

STOCHASTIC DUAL NEWTON ASCENT FOR EMPIRICAL RISK MINIMIZATION

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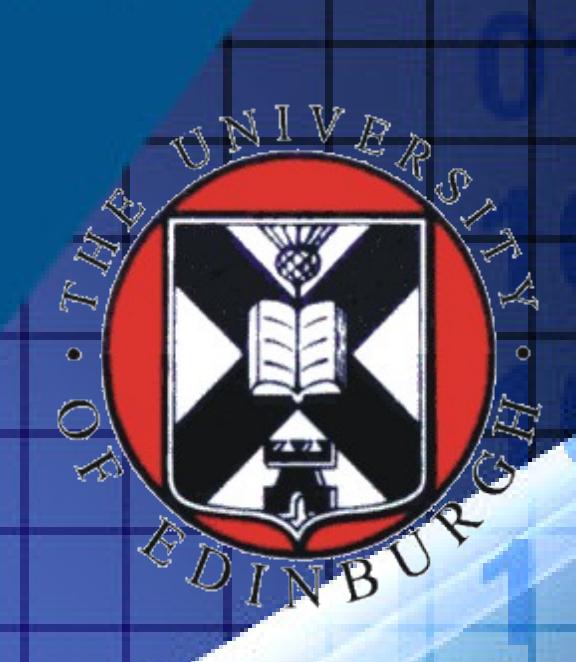
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Introduction

We study the problem of minimizing the average of a large number of **$1/\gamma$ -smooth convex functions** penalized with a **1-strongly convex regularizer**.

$$\min_{w \in \mathbb{R}^d} P(w) := \frac{1}{n} \sum_{i=1}^n \phi_i(\mathbf{a}_i^\top \mathbf{w}) + \lambda \mathbf{g}(\mathbf{w}). \quad (\text{P})$$

Each $a_i \in \mathbb{R}^d$ and we write $\mathbf{A} = [a_1, \dots, a_n] \in \mathbb{R}^{d \times n}$. Let g^* and $\{\phi_i^*\}_i$ be the Fenchel conjugate functions of g and $\{\phi_i\}_i$, respectively. In the case of g , for instance, we have $g^*(s) = \sup_{w \in \mathbb{R}^d} \langle w, s \rangle - g(w)$.

The (Fenchel) dual problem of (P) can be written as:

$$\max_{\alpha \in \mathbb{R}^n} D(\alpha) := \frac{1}{n} \sum_{i=1}^n -\phi_i^*(-\alpha_i) - \lambda g^*\left(\frac{1}{\lambda n} \mathbf{A}\alpha\right). \quad (\text{D})$$

The Algorithm

Sampling \hat{S} : A random subset of $\{1, 2, \dots, n\}$ such that $\forall i : \text{Prob}(i \in \hat{S}) > 0$ and $\text{Prob}(\hat{S} = \emptyset) = 0$.

Algorithm 1: SDNA Algorithm

- 1: **Initialization:** $\alpha^0 \in \mathbb{R}^n$; $\bar{\alpha}^0 = \frac{1}{\lambda n} \mathbf{A}\alpha^0$
- 2: **for** $k = 0, 1, 2, \dots$ **do**
- 3: Primal update: $w^k = \nabla g^*(\bar{\alpha}^k)$
- 4: **Generate a random set of blocks** $S_k \sim \hat{S}$
- 5: Compute:

$$\Delta\alpha^k = \arg \min_{\mathbf{h} \in \mathbb{R}^n} \langle \mathbf{A}^\top w^k, \mathbf{I}_{S_k} \mathbf{h} \rangle + \frac{1}{2} \mathbf{h}^\top \mathbf{X}_{S_k} \mathbf{h} \\ + \sum_{i \in S_k} \phi_i^*(-\alpha_i^k - \mathbf{h})$$

- 6: Dual update: $\alpha^{k+1} := \alpha^k + (\Delta\alpha^k)_{S_k}$
- 7: Average update: $\bar{\alpha}^{k+1} = \bar{\alpha}^k + \frac{1}{\lambda n} \sum_{i \in S_k} \Delta\alpha_i^k a_i$
- 8: **end for**

Where $\mathbf{X} = \mathbf{A}^\top \mathbf{A}$ and \mathbf{X}_{S_k} is the matrix obtained from \mathbf{X} retaining elements \mathbf{X}_{ij} for which both $i, j \in S_k$ and zeroing out all other elements.

Iteration Complexity of SDNA

Theorem: Let \hat{S} be a uniform sampling and let $\tau := \mathbf{E}[|\hat{S}|]$. The output sequence $\{w^k, \alpha^k\}_{k \geq 0}$ of Algorithm 1 satisfies:

$$\mathbf{E}[P(w^k) - D(\alpha^k)] \leq \frac{(1 - \sigma)^k}{\theta(\hat{S})} (D(\alpha^*) - D(\alpha^0)),$$

where $\sigma := \frac{\tau \min(1, s_1)}{n}$, $\theta(\hat{S}) := \min_i \frac{p_i \lambda \gamma n}{v_i + \lambda \gamma n}$, $s_1 = \lambda \min \left[\left(\frac{1}{\tau \gamma \lambda} \mathbf{E}[(\mathbf{A}^\top \mathbf{A})_{\hat{S}}] + \mathbf{I} \right)^{-1} \right]$ and $v \in \mathbb{R}_{++}^n$ is a vector satisfying:

$$\mathbf{E}[(\mathbf{A}^\top \mathbf{A})_{\hat{S}}] \preceq \text{diag}(p) \cdot \text{diag}(v). \quad (1)$$

Comparison with Mini-Batch SDCA

Algorithm 2: Minibatch SDCA

- 1: **Parameters:** uniform sampling \hat{S} , vector $v \in \mathbb{R}_{++}^n$
- 2: **Initialization:** $\alpha^0 \in \mathbb{R}^n$; set $\bar{\alpha}^0 = \frac{1}{\lambda n} \mathbf{A}\alpha^0$
- 3: **for** $k = 0, 1, 2, \dots$ **do**
- 4: Primal update: $w^k = \nabla g^*(\bar{\alpha}^k)$
- 5: Generate a random set of blocks $S_k \sim \hat{S}$
- 6: Compute for each $i \in S_k$
- 7: $h_i^k = \arg \min_{h_i \in \mathbb{R}} h_i(a_i^\top w^k) + \frac{v_i}{2} |h_i|^2 + \phi_i^*(-\alpha_i^k - h_i)$
- 8: Dual update: $\alpha^{k+1} := \alpha^k + \sum_{i \in S_k} h_i^k e_i$
- 9: Average update: $\bar{\alpha}^{k+1} = \bar{\alpha}^k + \frac{1}{\lambda n} \sum_{i \in S_k} h_i^k a_i$
- 10: **end for**

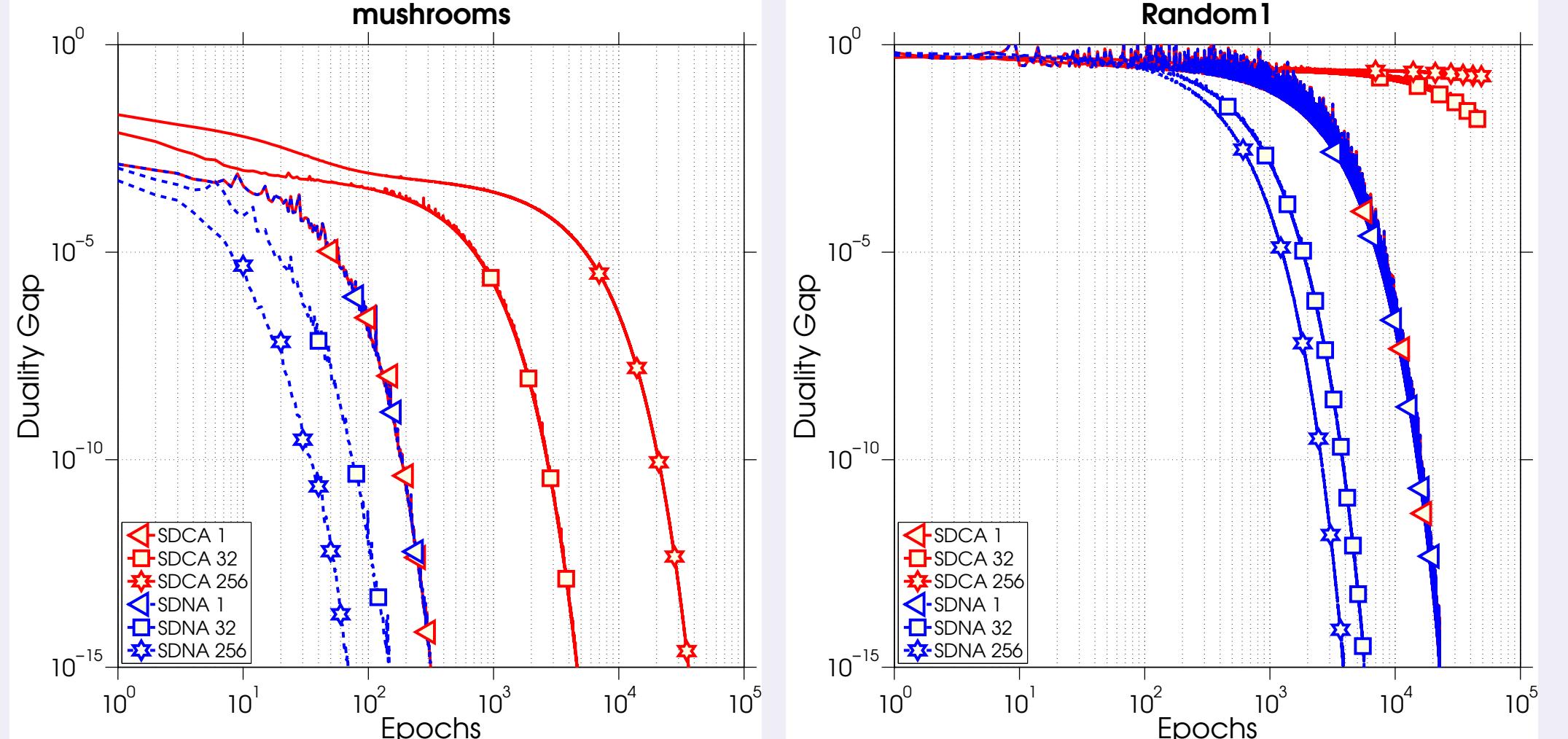
Theorem: If (1) holds, then the output sequence $\{w^k, \alpha^k\}_{k \geq 0}$ of Algorithm 2 satisfies:

$$\mathbf{E}[P(w^k) - D(\alpha^k)] \leq \frac{(1 - \theta(\hat{S}))^k}{\theta(\hat{S})} (D(\alpha^*) - D(\alpha^0)).$$

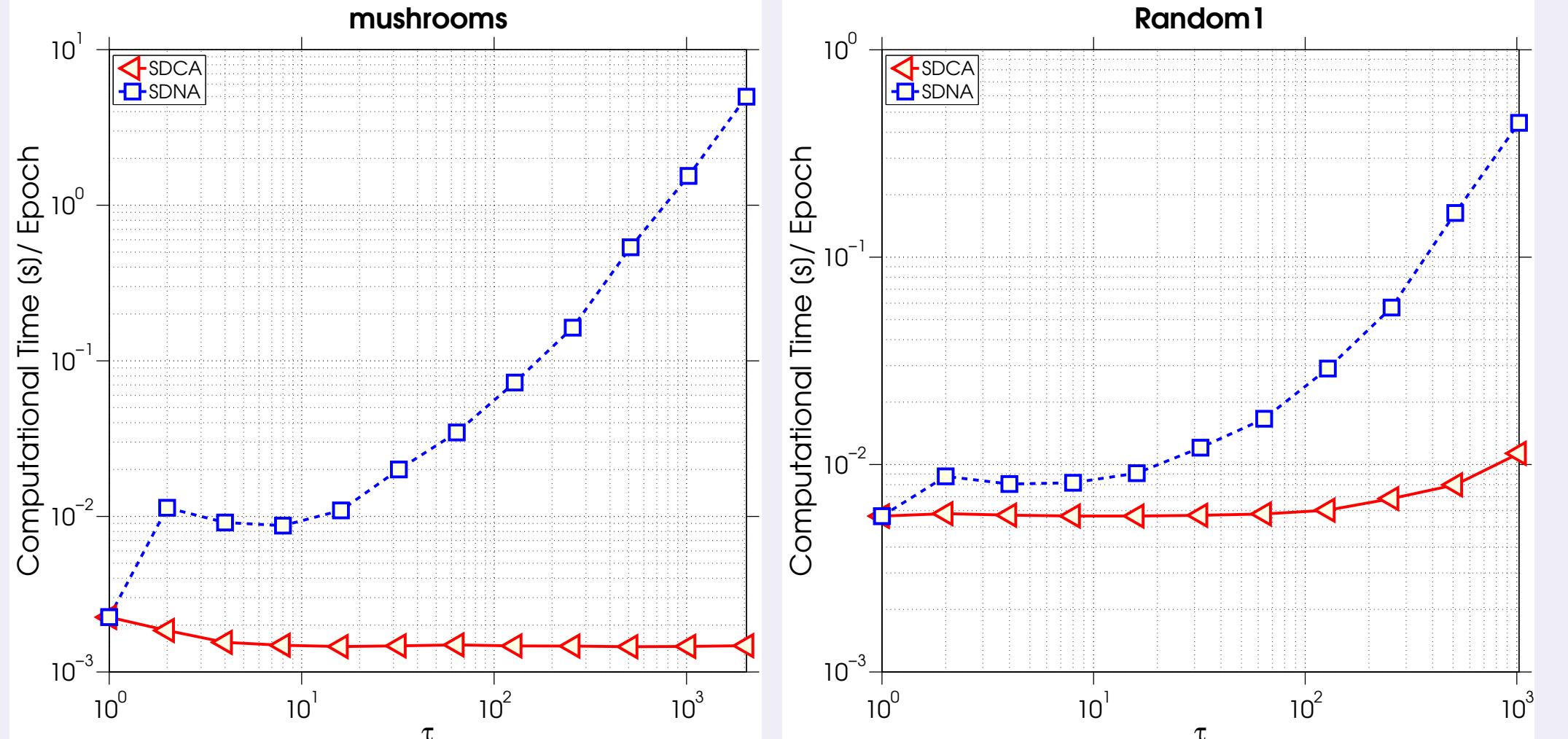
Moreover, $\theta(\hat{S}) \leq \sigma$.

Numerical Experiments

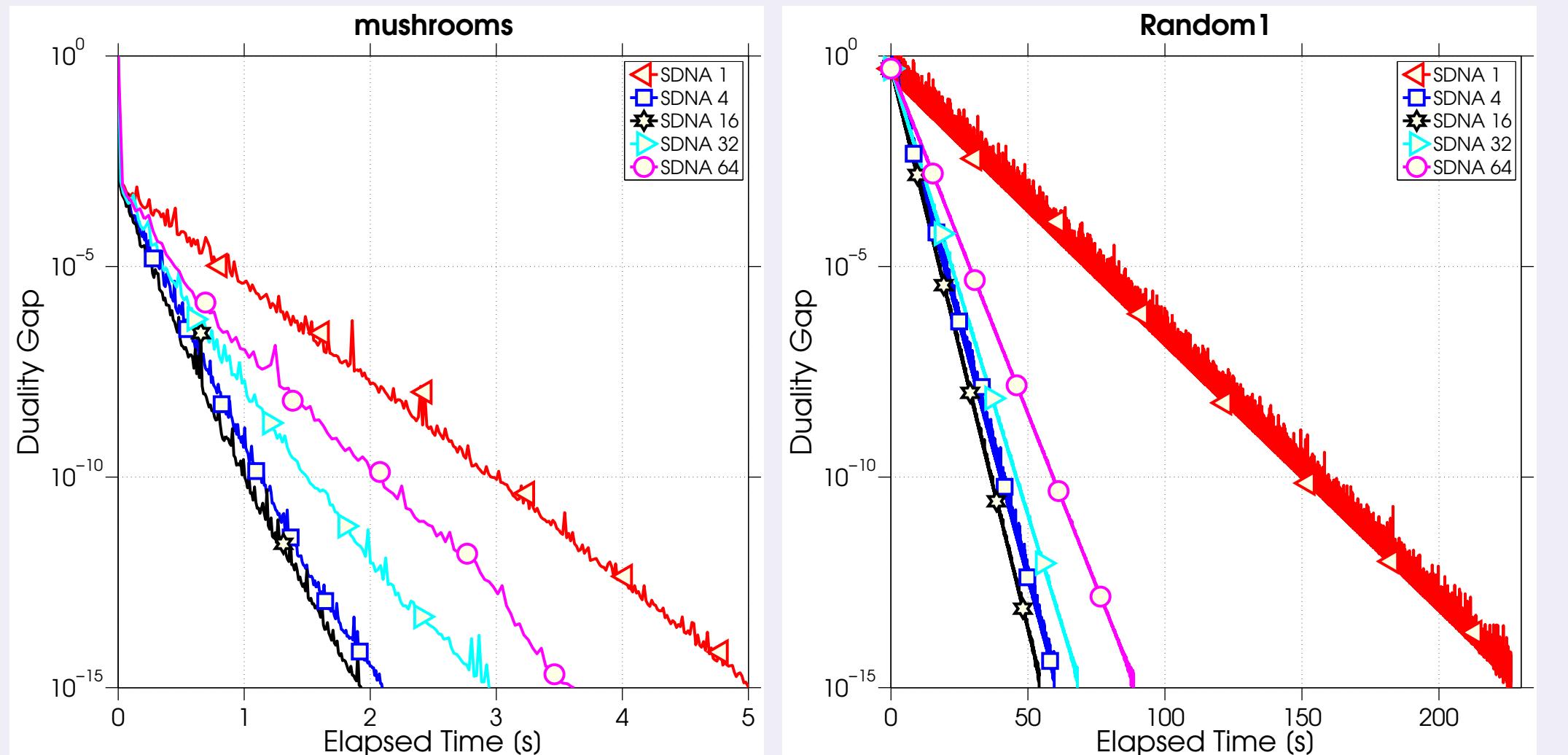
Comparison of SDNA and SDCA for minibatch sizes $\tau = 1, 32, 256$ on a real (left) and synthetic (right) dataset. The methods coincide for $\tau = 1$.



Time it takes for SDNA and SDCA to process a single epoch as a function of the minibatch size τ .



Runtime of SDNA for minibatch sizes $\tau = 1, 4, 16, 32, 64$.



References

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