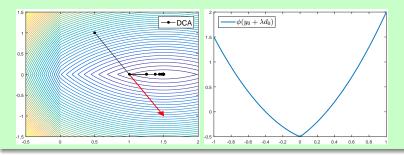
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Proposition

Let $\phi = g - h$, where $g : \mathbb{R} \to \mathbb{R}$ and $h : \mathbb{R} \to \mathbb{R}$ are convex and h is differentiable. If $0 \notin \partial_C \phi(y_k)$, then $\phi'(y_k; y_k - x_k) < 0$.

Convergence of BDCA

$$(\mathcal{P})$$
 minimize $\phi(x) := g(x) - h(x)$

Our convergence results follow the ideas from



H. Attouch, J. Bolte: On the convergence of the proximal algorithm for nonsmooth functions involving analytic features. *Math. Program.* 116 (2009), 5–16.

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For any $x_0 \in \mathbb{R}^m$, either BDCA returns a critical point of (\mathcal{P}) or it generates an infinite sequence such that the following holds.



 \bullet $\phi(x_k)$ is monotonically decreasing and convergent to some ϕ^* .

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- \bullet $\sum_{k=0}^{+\infty} \|d_k\|^2 < +\infty$. Further, if there is some $\bar{\lambda}$ such that $\lambda_k \leq \bar{\lambda}$ for all k, then $\sum_{k=0}^{+\infty} ||x_{k+1} - x_k||^2 < +\infty$.

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The Kurdyka-Łojasiewicz property

Definition

Let $f: \mathbb{R}^m \to \mathbb{R}$ be a locally Lipschitz function. We say that f satisfies the strong Kurdyka–Łojasiewicz inequality at $x^* \in \mathbb{R}^m$ if there exist $\eta \in]0, +\infty[$, a neighborhood U of x^* , and a concave function $\varphi: [0, \eta] \to [0, +\infty[$ such that:

- $\Phi(0) = 0;$
- \circ φ is of class \mathcal{C}^1 on $]0, \eta[$;
- **a** $\varphi' > 0$ on $]0, \eta[$;
- of for all $x \in U$ with $f(x^*) < f(x) < f(x^*) + \eta$ we have

$$\varphi'(f(x) - f(x^*)) \operatorname{dist}(0, \partial_C f(x)) \ge 1.$$

Here $\partial_C f$ stands for the Clarke subdifferential

$$\partial_C f(\bar{x}) = \operatorname{co}\left\{\lim_{x \to \bar{x}, \, x \notin \Omega_f} \nabla f(x)\right\},$$

where co stands for the convex hull and Ω_f denotes the set of Lebesque measure zero where f fails to be differentiable.

Convergence under the Kurdyka-Łojasiewicz property

$$(\mathcal{P})$$
 minimize $\phi(x) := g(x) - h(x)$

Theorem (Convergence)

Let $\{x_k\}$ be the sequence generated by the BDCA. Suppose that $\{x_k\}$ has a cluster point x^* , that ∇g is locally Lipschitz around x^* and that ϕ satisfies the strong Kurdyka–Łojasiewicz inequality at x^* .

Then $\{x_k\}$ converges to x^* , which is a critical point of (\mathcal{P}) .

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Proof

- Technical but "standard".
- λ_k can be zero or unbounded!
- We either need Clarke's subdifferential or to assume that $-\phi$ satisfies the Kurdyka–Łojasiewicz inequality:

$$\nabla g(y_k) - \nabla g(x_k) \in \partial h(x_k) - \nabla g(x_k) = \partial_C (-\phi(x_k)) = -\partial_C \phi(x_k)$$

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Theorem (Rate)

Suppose that the sequence $\{x_k\}$ generated by the BDCA has the limit point x^* , that ∇g is locally Lipschitz continuous around x^* and ϕ satisfies the strong Kurdyka–Łojasiewicz inequality at x^* with $\varphi(t) = Mt^{1-\theta}$ for some M > 0 and $0 < \theta < 1$. Then:

 \bullet if $\theta = 0$, then $\{x_k\}$ converges in a finite number of steps to x^* ;

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- \bullet if $\theta \in [0, \frac{1}{2}]$, then $\{x_k\}$ converges linearly to x^* ;
- \bullet if $\theta \in \left[\frac{1}{2}, 1\right[$, then $\exists \eta > 0$ s.t. $||x_k x^*|| \le \eta k^{-\frac{1-\theta}{2\theta-1}}$ for all large k.

How to choose the trial step size $\overline{\lambda}_k$?

BDCA (Boosted DC Algorithm)

Fix $\alpha > 0$ and $0 < \beta < 1$. Let x_0 be any initial point and set k := 0.

- Select $u_k \in \partial h(x_k)$ and $y_k \in \partial g^*(u_k)$.
- Set $d_k := y_k x_k$. If $d_k = 0 \Rightarrow$ stop and return x_k .
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- **3** Set $x_{k+1} := y_k + \lambda_k d_k, k := k + 1$, and **go to** Step 1.

One possibility would be to set $\overline{\lambda}_k = \overline{\lambda}$ for all k.

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Fix $\alpha > 0$ and $0 < \beta < 1$. Let x_0 be any initial point and set k := 0.

- \bigcirc Select $u_k \in \partial h(x_k)$ and $y_k \in \partial g^*(u_k)$.
- 2 Set $d_k := y_k x_k$. If $d_k = 0 \Rightarrow$ stop and return x_k .
- **3** Choose any $\lambda_k \geq 0$. Set $\lambda_k := \overline{\lambda}_k$. while $\phi(y_k + \lambda_k d_k) > \phi(y_k) - \alpha \lambda_k^2 ||d_k||^2$ do $\lambda_k := \beta \lambda_k$.
- **9** Set $x_{k+1} := y_k + \lambda_k d_k$, k := k+1, and **go to** Step 1.

One possibility would be to set $\overline{\lambda}_k = \overline{\lambda}$ for all k. Instead, we propose:

Self-adaptive trial step size

Fix $\gamma > 1$. Set $\overline{\lambda}_0 := 0$. Choose some $\overline{\lambda}_1 > 0$ and obtain λ_1 by BDCA. For any $k \geq 2$:

- if $\lambda_{k-2} = \overline{\lambda}_{k-2}$ and $\lambda_{k-1} = \overline{\lambda}_{k-1}$ then set $\overline{\lambda}_k := \gamma \lambda_{k-1}$; **else** set $\overline{\lambda}_{k} := \lambda_{k-1}$.
- Obtain λ_k from $\overline{\lambda}_k$ by the backtracking step of BDCA.

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Experiment 1: Finding steady states of biochemical networks

We were interested in finding a solution to the problem

$$\underset{x \in \mathbb{R}^m}{\text{minimize}} \ \phi(x) := \|p(x) - c(x)\|^2$$

where

$$p(x) := [F, R] \exp \left(p + [F, R]^T x \right)$$
 and $c(x) := [R, F] \exp \left(p + [F, R]^T x \right)$,

and $F, R \in \mathbb{Z}_{>0}^{m \times n}$ (*m* molecular species, *n* reversible elementary reactions).

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• It is not difficult to prove that f is real analytic $\Rightarrow f$ satisfies the Łojasiewicz property with some exponent $\theta \in [0, 1)$.

The Boosted DC Algorithm

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and $F, R \in \mathbb{Z}_{>0}^{m \times n}$ (m molecular species, n reversible elementary reactions).

- It is not difficult to prove that f is real analytic \Rightarrow f satisfies the Łojasiewicz property with some exponent $\theta \in [0, 1)$.
- We can then apply BDCA to the functions

$$g(x) := 2 \Big(\|p(x)\|^2 + \|c(x)\|^2 \Big) + \frac{\rho}{2} \|x\|^2 \quad \text{and} \quad h(x) := \|p(x) + c(x)\|^2 + \frac{\rho}{2} \|x\|^2,$$

for any $\rho > 0$. Our results guarantee the convergence of the sequence generated by BDCA, as long as the sequence is bounded.

Finding steady states of biochemical networks

A boring table of computational results...

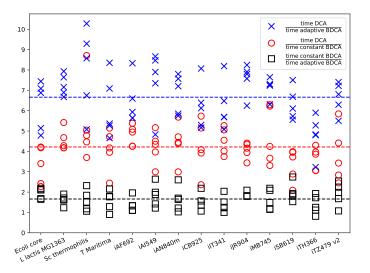
Taking $\rho := 100$, $\overline{\lambda}_k := 50$ (constant), $\beta := 0.5$ and $\alpha := 0.4$, we obtain:

DATA			ALGORITHMS: Time Spent (seconds)						RATIO (avg.)	
Model Name	m	n	BDCA			DCA			DCA/BDCA	
			min.	max.	avg.	min.	max.	avg.	iter.	time
Ecoli core	72	94	16	26	20	68	105	87	4.9	4.4
L lactis MG1363	486	615	2926	4029	3424	14522	18212	16670	5.2	4.9
Sc thermophilis	349	444	291	553	358	1302	2004	1611	4.9	4.5
T Maritima	434	554	1333	2623	1920	5476	12559	8517	4.7	4.4
iAF692	466	546	1677	2275	1967	8337	11187	9466	5.3	4.8
iAl549	307	355	177	254	209	665	1078	913	4.9	4.4
iAN840m	549	840	3229	6939	4721	16473	28957	21413	5.0	4.5
iCB925	416	584	1831	2450	2133	7358	11465	9887	5.0	4.6
iIT341	425	504	1925	2883	2302	9434	20310	12262	5.7	5.3
iJR904	597	915	6363	9836	7623	24988	43640	33621	4.4	4.8
iMB745	528	652	2629	5091	4252	16438	25172	20269	5.0	4.8
iSB619	462	598	2407	5972	3323	8346	25468	13967	4.3	4.2
iTH366	587	713	3310	5707	4464	13613	30044	20715	5.0	4.6
iTZ479 v2	435	560	1211	2656	2216	7368	12592	10120	4.9	4.6

For each model, we selected a random kinetic parameter $p \in [-1, 1]^{2n}$ and 10 initial random points $x_0 \in [-2, 2]^m$. BDCA was run 1000 iterations. DCA was run until it reached the same value obtained by BDCA.

Finding steady states of biochemical networks

Comparison of the constant and self-adaptive trial step size strategy for BDCA



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The COnstraint-Based Reconstruction and Analysis Toolbox

View The COBRA Toolbox source code on GitHub











The COnstraint-Based Reconstruction and Analysis Toolbox is a MATLAB software suite for quantitative prediction of cellular and multicellular biochemical networks with constraint-based modelling. It implements a comprehensive collection of basic and advanced modelling methods, including reconstruction and model generation as well as biased and unbiased model-driven analysis methods.

It is widely used for modelling, analysing and predicting a variety of metabolic phenotypes using genome-scale biochemical networks.

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The Minimum Sum-of-Squares Clustering Problem

Clustering is an unsupervised technique for data analysis whose objective is to group a collection of objects into clusters based on similarity.

- Let $A = \{a^1, \dots, a^n\}$ be a finite set of points in \mathbb{R}^m , which represent the data points to be grouped.
- The goal is to partition A into k disjoint subsets A^1, \ldots, A^k , called clusters, such that a clustering criterion is optimized.

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The *Minimum Sum-of-Squares Clustering* criterion, one tries to minimize the Euclidean distance of each data point to the centroid of its clusters, denoted by $X := (x^1, \dots, x^k) \in \mathbb{R}^{m \times k}$:

$$\underset{X \in \mathbb{R}^{m \times k}}{\text{minimize}} \ \phi(X) := \frac{1}{n} \sum_{i=1}^{n} \min_{j=1,...,k} \|x^{j} - a^{i}\|^{2}$$

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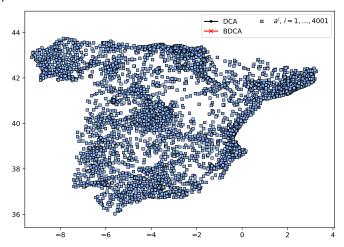
$$\underset{X \in \mathbb{R}^{m \times k}}{\text{minimize}} \ \phi(X) := \frac{1}{n} \sum_{i=1}^{n} \min_{j=1,\dots,k} \|x^{j} - a^{i}\|^{2} = g(X) - h(X),$$

where

$$g(X) := \frac{1}{n} \sum_{i=1}^{n} \sum_{i=1}^{k} \left\| x^{j} - a^{i} \right\|^{2} + \frac{\rho}{2} \|X\|^{2},$$
 (strongly convex and smooth)

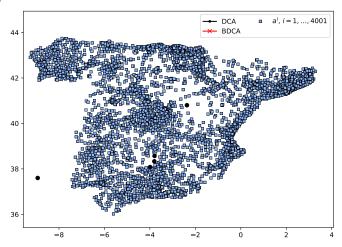
$$h(X) := \frac{1}{n} \sum_{i=1,\dots,k}^{n} \max_{j=1,\dots,k} \sum_{i=1,\dots,k}^{k} \left\| x^t - a^i \right\|^2 + \frac{\rho}{2} \|X\|^2.$$
 (strongly convex but nonsmooth).

Experiment 2: Clustering the Spanish cities in the peninsula



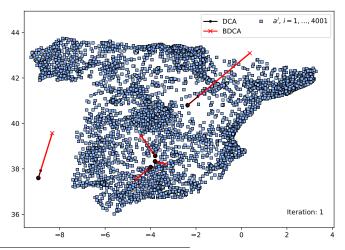
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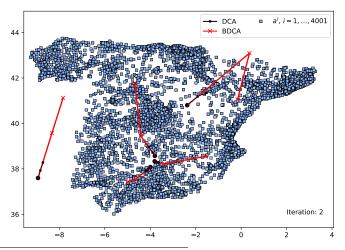
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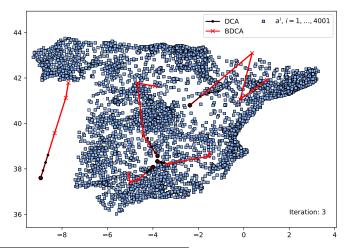
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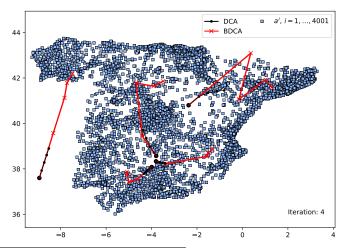
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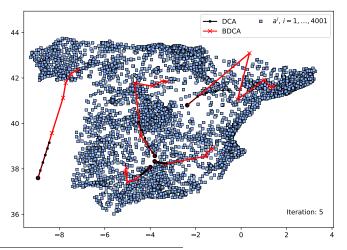
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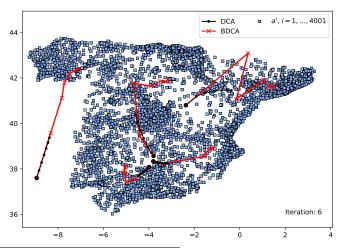
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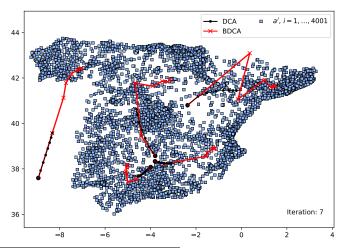
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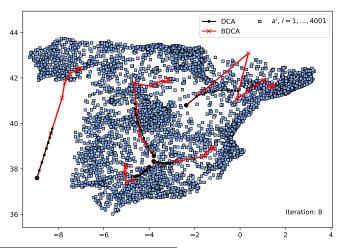
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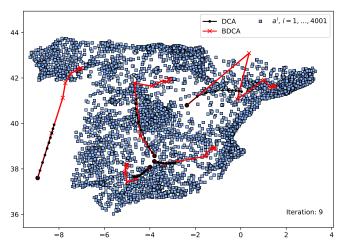
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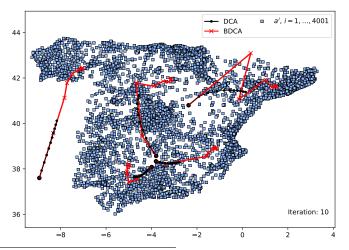
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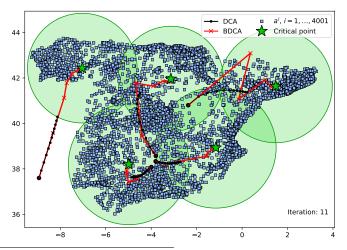
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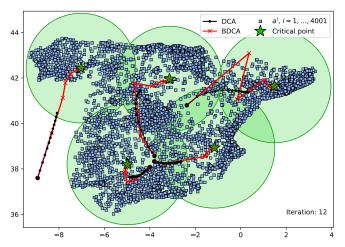
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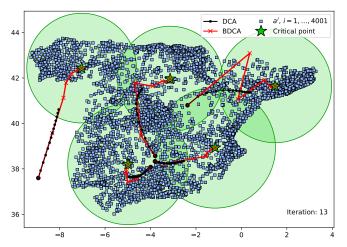
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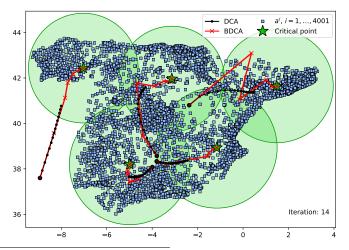
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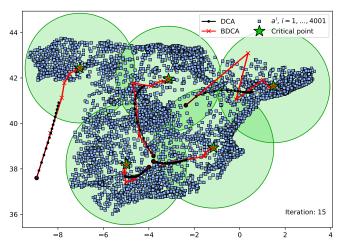
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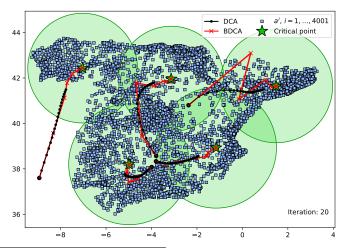
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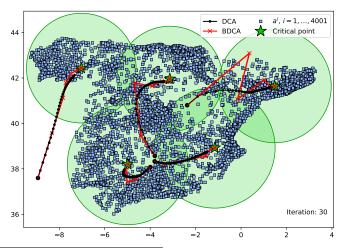
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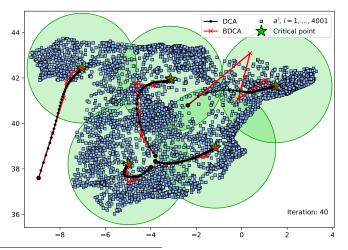


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Numerical experiments

Experiment 2: Clustering the Spanish cities in the peninsula

PROBLEM: Find a partition into 5 clusters of the 4001 Spanish cities in the peninsula with more than 500 residents¹.

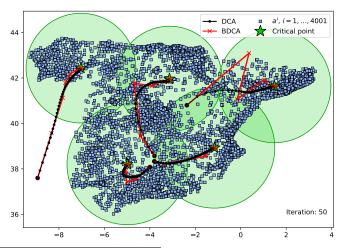


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The Boosted DC Algorithm References

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PROBLEM: Find a partition into k clusters of the 4001 Spanish cities in the peninsula with more than 500 residents, with $k \in \{5, 10, 15, 20, 25, 50, 75, 100\}$.

For 100 random starting points, BDCA was stopped when the relative error of ϕ was smaller than 10^{-3} . Then, DCA was run from the same starting point until the same value of the objective function was reached (which did not happen in 31 instances).

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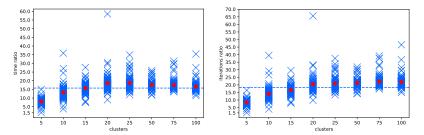


Figure: Comparison between DCA and BDCA. We represent the ratios of running time (left) and number of iterations (right) between DCA and BDCA.

Experiment 3: Clustering random points in an *m*-dimensional box

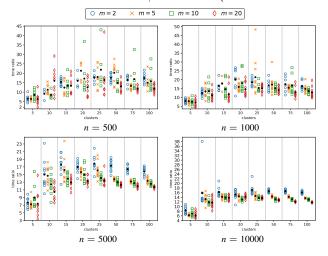
We took n random points in \mathbb{R}^m (normal distribution), with $n \in \{500, 1000, 5000, 10000\}$ and $m \in \{2, 5, 10, 20\}$. For each (n, m), 10 random starting points were chosen. Then:

- BDCA was run to solve the *k*-clustering, with $k \in \{5, 10, 15, 20, 25, 50, 75, 100\}$.
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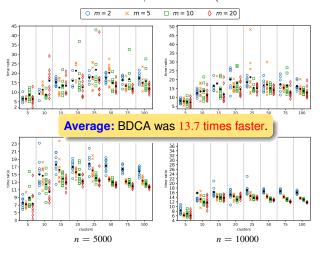
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The Multidimensional Scaling Problem

Suppose that we have a table of distances between some objects, known as the dissimilarity matrix. If the objects are n points x^1, x^2, \ldots, x^n in \mathbb{R}^q , the dissimilarity matrix can be defined by the Euclidean distance between them:

$$\delta_{ij} = \|x^i - x^j\| := \mathsf{d}_{ij}(X),$$

where we denote by *X* the $n \times q$ matrix whose rows are x^1, x^2, \dots, x^n .

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where we denote by X the $n \times q$ matrix whose rows are x^1, x^2, \dots, x^n . Given a target dimension $p \le q$, the MDS problem consists in finding n points in \mathbb{R}^p , which are represented by an $n \times p$ matrix X^* , such that

$$Stress(X^*) := \sum_{i < j} w_{ij} \left(\mathsf{d}_{ij}(X^*) - \delta_{ij} \right)^2$$

is smallest, where $w_{ij} \ge 0$ are weights ($w_{ij} = 0$ if δ_{ij} is missing).

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is smallest, where $w_{ii} > 0$ are weights ($w_{ii} = 0$ if δ_{ii} is missing). This can be equivalently formulated as a DC problem by setting

$$g(X) := \frac{1}{2} \sum_{i < j} w_{ij} \mathbf{d}_{ij}^2(X) + \frac{\rho}{2} ||X||^2,$$

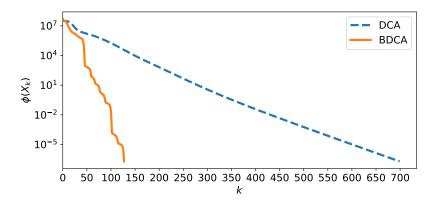
$$h(X) := \sum_{i < j} w_{ij} \delta_{ij} \mathsf{d}_{ij}(X) + \frac{\rho}{2} \|X\|^2,$$

for some $\rho \geq 0$. Moreover, it is clear that g is differentiable while h is not, but ∂h can be explicitly computed.

Experiment 4: MDS for Spanish cities

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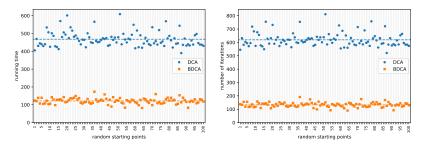
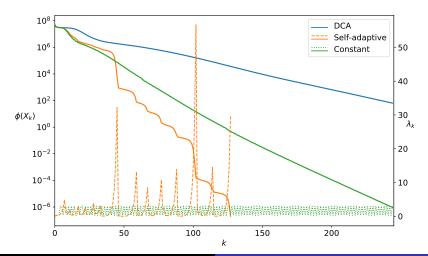


Figure: Running time (left) and number of iterations (right) of DCA and BDCA for 100 random instances.

Experiment 4: MDS for Spanish cities



References

Main References



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