

BLAS for Tensors: What, Why, and How

Devin Matthews

Outline

- I. The role of interfaces in domain applications
- II. BLAS as an example interface
- III. BLIS as a better BLAS
- IV. Tensors
- V. Tensor interfaces now
- VI. A “Tensor BLAS”

Math to Code: Fundamental Considerations

What domain scientists want (math):

$$\langle 0 | \delta\Lambda^{(1)}[[\bar{H}, \delta T^{(1)}], \delta T^{(2)}] | 0 \rangle \leftarrow \frac{1}{4} \lambda_{abc}^{ijk(1)} \bar{H}_{ie}^{ma(3)} t_{mjk}^{ebc(1)}$$
$$\left(\frac{-i\hbar}{c} \gamma^0 \frac{\partial}{\partial t} - i\hbar \gamma^j \partial_j + mc \right) \psi(x) = (-\gamma^0 p^0 + \gamma^j p^j + mc) \psi(x)$$

$$P(Z_{(m,n)} = k \mid \mathbf{Z}_{-(m,n)}, \mathbf{W}; \alpha, \beta)$$
$$\propto P(Z_{(m,n)} = k, \mathbf{Z}_{-(m,n)}, \mathbf{W}; \alpha, \beta)$$
$$= \left(\frac{\Gamma \left(\sum_{i=1}^K \alpha_i \right)}{\prod_{i=1}^K \Gamma(\alpha_i)} \right)^M \prod_{j \neq m} \frac{\prod_{i=1}^K \Gamma(n_{j,(.)}^i + \alpha_i)}{\Gamma \left(\sum_{i=1}^K n_{j,(.)}^i + \alpha_i \right)}$$

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DGEMM (BLAS)

SCSRMM (SparseBLAS)

MPI_Reduce_scatter_block (MPI)

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Data layout ————— Performance — Alignment/caching

Numerical representation

Architectural optimizations

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Features of BLAS

```
DGEMM (CHARACTER*1 TRANSA,  
       CHARACTER*1 TRANSB,  
       INTEGER M,  
       INTEGER N,  
       INTEGER K,  
       REAL*8 ALPHA,  
       REAL*8 (*) A,  
       INTEGER LDA  
       REAL*8 (*) B,  
       INTEGER LDB  
       REAL*8 BETA  
       REAL*8 (*) C,  
       INTEGER LDC)
```

User/external code owns the data.

Data and specification are separate. Allows easy hacking (e.g. submatrices, resizing, etc.), but can be error-prone.

All information about the operation is explicit. Can be unwieldy for users but good for flexibility.

BLAS: the Good and the Bad

(a.k.a. How to Start a Flame War)

Good:

- Easier than writing three loops.
- Flexible enough for end users and library writers.
- High-performance implementations exist.
- Bindings in many languages.
- Can be wrapped in a more user-friendly interface.

Bad:

- FORTRAN dependency.
- Requires unit stride.
- No conjugation without transpose.
- Some obvious missing features.
- User must allocate data and deal with alignment etc.
- Opaque.
- Poor threading control.
- No mixed-precision support.

How People Really (Ab)use BLAS

`dcopy(n, &constant, 0, array, 1)`
(i.e. fill array)

Actually transpose a matrix
(and other loop code)

`dscal(n, beta, y, 1)`
`daxpy(n, alpha, x, 1, y, 1)`
(i.e. `daxpby`)

Lots of copying and data movement
BLAS call
Lots more data movement

`daxpy(n, alpha1, x_1, 1, y, 1)`
`daxpy(n, alpha1, x_2, 1, y, 1)`
`daxpy(n, alpha2, x_3, 1, y, 1)`

...

`ddot(n, &one, 0, array, 1)`
(i.e. *non*-absolute sum)

Separate real and imaginary
arrays/matrices

BLIS

```
DGEMM(CHARACTER*1 TRANSA,  
      CHARACTER*1 TRANSB,  
      INTEGER M,  
      INTEGER N,  
      INTEGER K,  
      REAL*8 ALPHA,  
      REAL*8 (*) A,  
      INTEGER LDA  
      REAL*8 (*) B,  
      INTEGER LDB  
      REAL*8 BETA  
      REAL*8 (*) C,  
      INTEGER LDC)
```

```
void bli_dgemm( trans_t transa,  
                trans_t transb,  
                dim_t    m,  
                dim_t    n,  
                dim_t    k,  
                double*  alpha,  
                double*  a,  
                inc_t   rsa, inc_t csa,  
                double*  b,  
                inc_t   rsb, inc_t csb,  
                double*  beta,  
                double*  c,  
                inc_t   rsc, inc_t csc );  
  
void bli_gemm( obj_t*  alpha,  
               obj_t*  a,  
               obj_t*  b,  
               obj_t*  beta,  
               obj_t*  c )
```

Tensors

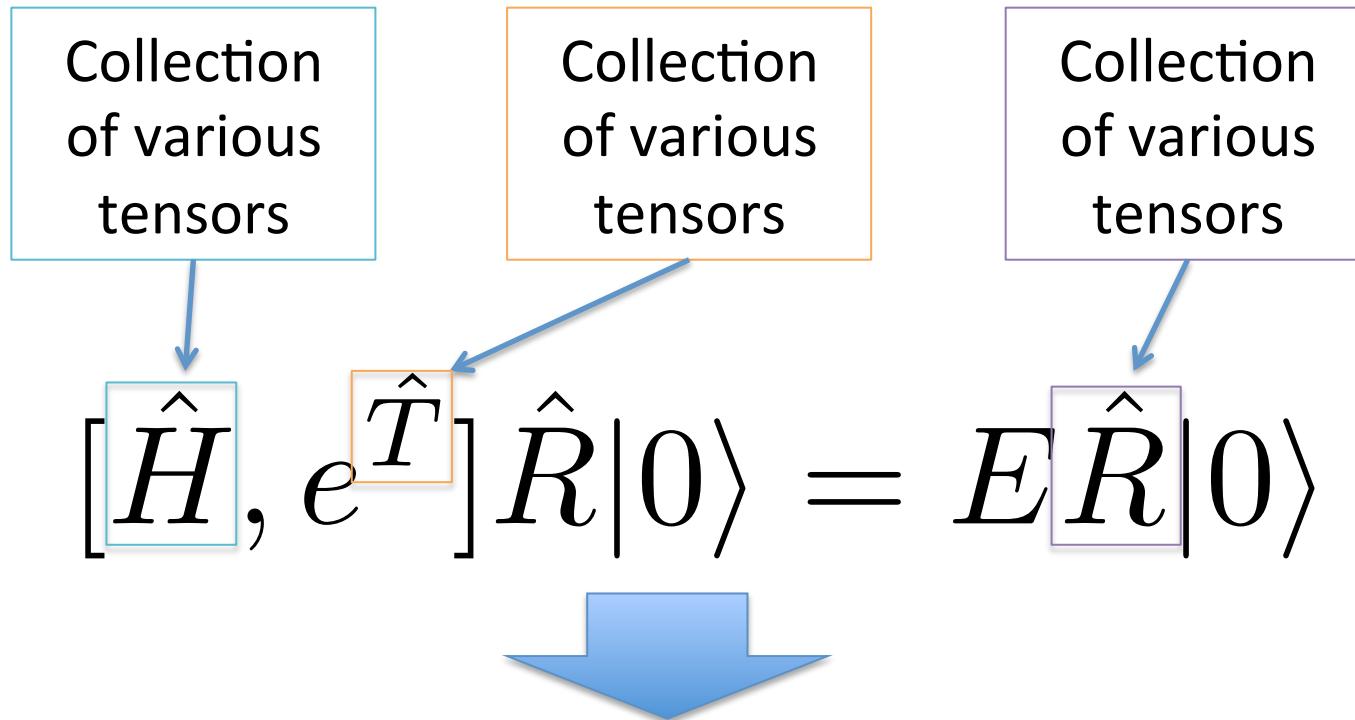
- Tensors are essentially multi-dimensional arrays:

double T[na][nb][ni][nj]; \longleftrightarrow $T_{ij}^{ab} \in \mathbb{R}^{n_a \times n_b \times n_i \times n_j}$

- Matrices are 2-D tensors.
- Tensor indices are usually explicit. Einstein notation is very helpful:

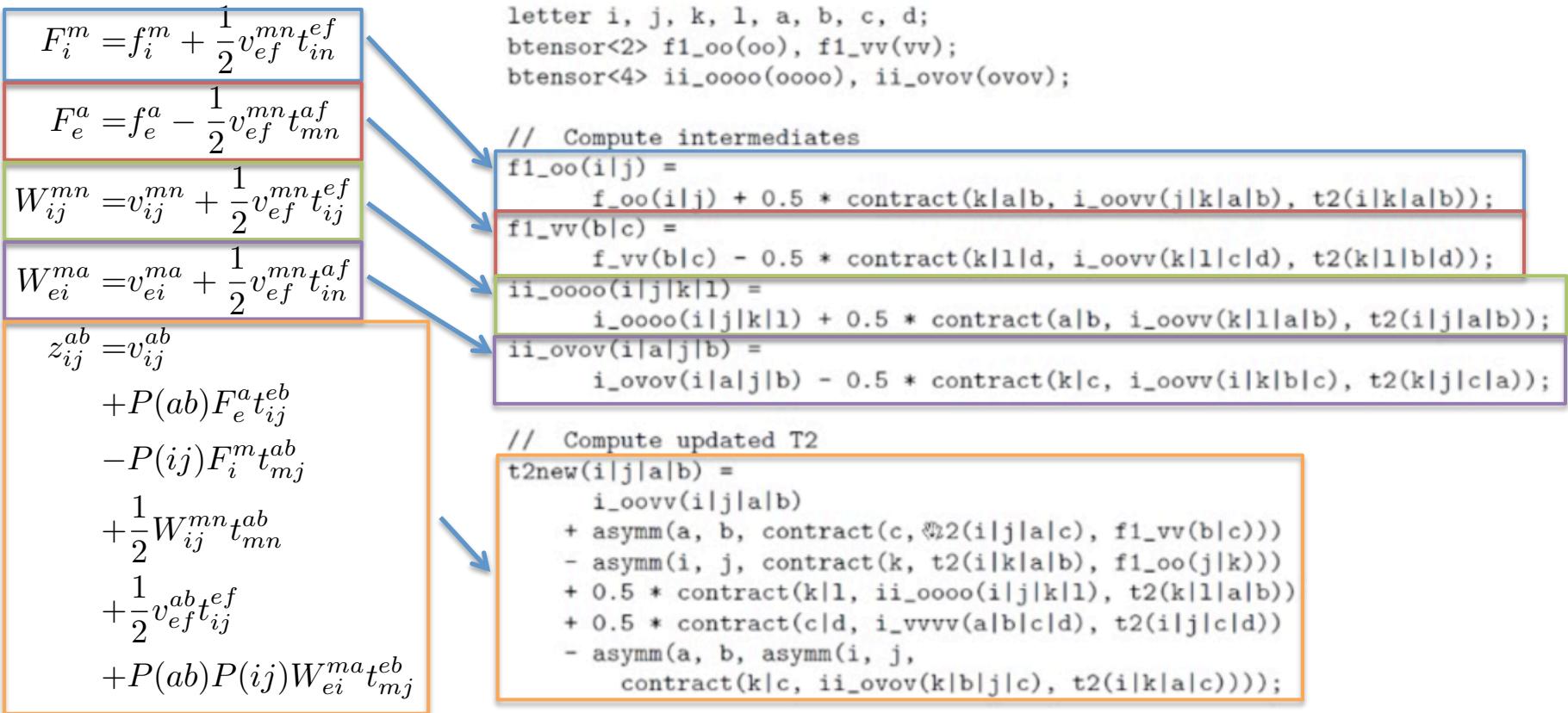
$$\begin{aligned} z_{ijk}^{abc} &= (1 + P_{ck}^{ai} + P_{ck}^{bj}) \left[4\check{t}_{ijm}^{abe} \check{t}_{nk}^{fc} \check{v}_{ef}^{mn} - 2(1 + P_{bj}^{ai}) \check{t}_{ijm}^{aeb} \check{t}_{nk}^{fc} \check{v}_{ef}^{mn} \right. \\ &\quad - 2\check{t}_{ijm}^{abe} \check{t}_{nk}^{cf} \check{v}_{ef}^{mn} - 2\check{t}_{ijm}^{abe} \check{t}_{nk}^{fc} \check{v}_{fe}^{mn} \\ &\quad + (1 + P_{bj}^{ai}) \check{t}_{ijm}^{aeb} \check{t}_{nk}^{cf} \check{v}_{ef}^{mn} + (1 + P_{bj}^{ai}) \check{t}_{ijm}^{aeb} \check{t}_{nk}^{fc} \check{v}_{fe}^{mn} \\ &\quad \left. + \check{t}_{ijm}^{abe} \check{t}_{nk}^{cf} \check{v}_{fe}^{mn} + (1 + P_{bj}^{ai}) \check{t}_{ijm}^{aec} \check{t}_{nk}^{bf} \check{v}_{fe}^{mn} \right]. \end{aligned}$$

Tensors in Chemistry



- Sequence of tensor contractions, summations, etc.
- Need to account for physics: spin, spatial symmetry, and so on.
- Some tensors are very big, some are very small, many different dimensionalities.
- Often need (distributed), out-of-core storage.

High-level Interfaces: Chemistry



Low-level Interfaces: Blitz++, Eigen, Boost, BTAS, etc.

- Handle allocation, alignment, indexing, etc. “Native” efficiency.

```
Array<double,4> pqrs(np, nq, nr, ns);  
pqrs[0][1][6][3] = 0.122;
```

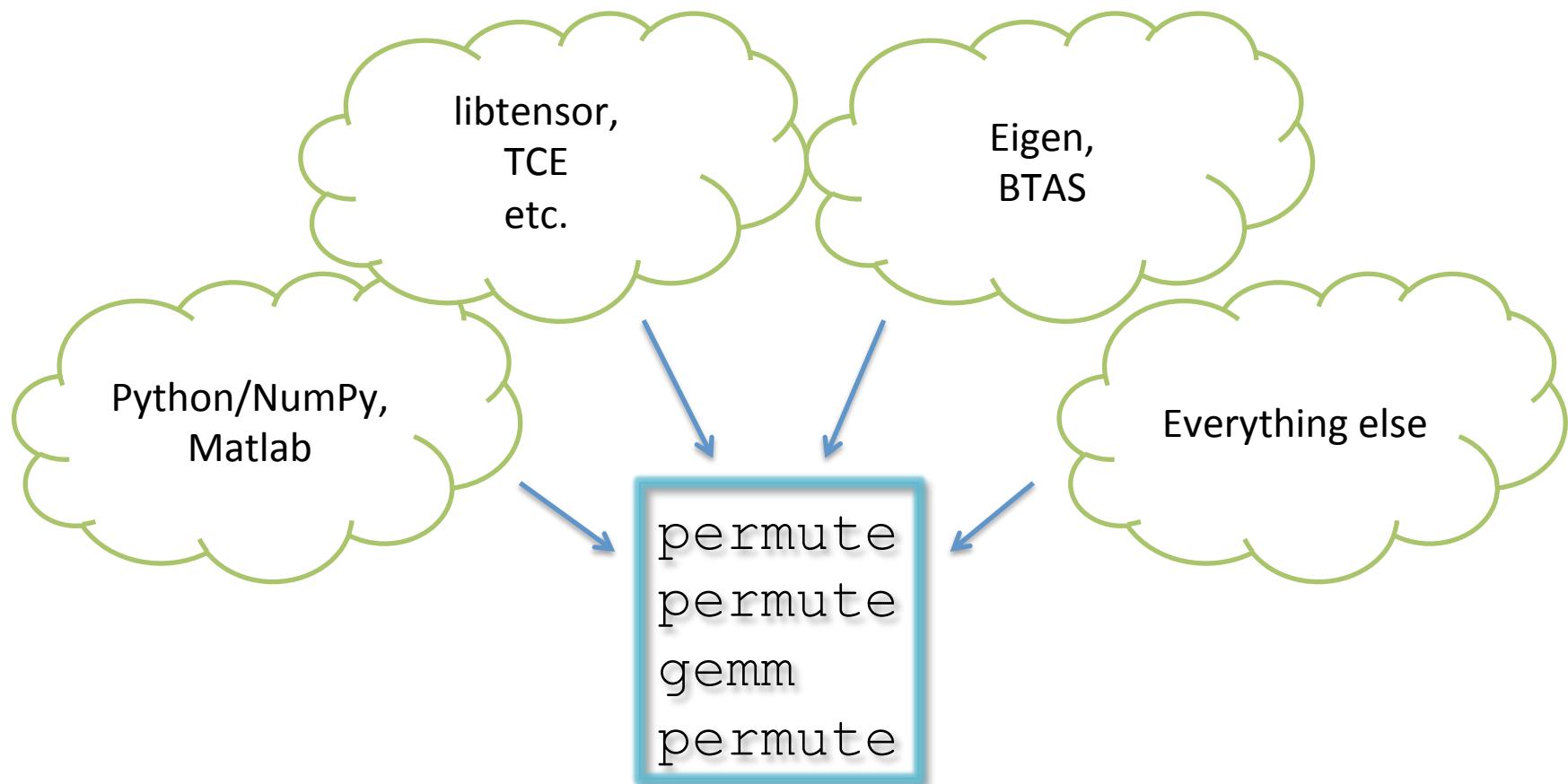
- C++ allows for efficient and expressive interfaces (fixed vs. variable dimensionality, static typing, operator overloading, operation trees, etc.).

```
Array<int,3> A(4, 10, 2);  
Array<int,1> G = A(2, 7, Range::all());
```

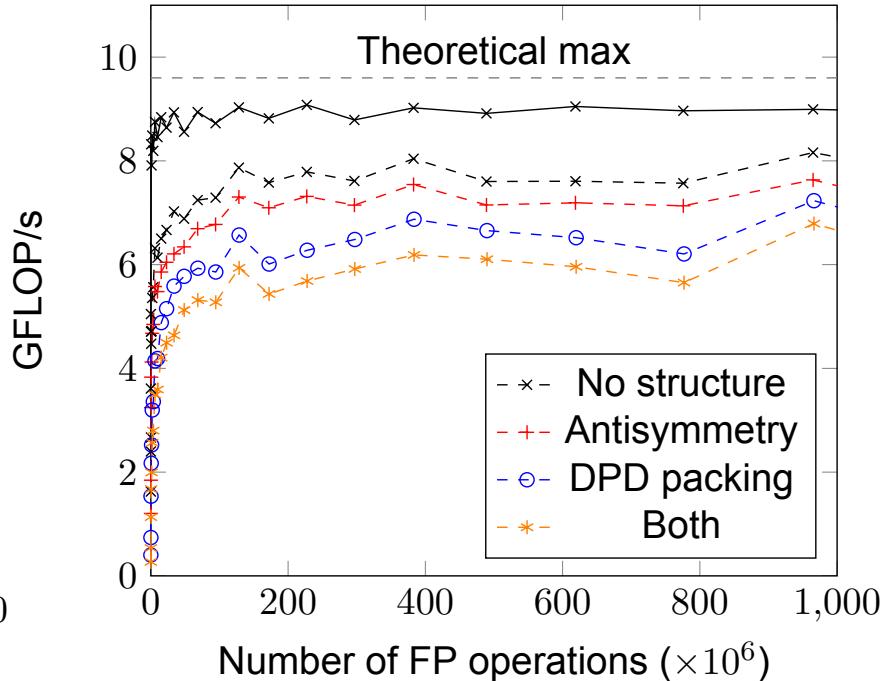
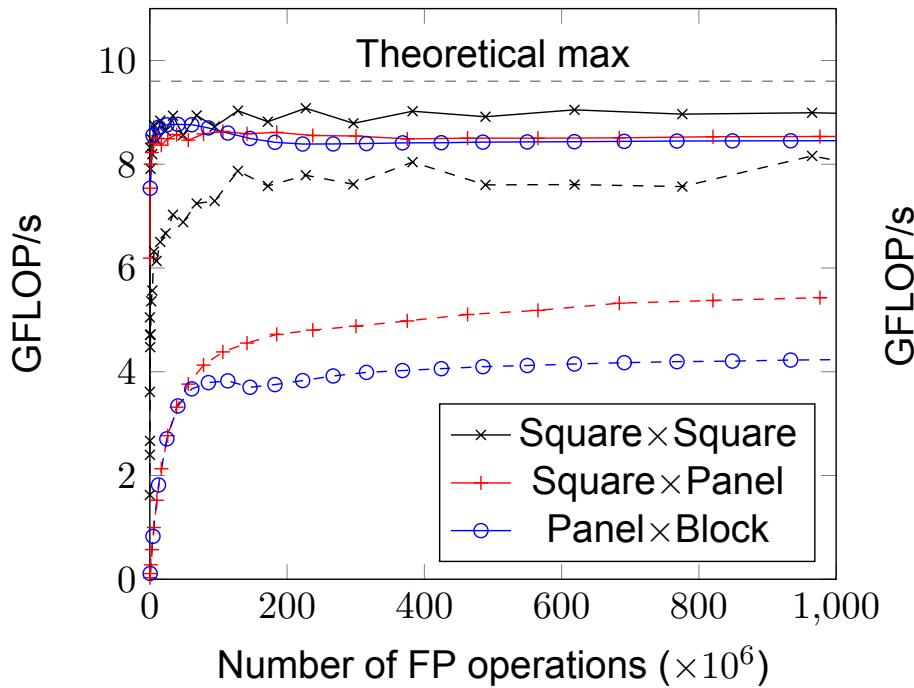
- Limited computational support (i.e. Level 1-type operations, exptl. contraction support in Eigen).

```
C(i,j) = sum(A(i,k), B(k,j), k) + Cprime(i,j);
```

Under the Hood: BLAS!

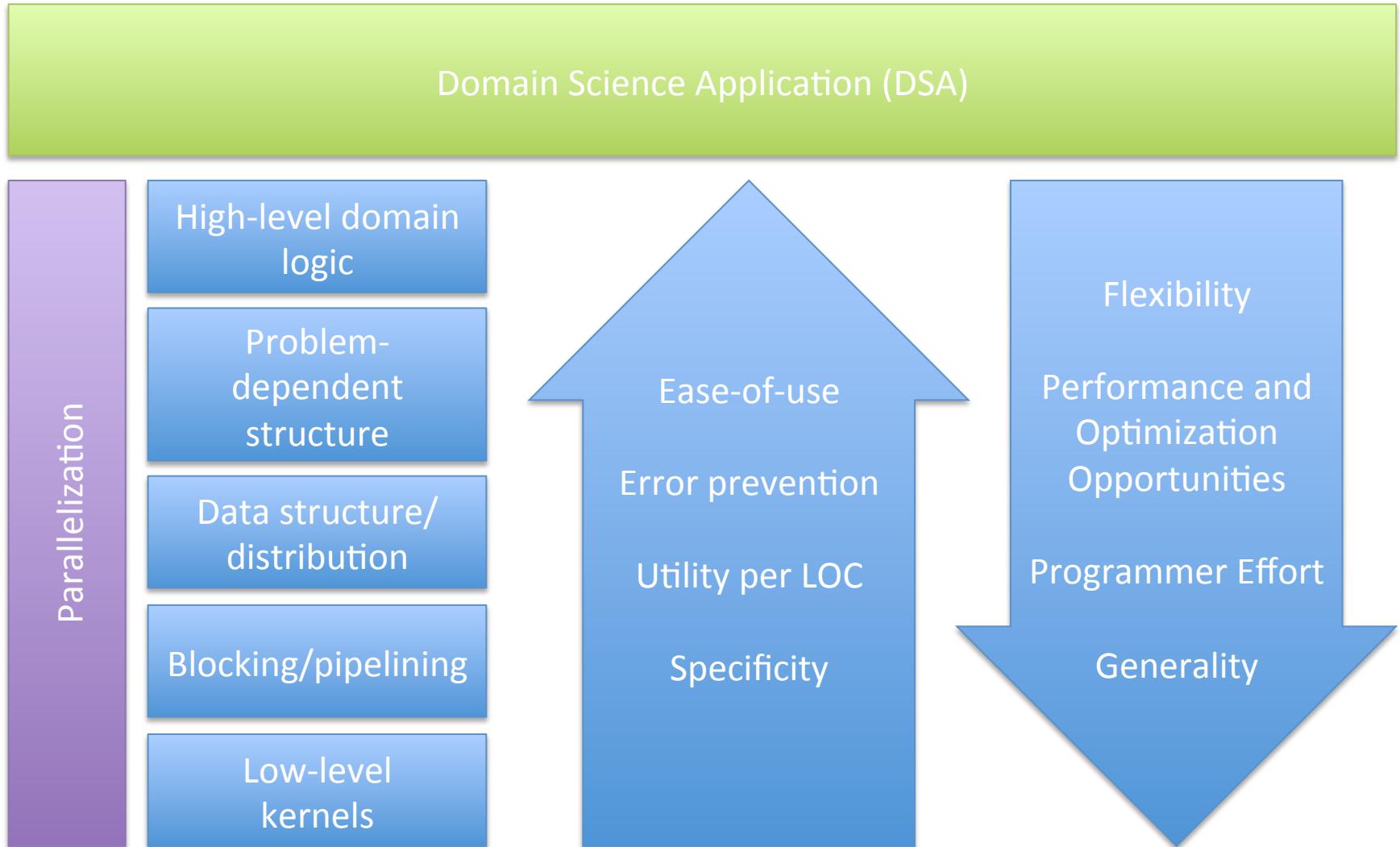


Why not BLAS?

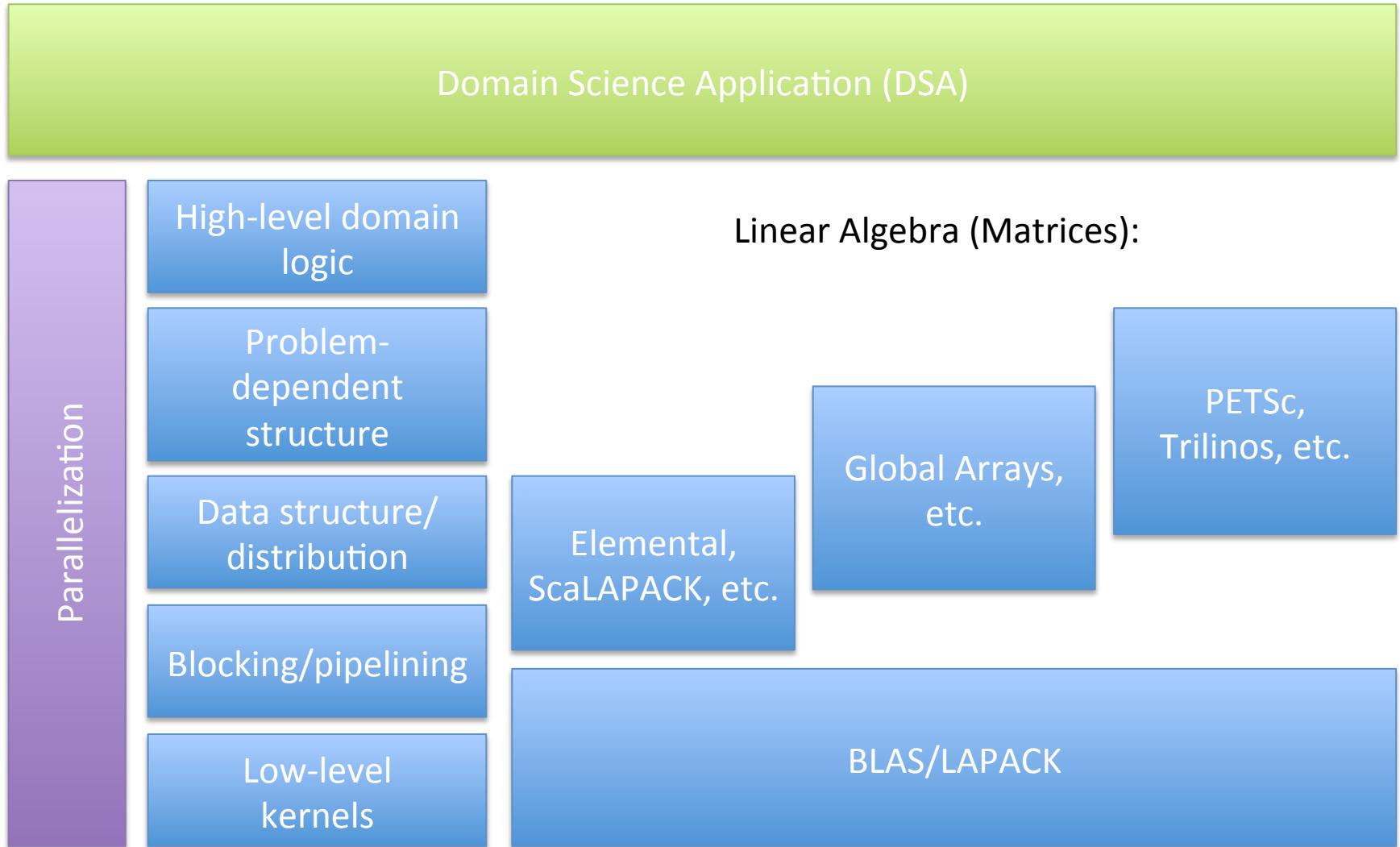


Solid lines: matrices
Dashed lines: tensors

Where to Draw the Line?



Where to Draw the Line?



Where to Draw the Line?

Domain Science Application (DSA)

Parallelization

High-level domain logic

Problem-dependent structure

Data structure/
distribution

Blocking/pipelining

Low-level kernels

Multilinear Algebra (Tensors):

libtensor,
TCE,
TiledArrays,
etc.

CTF, ROTE

??? (BLAS for now)

What: A (Possible) “Tensor BLAS”

```
err_t tensor_dcontract(
    double alpha,
    const double* A,
    gint_t ndim_A,
    const dim_t* len_A,
    const inc_t* stride_A,
    const idx_t* idx_A,
    const double* B,
    gint_t ndim_B,
    const dim_t* len_B,
    const inc_t* stride_B,
    const idx_t* idx_B,
    double beta,
    double* C,
    gint_t ndim_C,
    const dim_t* len_C,
    const inc_t* stride_C,
    const idx_t* idx_C);
```

- Data externally specified as in BLAS.
- Custom integral types for lengths, strides, number of dimensions.
- Any non-negative number of dimensions.
- Integral error code.
- Contracted/non-contracted dimensions specified by index strings (integral, string literal, etc.) + Einstein notation.
- No “TRANSA” etc.

What: A (Possible) “Tensor BLAS”

BLAS		Tensor BLAS	
Level 3		Binary	CONTRACT, WEIGHT, etc. → MULT
Level 2		Unary	TRANSPOSE, TRACE, etc. → SUM
DOT, COPY, AXPY, etc.	Level 1	Local	REDUCE, SCALE, etc.

Why:

- Flexibility:
 - Any storage order is allowed: column-major, row-major, or a mix.
Strides do not need to be multiples of each other.
 - Transposition and contracted/non-contracted indices are implicit.
Index names are not prescribed.

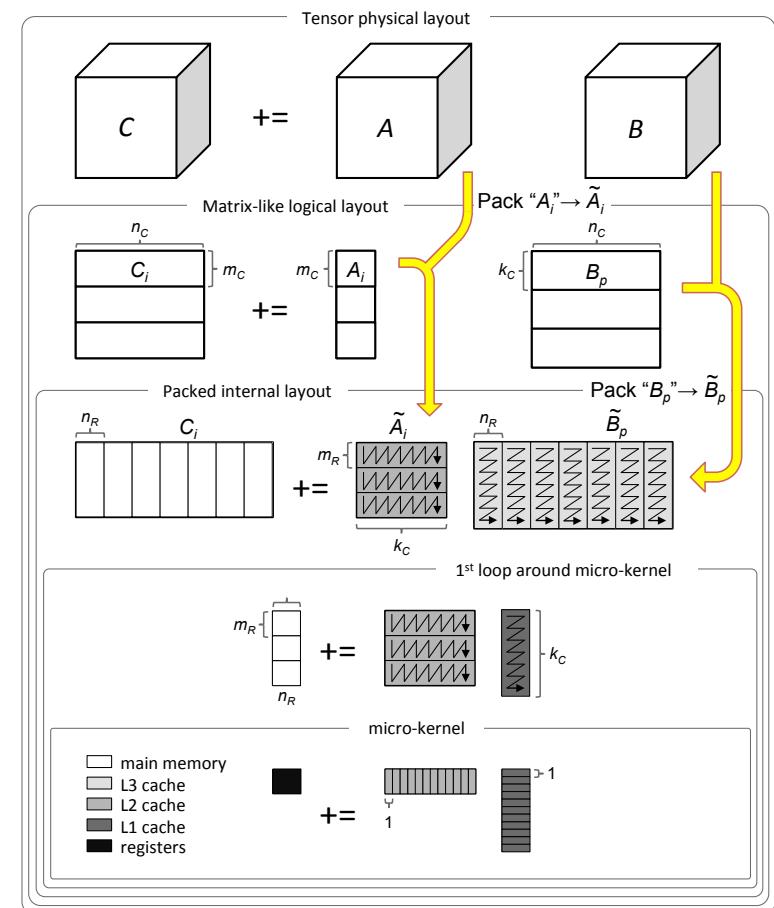
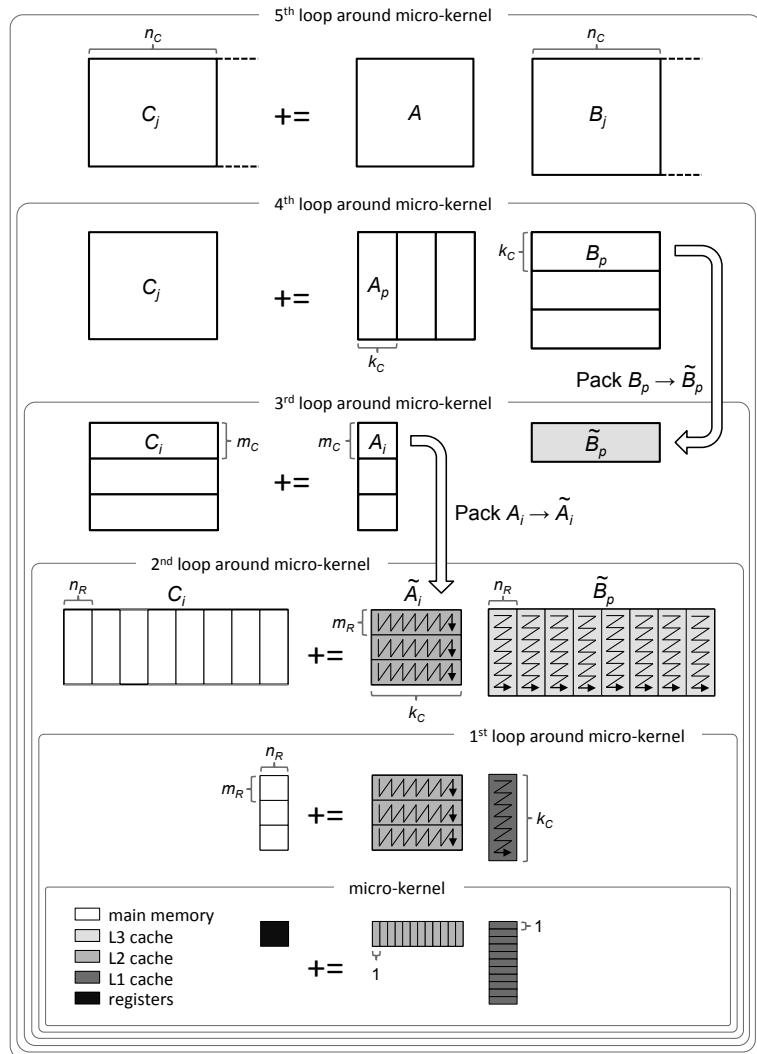
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 - Types (esp. integral) are user-definable, as in BLIS. No 32/64-bit confusion.
 - Pure C interface.

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 - Pure C interface.
- Extensibility:
 - All information needed for the operation is explicit (as in BLAS). Can be used directly or wrapped in another interface.

How: BLIS



Thanks

The Science of
High-Performance
Computing Group



THE UNIVERSITY OF
TEXAS
AT AUSTIN

