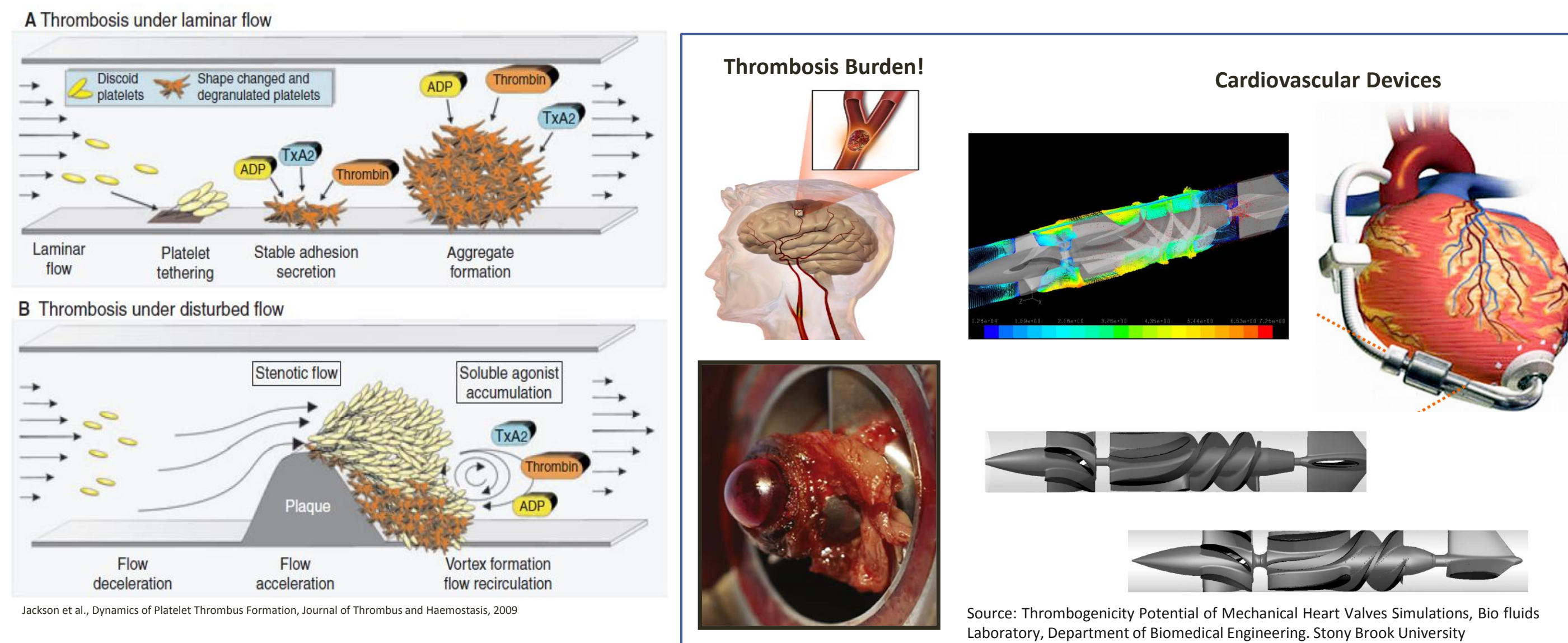


Motivation



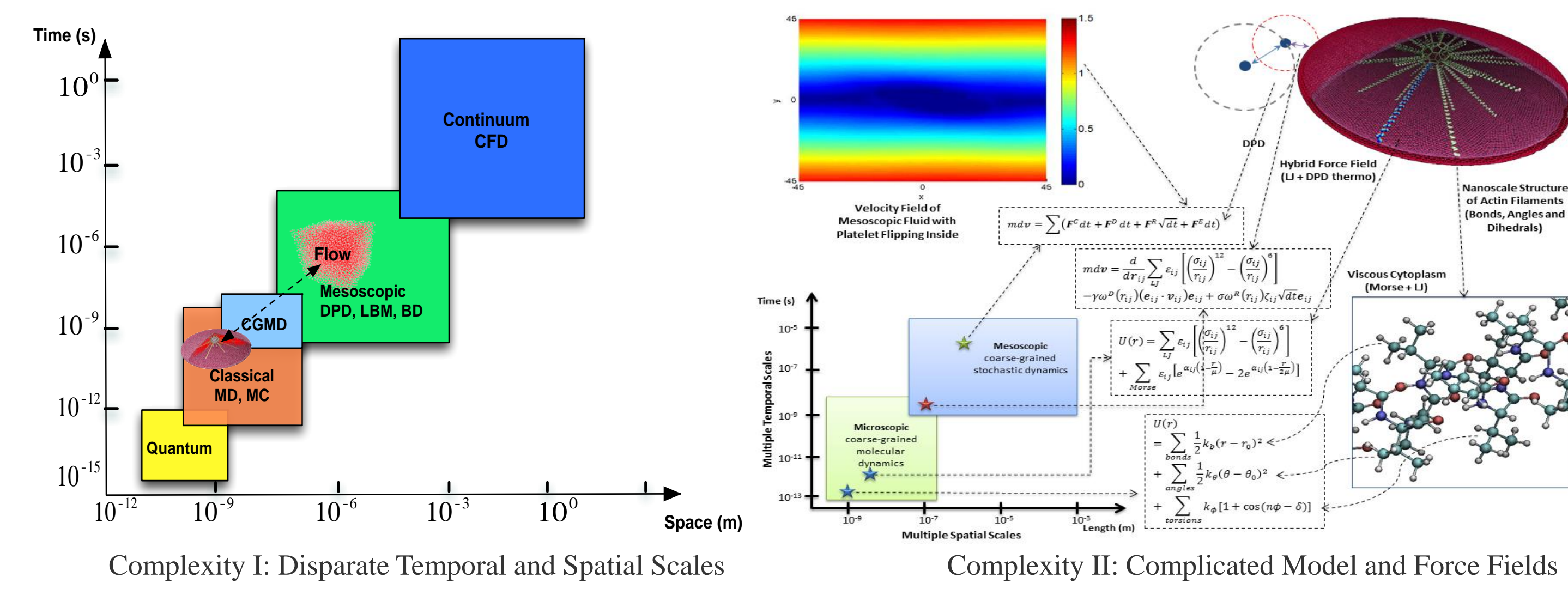
This objective of this project is to efficiently simulate flow-induced platelet activation in order to better understand thrombosis formation mechanisms. The methodologies include:

- Mathematical modeling of viscous blood flows and human platelet cell
- Multiscale coupling methods
- Data analysis of thermodynamic properties
- Algorithmic acceleration
- Heterogeneous computing
- Visualization

Multiscale Fluid-Platelet Models

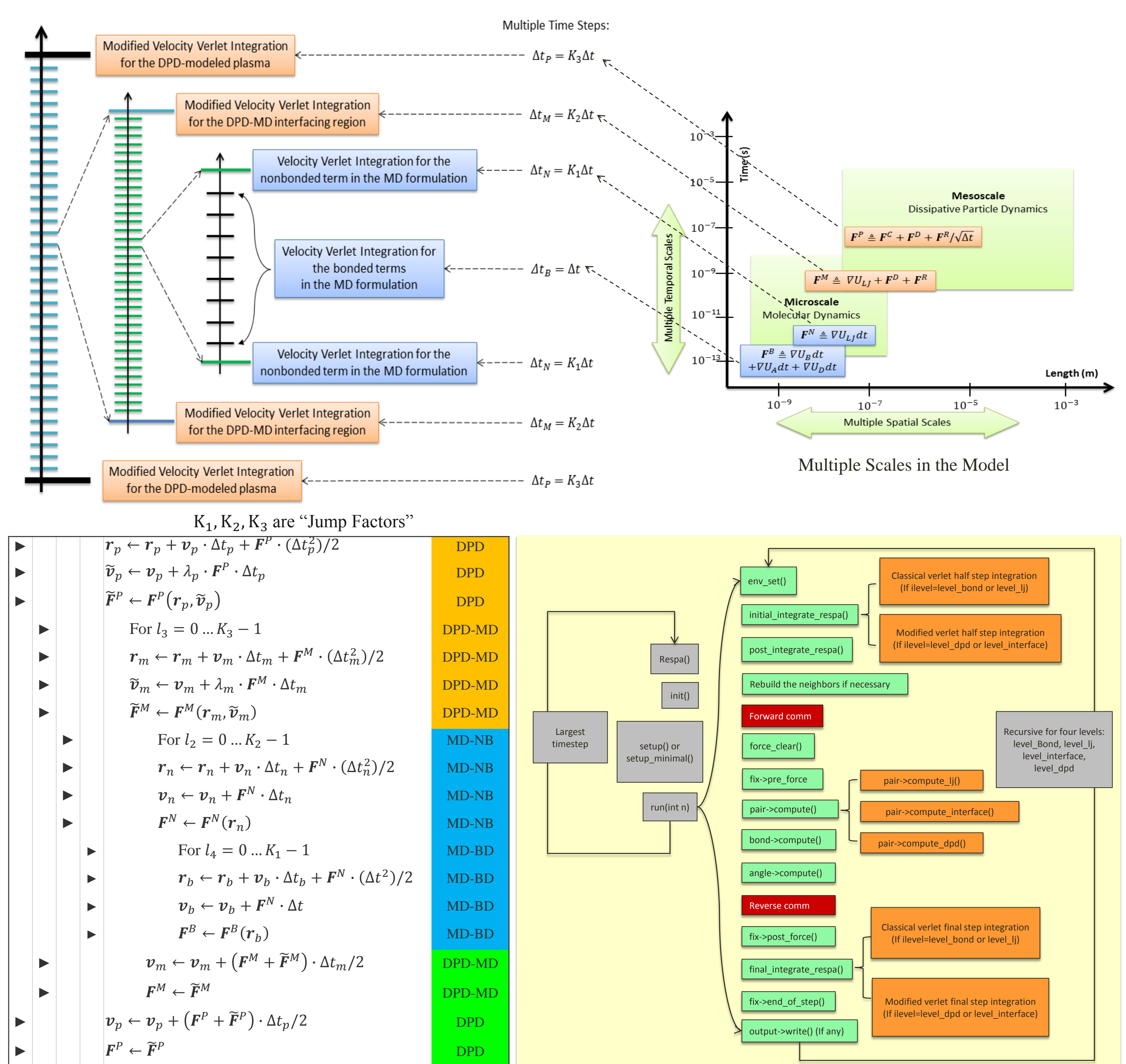
Scales	Nanoscale	Mesoscale
Simulation Domain	Platelet Cell	Blood Plasma
Methods	Coarse-Grained Molecular Dynamics (CGMD)	Dissipative Particle Dynamics (DPD)
Time Step	10~100 fs	0.01~1 μs
Length	1~20 Å	0.1 ~ 1 μm
Model Abstraction		
Force Fields	$V(r) = \sum k_b(r - r_0)^2 + \sum k_\theta(\theta - \theta_0)^2$ Bond and Angle Terms $+ \sum k_\phi[1 + \cos(n\phi - \delta)] + \sum \frac{q_i q_j}{4\pi\epsilon_0 r}$ Dihedral and Electrostatic $+ \sum 4\epsilon \left[\left(\frac{r}{r_0} \right)^{12} - \left(\frac{r}{r_0} \right)^6 \right]$ Van Der Waals (L-J) $+ \sum \epsilon \left[\alpha \left(1 - \frac{r}{R(\mu)} \right) - 2 \exp \left(\frac{\alpha}{2} \left(1 - \frac{r}{R(\mu)} \right) \right) \right]$ Modified Morse V is the total energy on each particle composed of platelet. It includes a classical MD potential for describing the actin filament structure, a modified Morse potential for describing the viscous cytoplasm structures, and a CGMD for describing the filamentous core and the membrane structures	$F_{ij} = F_{ij}^C + F_{ij}^D + F_{ij}^R$ (Groot and Warren 1997) $F_{ij}^C = \alpha\omega(r_{ij})e_{ij}$ Conservative Term $F_{ij}^D = -\gamma\omega^2(r_{ij})(e_{ij} \cdot v_{ij})e_{ij}$ Dissipative Term $F_{ij}^R = \sigma\omega(r_{ij})\xi_{ij}e_{ij}$ Random Term Where $r_{ij} = r_i - r_j$, $r_{ij} = r_{ij} $, $e_{ij} = \frac{r_{ij}}{ r_{ij} }$ The ξ_{ij} are symmetric random variables with zero mean and unit variance, uncorrelated for different pairs of particles and different times.
Properties Considerations	Parameterize the undetermined parameters to match physical properties: <ul style="list-style-type: none"> Platelet Cell Size Membrane Young's Modulus Membrane Shear Modulus Stretching Response Cell Plasma Compressibility Cell Plasma Viscosity Cell Plasma Pressure Cell Plasma Density Besides, we also need to consider computational feasibility and the ability of platelet model to become activated.	Parameterize the undetermined parameters and modify boundary conditions to match the physical properties: <ul style="list-style-type: none"> Viscosity Compressibility Reynolds Number Density Viscous Boundary Layers
Spatial Interfacing	Hybrid force field containing the dissipative and random terms from DPD and Lenard-Jones potential from MD. It's exploited to mimic friction between platelet membranes and surrounding blood flows. $F_{ij} = F_{ij}^L + F_{ij}^D + F_{ij}^R$ Parameterize the undetermined parameters to match: <ul style="list-style-type: none"> platelets flipping trajectory with analytical solution (Jeffery's orbit) in Couette flow Rotation angle: $\phi = \phi(\gamma t) = \text{atan} \left(\frac{1}{r_c} \tan \left[-\gamma t \frac{r_c}{r_c^2 + 1} + \tan^{-1}(r_c \tan \phi_0) \right] \right)$ 	

Computational Complexities

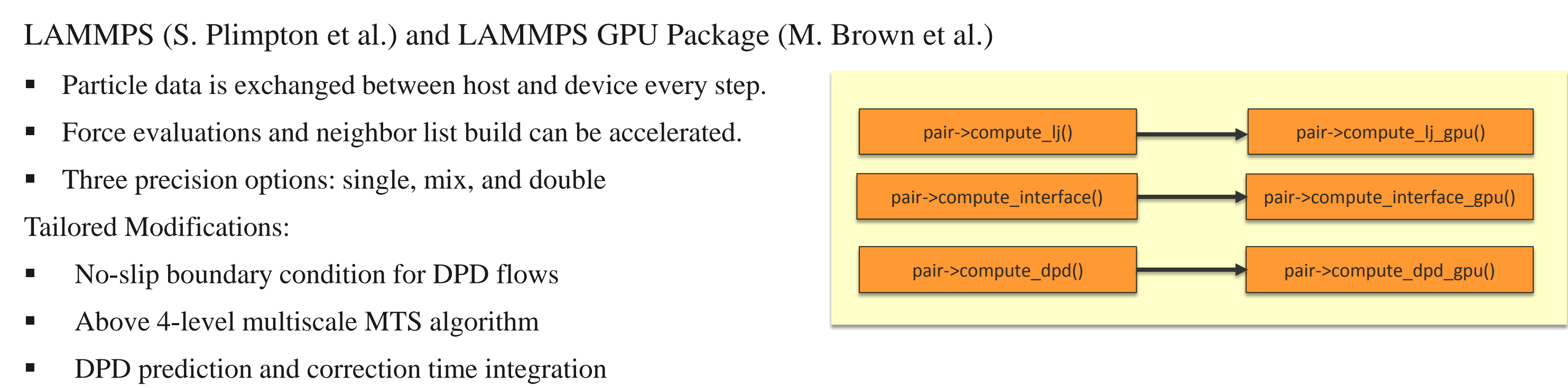


Categories	Single Platelet	Multiple Platelets
In Vacuum	~0.14 million particles	Complex interactions among platelets
In Blood Plasma	~0.6 million particles	~2.7 million particles for 4 platelets flipping in blood plasma ~10.9 million particles for 16 platelets flipping in blood plasma > 50 million particles for 100 platelets in blood plasma
In Blood Vessels	Many types of blood cells and complex interactions among those cells	
With Shear Stresses & Thermo Conditions	Much more complex inputs and outputs control	

Speedup Strategy I-Multiscale Multiple Time Stepping Algorithm



Speedup Strategy II-GPGPU Acceleration



Performance Results on Supercomputers

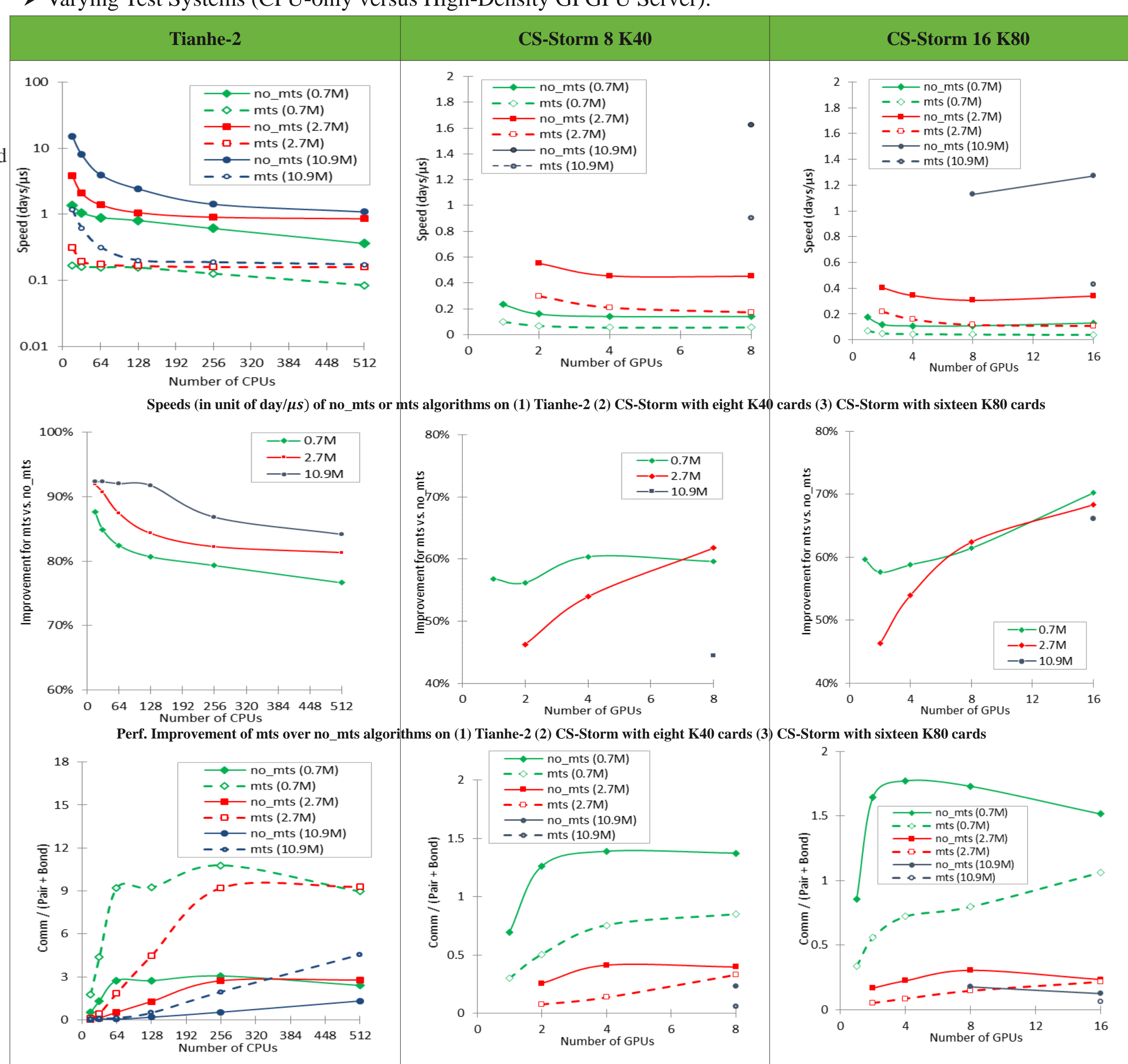
> Varying Problem Sizes:

Experiments	# of Platelets	# of Particles	Dimensions
Exp-S	1	680,718	45 × 90 × 45
Exp-M	4	2,722,872	90 × 90 × 90
Exp-L	16	10,891,488	180 × 90 × 180

> Varying MTS Jump Factors:

Case	Time steps for each scale				Configurations			
	CGMD-BD (Δt ₁ × 10 ⁻⁶)	CGMD-NB (Δt ₂ × 10 ⁻⁶)	DPD-CGMD (Δt ₃ × 10 ⁻⁶)	DPD (Δt ₄ × 10 ⁻⁶)	Δt × 10 ⁻⁶	K ₁	K ₂	K ₃
CaseA	2.5	2.5	25.0	500.0	500.0	1	10	20
CaseB	5.0	5.0	50.0	1000.0	1000.0	1	10	20
CaseC	5.0	5.0	50.0	500.0	500.0	1	10	10
CaseD	10.0	10.0	100.0	500.0	500.0	1	10	5
CaseE	10.0	10.0	100.0	1000.0	1000.0	1	10	10
STS	1.0	1.0	1.0	1.0	1.0	1	1	1

> Varying Test Systems (CPU-only versus High-Density GPGPU Server):



Summary and Future Work

- With combined algorithmic and hardware accelerations, we can efficiently simulate 1-ms the millisecond-scale hematology at resolutions of nanoscale platelets and mesoscale bio-flows using millions of particles.
- The rule of thumb is to consider the balance of speed and accuracy for an optimal MTS scheme and the balance of computation and communication for an optimal load-balancing scheme between accelerators and CPUs.
- Future work involves with the efforts to reduce communication overheads and simulate more complicated multiscale phenomena.

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