# TeraPCA: A fast and scalable method to study genetic variation in tera-scale genotypes

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#### **Problem statement**

- Principal Component Analysis (PCA) is a key tool in the study of population structure in human genetics.
- As modern datasets become increasingly larger in size, traditional approaches based on loading the entire dataset in the system memory (RAM) become impractical and out-of-core implementations are the only viable alternative.

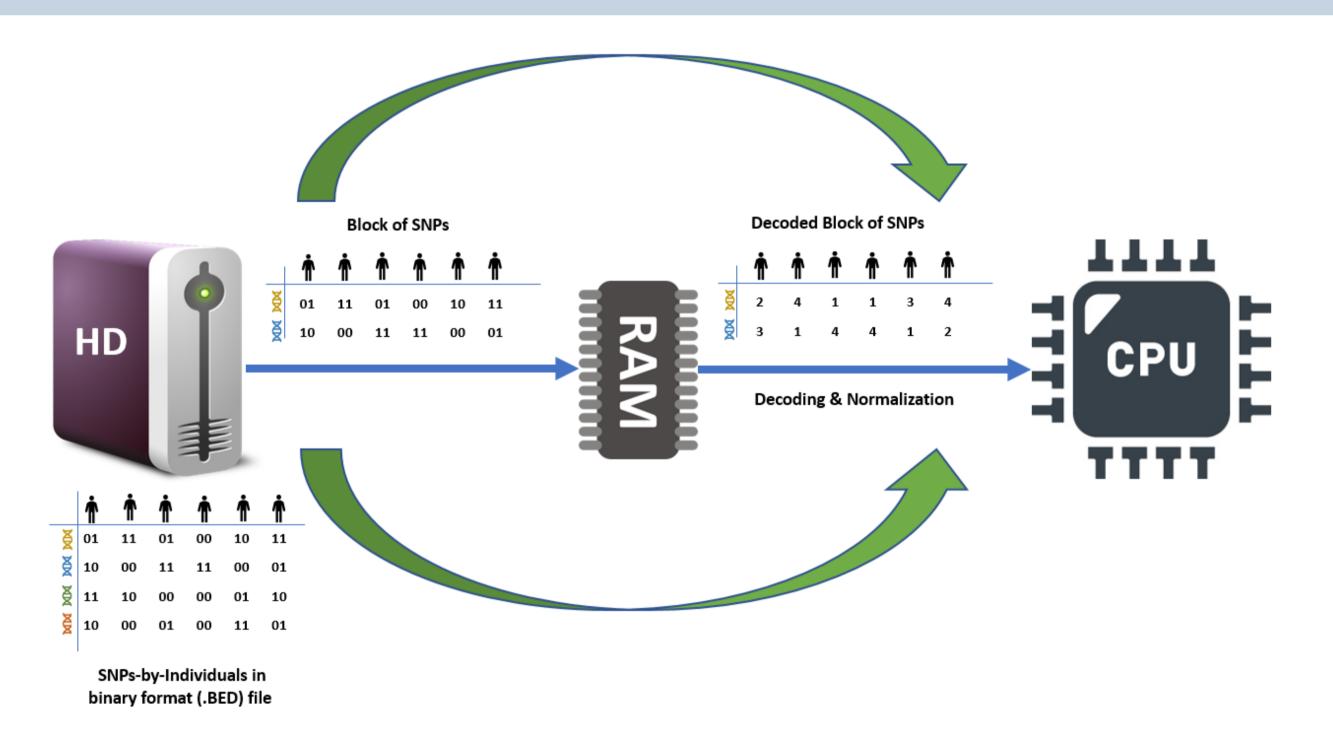
## The TeraPCA library

Our contribution is summarized in TeraPCA, a C++ library to perform out-of-core PCA of large genetics datasets:

- ► TeraPCA computes the sought Principal Components by partially solving a symmetric eigenvalue problem.
- This eigenvalue problem is solved by Randomized Subspace Iteration.

Why it works: typical applications in genetics only require a very small number of PCs (e.g., 10) within a small accuracy (e.g., two-three digits). Most importantly, Randomized Subspace Iteration features block iteration thus allowing higher granularity in out-of-core settings.

### TeraPCA in a Nutshell



Algorithm Randomized Subspace Iteration

**Input:**  $A^{\top} \in \mathbb{R}^{n \times m}$ , initial guess matrix  $X_0 \in \mathbb{R}^{m \times s}$  with elements drawn i.i.d. from the normal distribution  $\mathcal{N}(0,1)$ ,  $k \geq 1$ , and  $s \geq k$ .

**Output:** The k leading approximate left singular vectors of A.

- 1:  $C = A(A^{T}X_{0})$
- 2: repeat
- $Q = \operatorname{orth}(C)$
- 4:  $C = AA^{\top}Q$
- 5:  $M = Q^{\top}C$
- 6: Compute the eigenvalue decomposition  $M = XDX^{T}$
- 7: C = QX
- 8: until convergence
- 9: **return** first *k* columns of Q

#### **Algorithm** Out-of-core MMV $C = A(A^TX)$

**Input:**  $\zeta > 0$ ,  $m \times s$  matrix X.

**Output:**  $m \times s$  matrix C.

- 1: C = 0
- 2: **for**  $i = 1 : \zeta$  **do**
- Fetch the i-th row-block of  $A^{ op}$
- 4:  $C = C + A_i(A_i^\top X)$
- 5: end for

## Datasets & Experimental Setup

- Our goal is to approximate the **ten** leading Principal Components (PCs). For TeraPCA we set the dimension (*s*) of the initial approximation subspace equal to **twenty**.
- All our experiments ran at Purdue's Brown cluster on a dedicated node which features an Intel Xeon Gold 6126 @ 2.6 GHz processor, 96 GB RAM and 64-bit CentOS Linux 7 operating system.

Dataset	Size (.PED file)	Size (.BED file)	# Samples	# SNPs
$S_1$ (simulated)	19 GB	120 MB	5,000	1,000,000
$S_2$ (simulated)	38 GB	239 MB	10,000	1,000,000
$S_3$ (simulated)	373 GB	24 GB	100,000	1,000,000
$S_4$ (simulated)	1.9 TB	117 GB	500,000	1,000,000
$S_5$ (simulated)	3.7 TB	233 GB	1,000,000	1,000,000
$S_6$ (simulated)	38 GB	2.4 GB	100,000	100,000
$S_7$ (simulated)	150 GB	9.4 GB	2,000	20,000,000
HGDP	615 MB	39 MB	1,043	154,417
1000 Genomes	8.4 GB	483 MB	2,504	808,704
PRK	2 GB	126 MB	4,706	111,831
T2D	1.8 GB	111 MB	6,370	72,457

- TeraPCA GitHub Repository: https://github.com/aritra90/TeraPCA
- Data Simulator GitHub Repository: https://github.com/eugeniamaria/DataSimulator

## Time comparisons

Comparison with FlashPCA2 (only 2GB RAM was allowed)

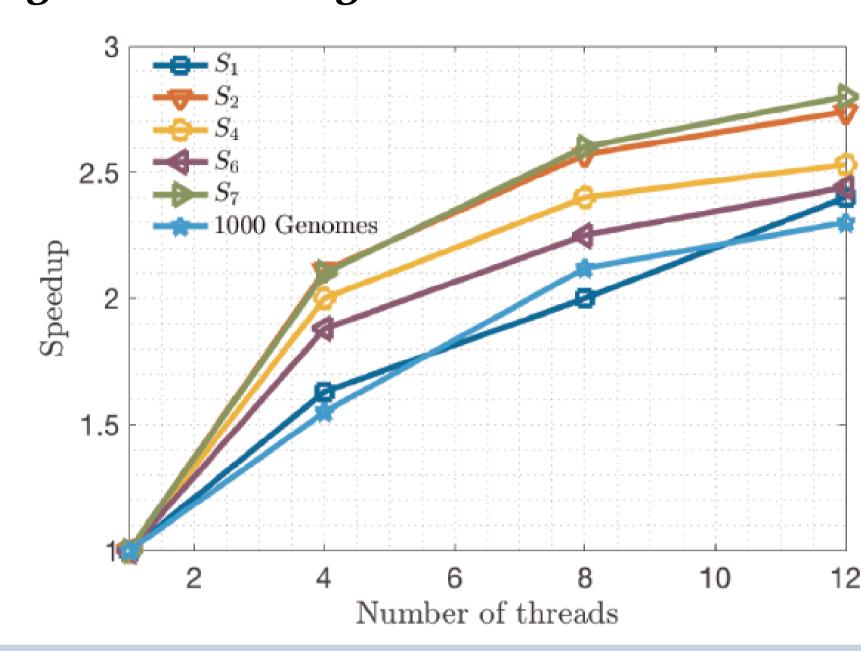
**Table:** TeraPCA vs FlashPCA2 (\* indicates no convergence after 50 hrs).

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Dataset	TeraPCA	FlashPCA2	Speed-up
$S_1$	26.2 mins	33.3 mins	1.27
$S_2$	39.3 mins	87.5 mins	2.22
$S_3$	7.9 hrs	35.6 hrs	4.50
$S_4$	7.3 hrs	n/a*	$\infty$
$S_5$	13.2 hrs	n/a*	$\infty$
$S_6$	39.5 mins	141.1 mins	3.57
$S_7$	37.3 mins	106.5 mins	2.86
HGDP	6.5 secs	7.7 secs	1.22
1000 Genomes	4.3 mins	3.5 mins	0.81
T2D	96 secs	119 secs	1.24
PRK	76 secs	73 secs	0.96

# TeraPCA has an advantage over FlashPCA2 (which is based on Implicit Restarted Arnoldi) due to its block nature which allows to:

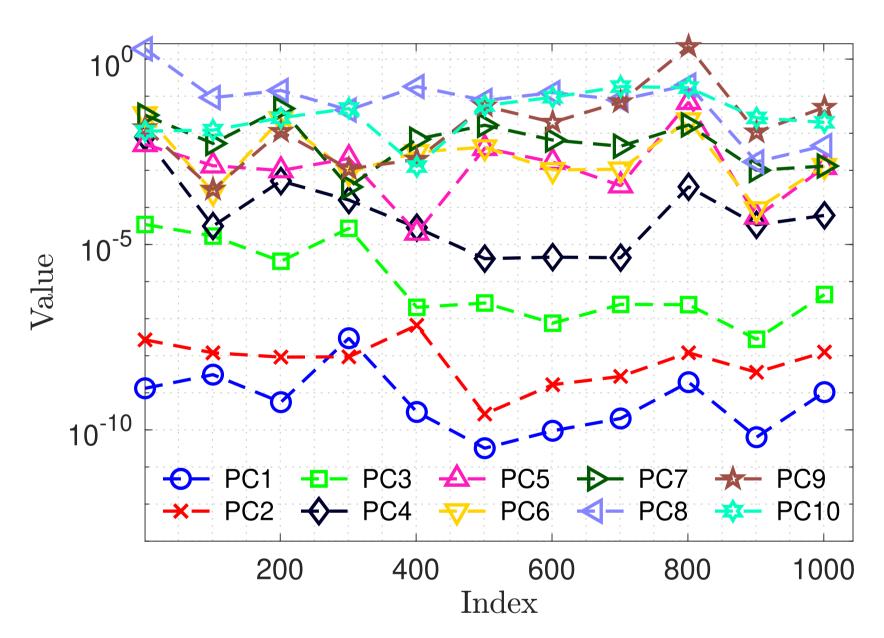
- search for multiple PCs simultaneously
- perform more computations per epoch
- take advantage of state-of-the-art dense linear algebra kernels (e.g., BLAS, LAPACK)

#### Speedup using Multithreading



### **Accuracy Results**

Accuracy of leading PCs



**Figure:** Element-wise relative error of the 10 leading PCs computed by TeraPCA versus those computed by LAPACK for the HGDP dataset.

#### Accuracy of leading eigenvalues

Table: Accuracy of the 10 leading eigenvalues computed for TeraPCA and FlashPCA2.

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eigenvalue	relative error		eigenvalue	relative error	
index	TeraPCA	FlashPCA2	index	TeraPCA	FlashPCA2
1	9.91E-15	1.74E-03	6	3.01E-06	7.63E-04
2	1.02E-13	1.30E-03	7	3.36E-06	1.47E-03
3	5.65E-11	1.49E-03	8	1.04E-05	6.81E-04
4	2.18E-08	1.31E-03	9	7.11E-05	1.28E-03
5	2.65E-06	1.10E-03	10	1.74E-04	7.44E-04

## Acknowledgements

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