
BLAS AND LAPACK

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Linear Algebra in Computational Chemistry

$$\mathbf{A}\mathbf{V} = \mathbf{\Lambda}\mathbf{V}$$

- * Eigenvalue Problems

- * The Schrödinger equation $\hat{H}\Psi = E\Psi$

- * Configuration interaction (Hamiltonian matrix)

- * Normal mode analysis (Hessian matrix)

- * Moments of inertia (Inertia tensor)

Linear Algebra in Computational Chemistry

$$\mathbf{Ax} = \mathbf{b}$$

- * Linear Equation Systems
 - * Orbital response equations (CPHF)
 - * Hessian matrix inversion
 - * Geometry step (potential-energy-surface scanning)

Linear Algebra in Computational Chemistry

$$\mathbf{AB} = \mathbf{C}$$

- * Matrix-Matrix Multiplication

- * Algebraic (basis-set) problems cast as matrix problems

- * Coupled cluster theory (many-body methods)

- * Self-consistent field theory (Roothaan's algorithm)

BLAS

- * Basic Linear Algebra Subprograms

- * BLAS1:

- * vector norms

- * dot products

- * vector scaling

- * addition of a scalar multiple of one vector to another (AXPY):

$$\mathbf{y} = \alpha \mathbf{x} + \mathbf{y}$$

BLAS

- * Basic Linear Algebra Subprograms

- * BLAS2:

- * matrix-vector operations:

$$\mathbf{y} = \alpha \mathbf{A} \mathbf{x} + \beta \mathbf{y}$$

BLAS

- * Basic Linear Algebra Subprograms

- * BLAS3:

- * matrix-matrix operations:

$$\mathbf{C} = \alpha \mathbf{A} \mathbf{B} + \beta \mathbf{C}$$

- * GEMM = GEneral Matrix Multiply:

LAPACK

- * Linear Algebra PACKage for solving:

- * Systems of linear equations:

$$\mathbf{Ax} = \mathbf{b}$$

- * Singular value problems;

$$\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}$$

- * Eigenvalue problems:

$$\mathbf{AV} = \mathbf{\Lambda}\mathbf{V}$$

QR Algorithm

$$\mathbf{A}\mathbf{V} = \mathbf{\Lambda}\mathbf{V}$$

QR Decomposition: A square matrix may be factored into a product of an orthogonal matrix and an upper-triangular matrix:

$$\mathbf{A} = \mathbf{Q}\mathbf{R}$$

$$\mathbf{Q}^T \mathbf{Q} = \mathbf{I}$$

$$\mathbf{A}_0 \equiv \mathbf{A} = \mathbf{Q}_0 \mathbf{R}_0$$

$$\mathbf{A}_1 \equiv \mathbf{R}_0 \mathbf{Q}_0 = \mathbf{Q}_0^T \mathbf{Q}_0 \mathbf{R}_0 \mathbf{Q}_0 = \mathbf{Q}_0^T \mathbf{A}_0 \mathbf{Q}_0 = \mathbf{Q}_0^{-1} \mathbf{A} \mathbf{Q}_0$$

...

$$\mathbf{A}_{k+1} \equiv \mathbf{R}_k \mathbf{Q}_k = \mathbf{Q}_k^T \mathbf{Q}_k \mathbf{R}_k \mathbf{Q}_k = \mathbf{Q}_k^T \mathbf{A}_k \mathbf{Q}_k = \mathbf{Q}_k^{-1} \mathbf{A}_k \mathbf{Q}_k$$

Naming Conventions

- * Precision:

- * S = single precision real (float)

- * D = double-precision real (double)

- * C = single-precision complex

- * Z = double-precision complex

- * Matrix type: GE = general; SY = symmetric

- * Drivers: SV = solve; EV = eigenvalues; SVD = duh

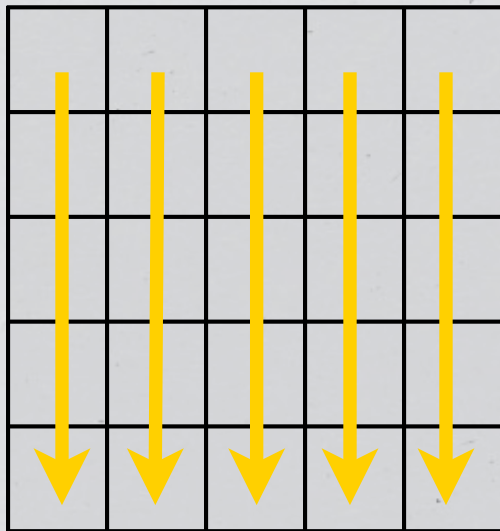
Library Interface: DGEMM

* $C = \alpha * A * B + \beta * C$

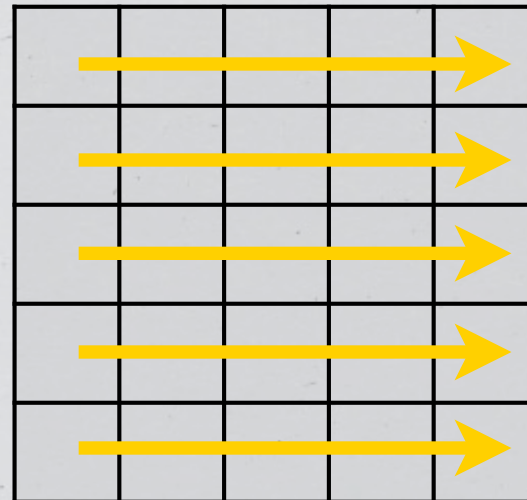
- * TRANSA = 'n' (normal) or 't' (transpose)
- * TRANSA = 'n' (normal) or 't' (transpose)
- * M = rows of matrix C and of matrix A or A-transpose
- * N = columns of matrix C and of matrix B or B-transpose
- * K = columns of A/A-transpose and rows of B/B-transpose
- * ALPHA = (double) scalar
- * A = (double) array (or double * in C/C++)
- * LDA = row-dim. (Fortran) or col.-dim. (C/C++) of matrix A
- * B = (double) array (or double * in C/C++)
- * LDB = row-dim. (Fortran) or col.-dim. (C/C++) of matrix B
- * BETA = (double) scalar
- * C = (double) array (or double * in C/C++)
- * LDC = row-dim. (Fortran) or col.-dim. (C/C++) of matrix C.

Fortran vs. C/C++

- * The ordering of the elements in memory of a matrix is different between Fortran and C/C++:
- * In Fortran: consecutive elements follow the **columns**
- * In C/C++: consecutive elements follow the **rows**



Fortran



C/C++

Fortran vs. C/C++

- * Given that the standard BLAS and LAPACK interfaces are defined to be Fortran77/90, some adjustments by C/C++ programs are necessary to call the functions correctly.

$$\mathbf{C} = \mathbf{A}\mathbf{B}$$

$$\mathbf{C}^T = (\mathbf{A}\mathbf{B})^T = \mathbf{B}^T \mathbf{A}^T$$

- * Thus, when calling DGEMM() from C/C++, we reverse the ordering of the matrices, **but keep the same ‘n’ and ‘t’** arguments.

Library Interface: DSYEV

* $A * V = W * V$

- * JOBZ = 'n' (eigenvalues only) or 'v' (also eigenvectors)
- * UPLO = 'l' (lower-triangle) or 'u' (upper-triangle) (not important for full matrix)
- * N = dimension of A
- * A = (double) array (or double * in C/C++) containing the matrix. This is replaced by the eigenvectors on exit.
- * LDA = row-dim. (Fortran) or col.-dim. (C/C++) of matrix A
- * W = (double) array (or double * in C/C++) containing the eigenvalues in ascending order on exit.
- * WORK = (double) array (or double * in C/C++) containing memory for temporary use by the function.
- * LWORK = (int) length of WORK.
- * INFO = 0 (if successful) on exit. (Other values indicate incorrect arguments or lack of convergence).

Optimized BLAS/LAPACK

Maximum optimization of BLAS/LAPACK is vital for all computational chemistry software, and many implementations exist:

- * **Netlib:** The original source of the code. Should never be used for production-level computations. (free)
- * **Intel Math Kernel Library (MKL):** Hand optimized using evil and ancient magic for Intel processors. (\$\$)
- * **IBM Engineering and Scientific Subroutine Library (ESSL):** Optimized for PowerPC architectures. (\$\$)
- * **Goto BLAS:** Hand-optimized in assembler by Kazushige Goto. Astonishingly fast for Intel Nehalem and AMD Opteron. (BSD)
- * **Automatically Tuned Linear Algebra Subroutines (ATLAS):** Self-tuning at compile time for a given architecture. (BSD)