

OAK RIDGE National Laboratory

Toward Continental Forest Dynamics Modeling at Individual-tree Resolution on Exascale Systems

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U.S. DEPARTMENT of ENERGY

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Forests are complex adaptive systems whose dynamics emerge from local interactions among trees.

Local interactions among trees shape forest structure and species composition.

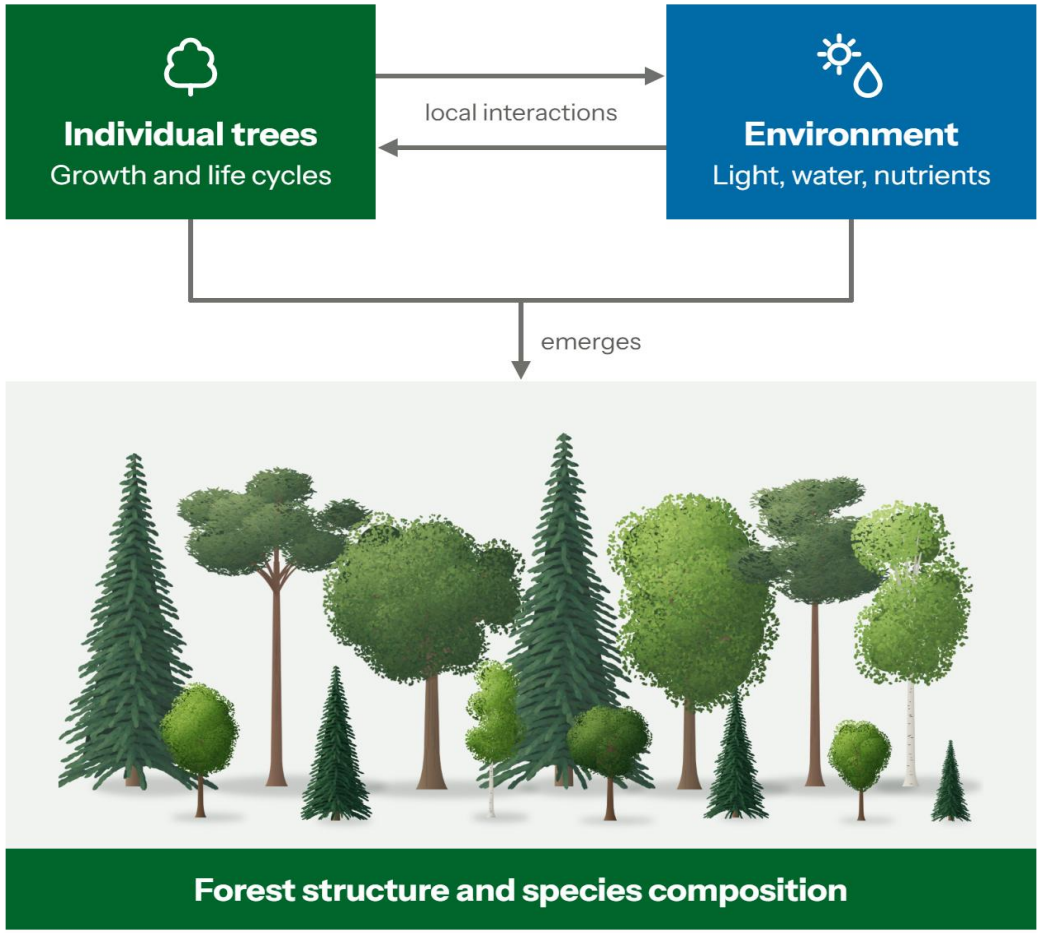
Individual-based models

Simulate tree life cycles and local competition for resources.

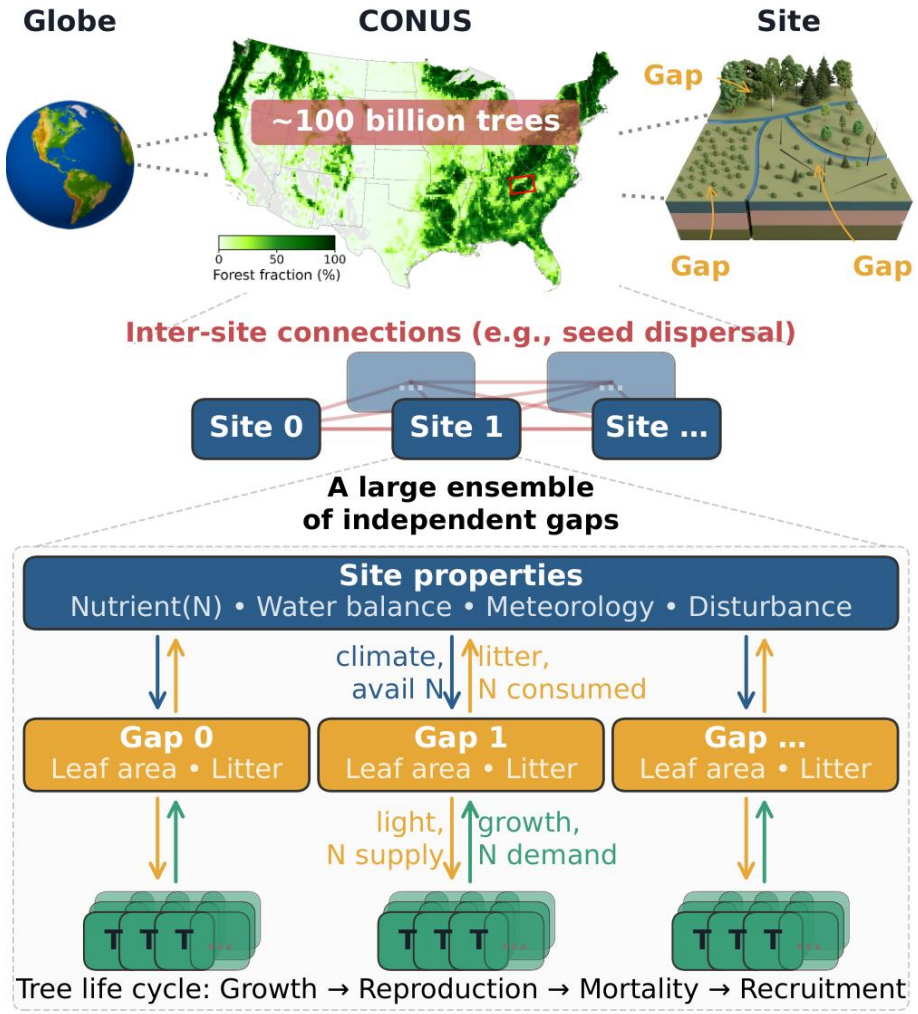
Forest gap models

Successful local and regional studies since the 1970s.

Botkin et al. (1972), J. Ecol. 60:849–872.
Shugart & West (1977), J. Environ. Manage. 5:161–179.



Gap models simulate forest succession through canopy gaps: large trees die, light increases and new trees grow.



A canopy opening admits light

When a large tree dies, its canopy opens.
More sunlight reaches seedlings and young trees.

Regeneration and competition

New trees establish and compete for resources.
As they grow, the canopy closes again.

Gap: one small forest patch

The model follows individual tree life cycles and resource competition within each patch.

Site: an ensemble of gaps

Gap patches share the same climate and soil but sample different forest histories.

Global forest dynamics are critical to Earth system modeling, but computational limits led researchers to aggregate trees.

Forests cover ~30% of Earth's land and harbor most terrestrial biodiversity.
They regulate regional and global weather and climate through exchanges of carbon, water and energy.

Earth system models couple land, atmosphere and ocean.
They need to predict forest change from continental to global scales.



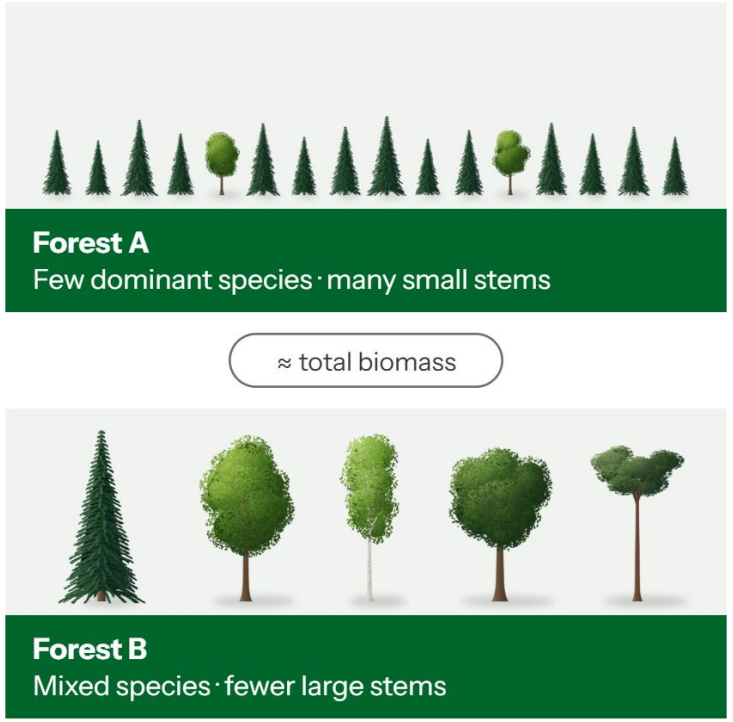
Aggregation can be insufficient for carbon prediction, and individual-tree models can address major uncertainties.

Aggregation limitations	Effects on predictions
Compressed species and trait diversity	Can miss species turnover and contrasting responses to climate and disturbance.
Averaged individual growth and mortality	Can bias carbon residence time and projected forest carbon sinks.
Simplified competition and disturbance	Can alter succession and forest recovery, even with similar initial biomass.

Spatial interactions shape forest change

Seeds arriving from other sites enable colonization.
Spreading disturbances alter tree survival and recovery.

Same biomass, different forests



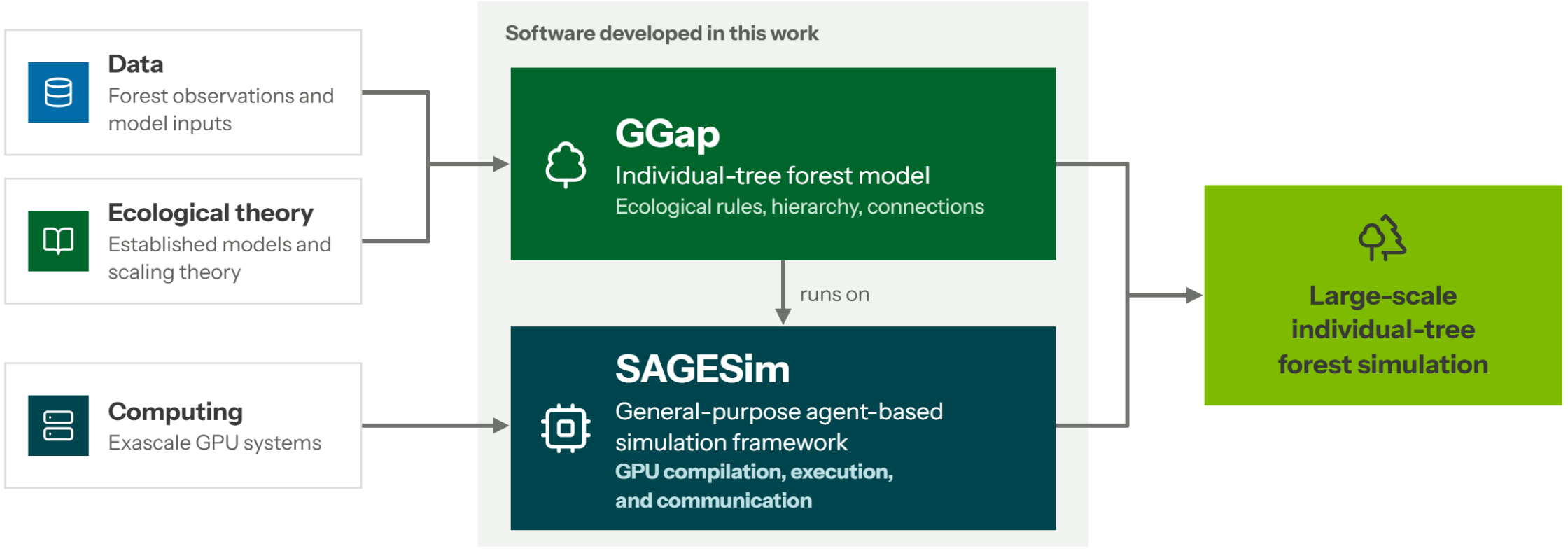
Conceptual example · crown shape and color indicate species

Exascale HPC provides the memory and parallel throughput needed for large individual-tree forest simulations.

Computational barrier	What exascale HPC provides
Billions of interacting agents Individual state across many sites	Distributed GPU memory Parallel updates across thousands of GPUs
Complex, spatially coupled processes Local competition and site-to-site exchange	GPU compute and memory bandwidth Fast interconnects for spatial exchange
Long simulation horizons Hundreds to thousands of annual steps	Sustained system-wide throughput Efficient execution of repeated updates

Scalable software is the missing link between HPC and forest simulation.

GGap brings an established gap model to continental-scale individual-tree simulation and adds explicit interactions among sites.



Site–Site interactions shape forest change, so predictions must account for them.

SAGESim: github.com/ORNL/SAGESim

GGap: github.com/bioatmosphere/GGap

Software design and implementation

SAGESim provides a general-purpose simulation framework.
GGap models individual trees and interactions among forest sites.

SAGESim is a general-purpose, pure-Python ABM framework that handles parallel updates and distributed GPU execution.

Python programming

Write Python code instead of GPU code.

AMD and NVIDIA GPU support

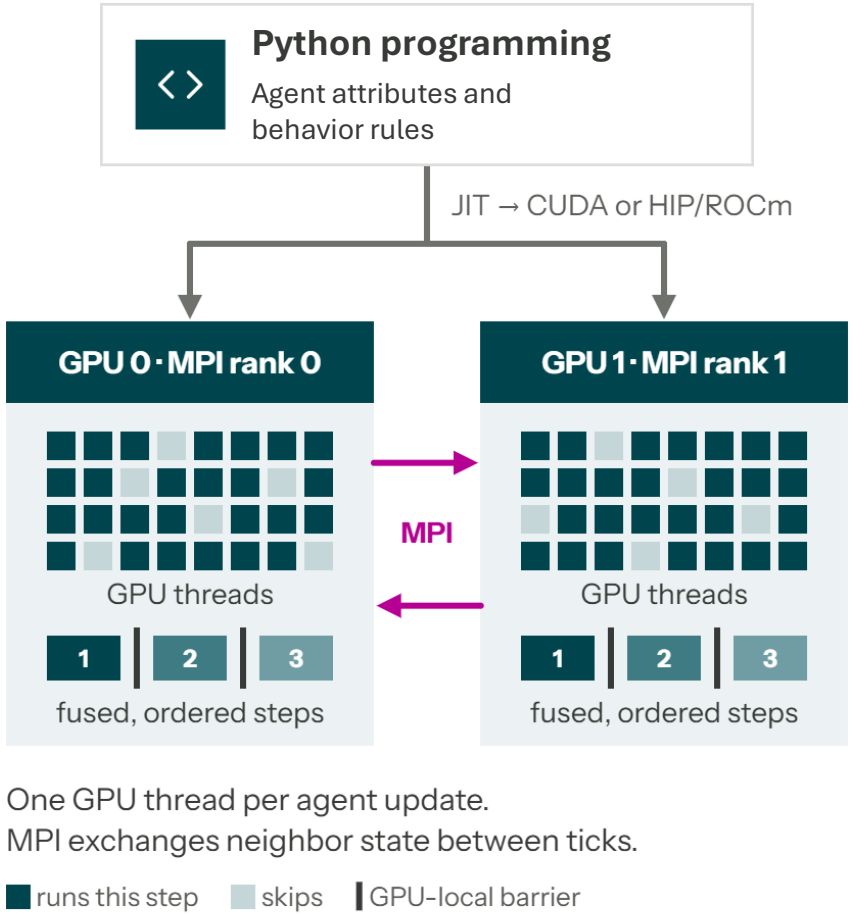
Run the same Python code on either GPU platform.

Ordered, parallel agent updates

Run dependent steps in one fused GPU kernel.

Runtime support

Sparse links, buffered state and reproducible RNG.



GGap: re-engineering the Fortran gap model enables large-scale forest simulation with spatially connected sites.

Original Fortran: nested loops	GGap: Site and Gap are agents
do s = 1, n_sites call update_site(s) do g = 1, n_gaps call update_gap(s, g) do t = 1, n_trees call update_tree(s, g, t) end do end do end do	**class Site**(Agent): neighbors = gaps, nearby_sites **class Gap**(Agent): neighbors = trees, parent_site **class Tree**(Agent): neighbors = parent_gap
Independent sites **No interactions between sites.**	**Spatially connected sites** **Site links add spatial interactions.**

Gap agents mediate Tree resources. Site agents coordinate Gaps and connect sites.

Example: 500 gaps × 1,000 Trees/gap = 500,000 Trees per site.

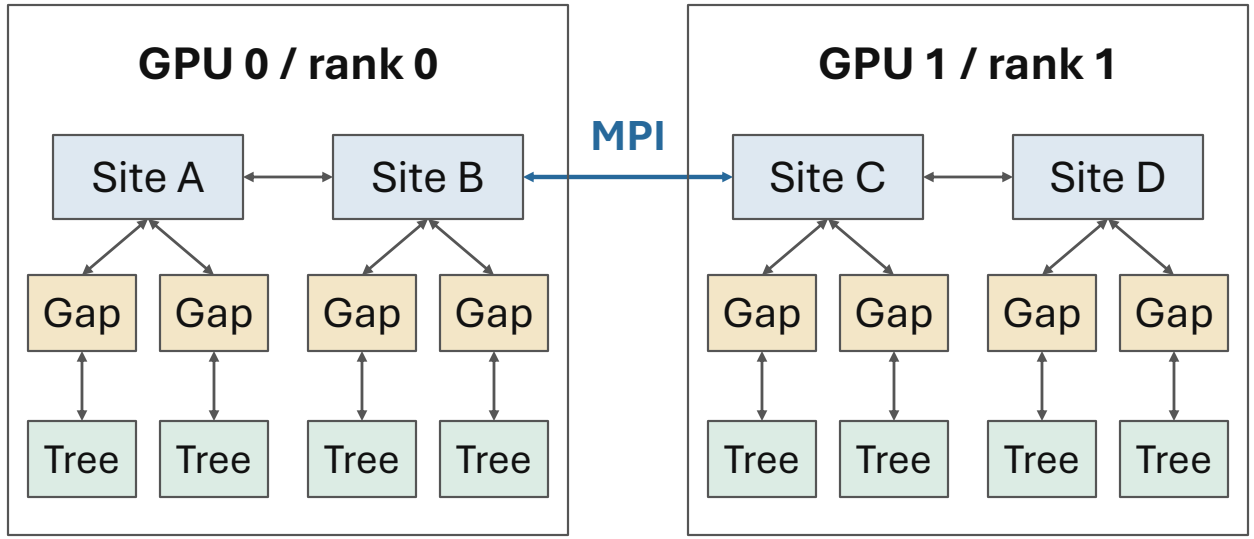
Naive all-to-all: ≈250 billion directed links. Hierarchy: 1,001,000.

GGap: each complete site stays on one GPU, keeping intensive work local and limiting MPI exchange to Site state.

Each complete site includes its Site, Gap and Tree agents.

Tree–Gap work
Growth, mortality, canopy competition and frequent resource exchange stay within the GPU.

Gap–Site exchange
Weather, nutrients and gap totals stay in GPU memory.

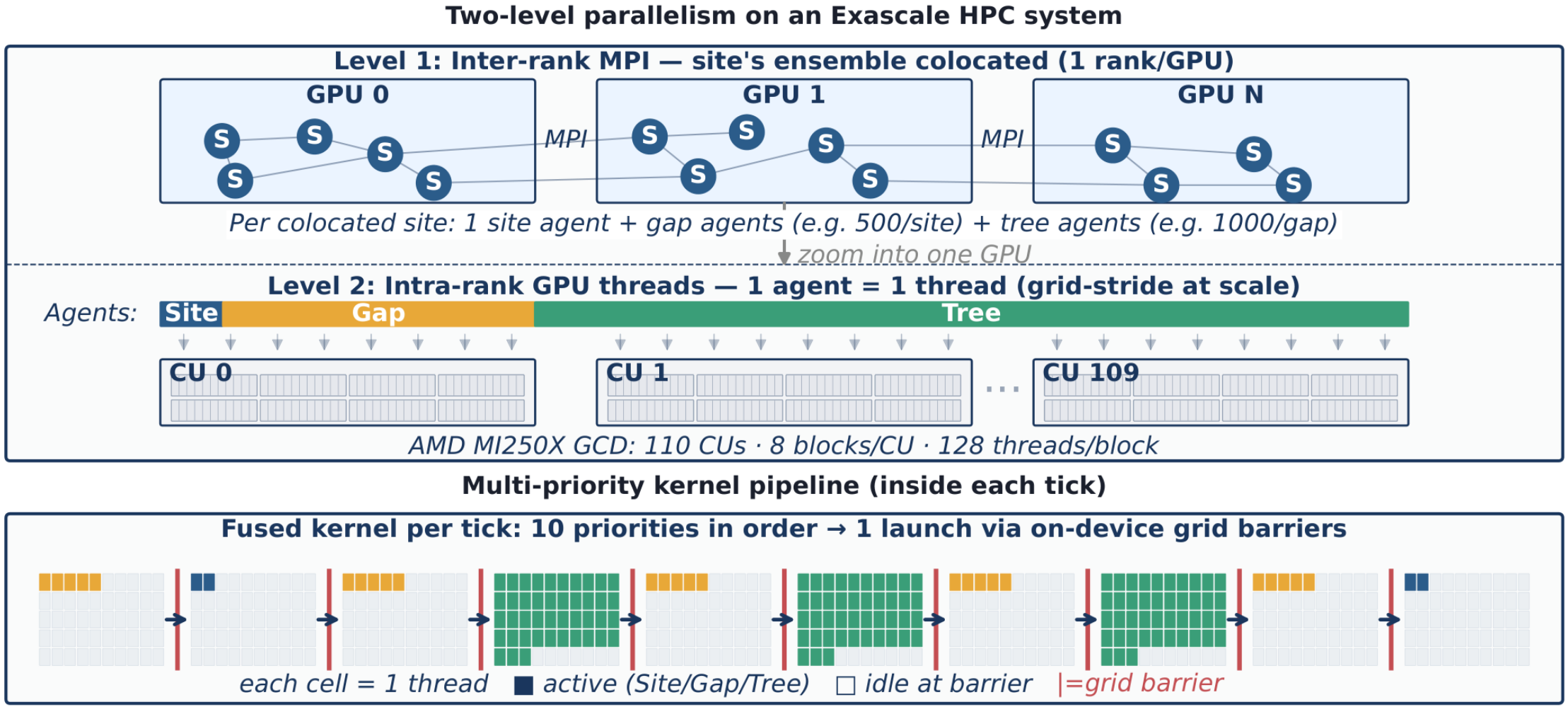


GGap: ten ordered annual step functions implement per-site ecology and inter-site seed dispersal in this initial version.

Priority	Agent	Ecological operation
P0	**Gap**	Build canopy LAI profile and aggregate tree litter
P1	**Site**	Update soil biogeochemistry, water balance, weather and disturbance
P2	**Gap**	Relay site weather and imported seeds
P3	**Tree**	Compute stress, potential growth and nitrogen demand
P4	**Gap**	Aggregate nitrogen demand and compute the supply ratio
P5	**Tree**	Update species seedbanks and seedlings
P6	**Gap**	Compute recruitment probability for each Tree slot
P7	**Tree**	Apply growth, mortality, litter production and recruitment
P8	**Gap**	Aggregate nitrogen consumed by trees
P9	**Site**	Close the nitrogen balance and disperse seeds among sites

Additional Site–Site connection such as fire spread or disease transmission, can be added only by modifying site step functions

GGap combines individual-tree ecology and spatial coupling with SAGESim's distributed GPU execution.

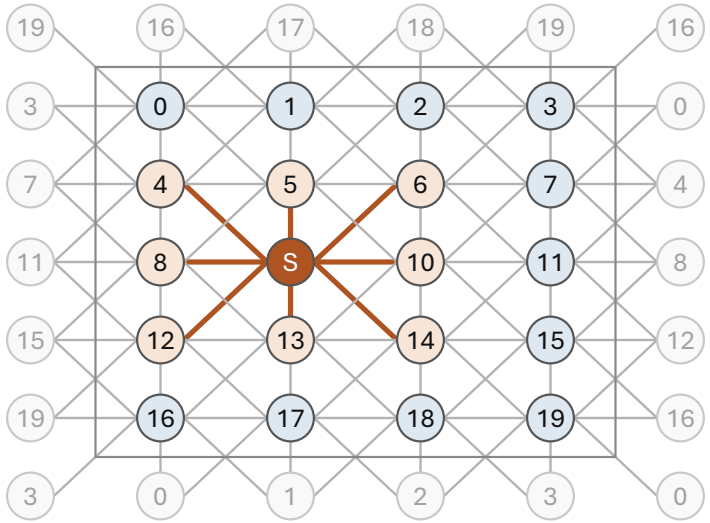


Scaling and performance analysis

Can we simulate sufficiently large forest domains,
and how efficiently?

A 2D torus supports controlled MPI scaling tests and a realistic network for local seed dispersal.

2D torus with eight neighbors



Orange links show eight nearby Sites.
Pale copies show periodic connections.

Controlled scaling of SAGESim's point-to-point MPI

Scaling tests need balanced compute and communication.
Equal site capacities control the compute workload.
A fixed degree and periodic boundaries keep connectivity balanced as we add sites in weak scaling.

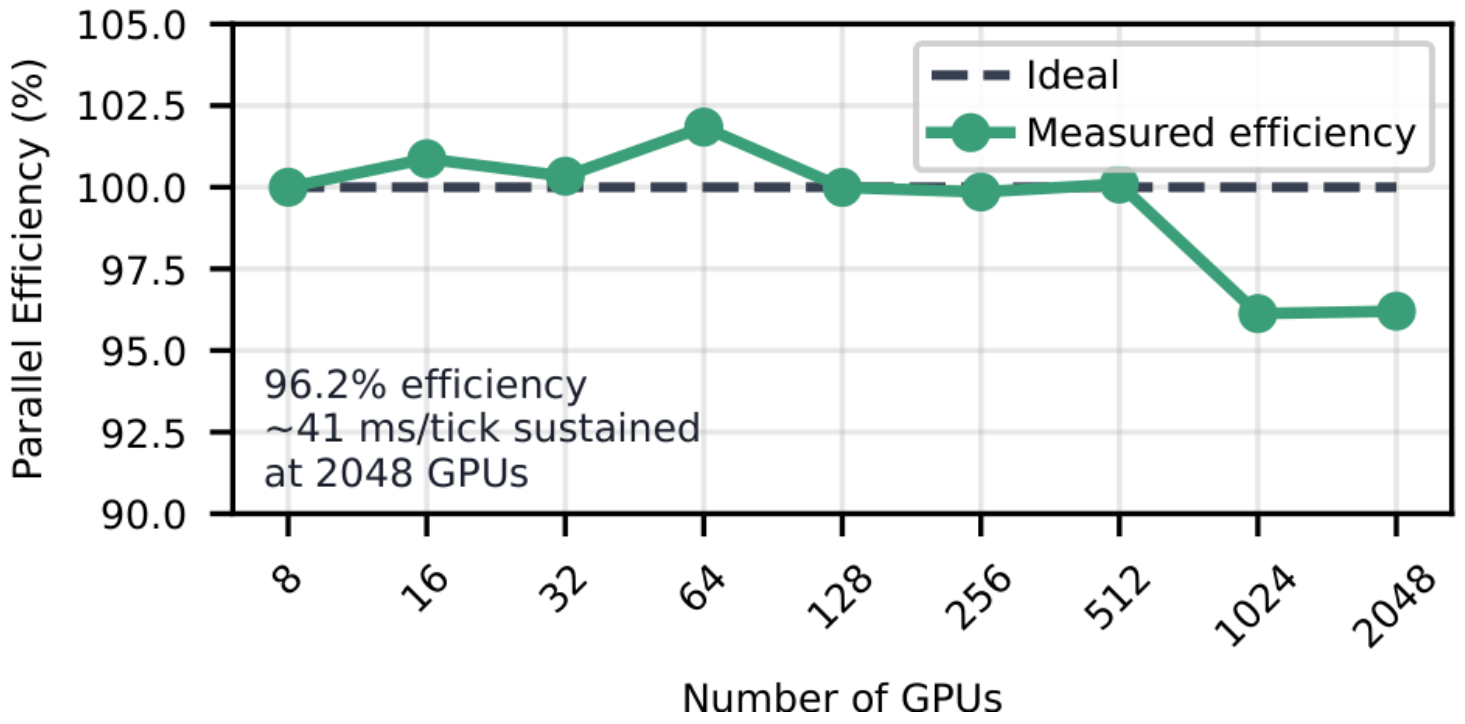
A realistic local seed-dispersal network

Seeds usually disperse to nearby locations.
Connecting each Site to its eight surrounding Sites represents this local exchange.

GGap achieves near-ideal weak scaling as its forest domain expands with the GPU allocation.

10 sites/GPU, 500 gaps/site, 1,000 Tree slots/gap. Frontier: 8 to 2,048 GPUs.

37.5% of Site–Site edges cross GPUs at every scale. Each run uses 1,000 ticks.



20,480 sites
10.25 billion agents

Continental-to-global simulation capacity

Larger domains at nearly constant time per tick.

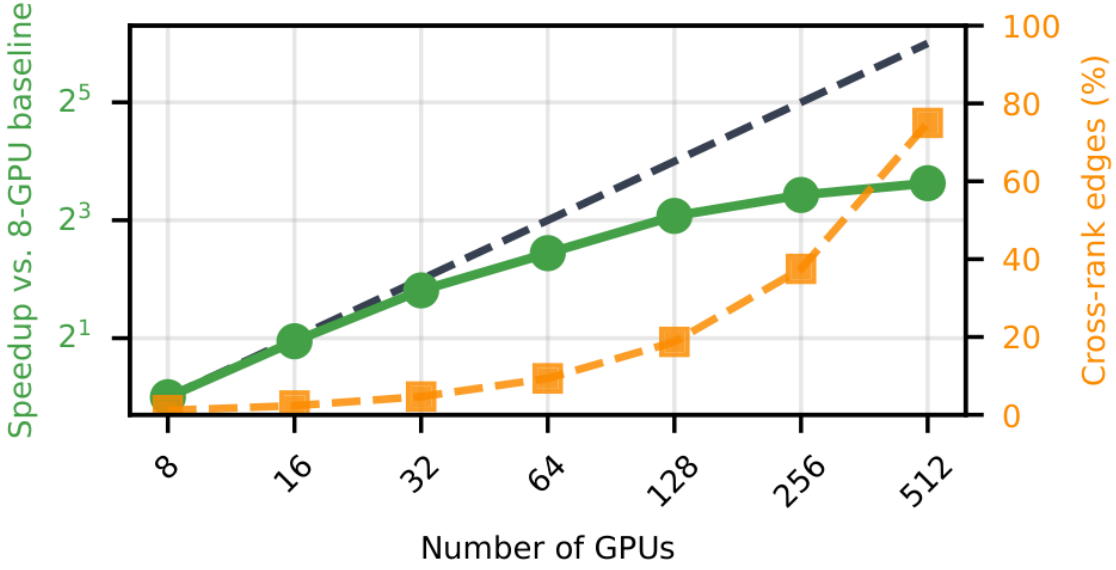
Strong scaling accelerates a fixed forest domain, with diminishing gains as GPU workloads become small.

Fixed 2,048 sites (≈205M agents), 200 gaps/site, 500 Tree slots/gap.

8 to 512 GPUs. 256 to 4 sites/GPU. Cross-GPU edges: 1.2% to 75% (24/rank).

12.4× speedup, 19.3% efficiency

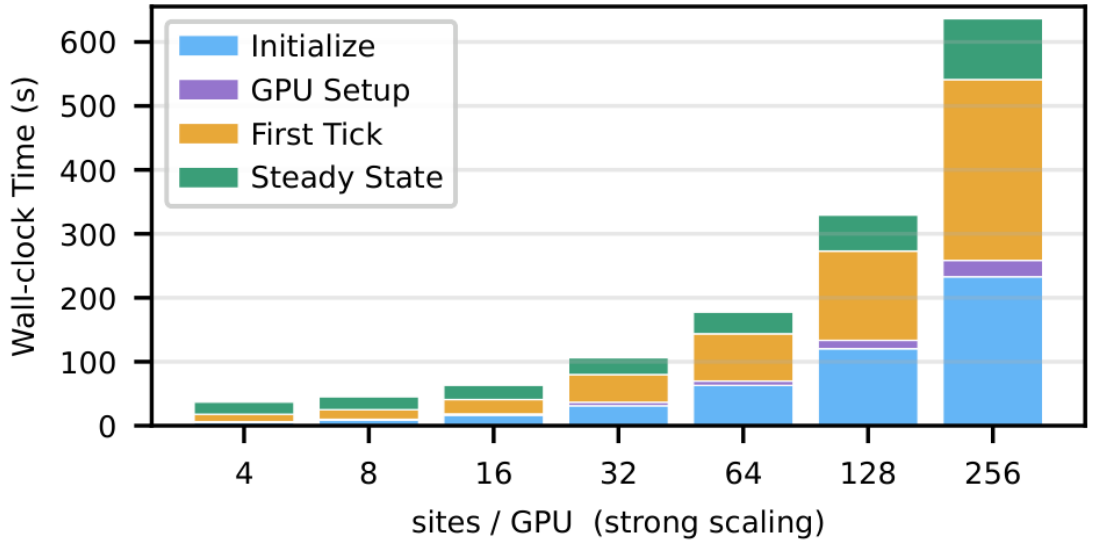
Green: measured. Gray dashed: ideal.



Speedup gains diminish as GPU count increases.

Runtime by phase (1,000 ticks)

Fewer sites/GPU means more GPUs.



Steady-state time improves 5× across the sweep.

The results establish GGap's computational capacity for continental-to-global forest studies and long simulations.

Demonstrated spatial capacity

20,480 sites and 10.25 billion agents tested. Moderate-resolution global domains need tens of thousands of sites.

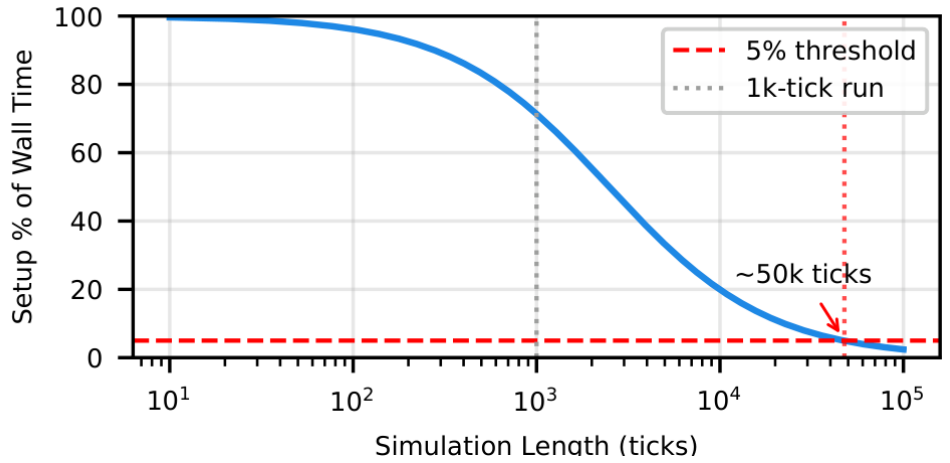
Long runs amortize one-time setup costs

Setup is paid once per run. Its fraction of runtime decreases as more ticks execute.

Faster repeated experiments

The fixed-domain run speeds up 12.4×, making repeated scenario and sensitivity experiments more practical.

One-time setup shrinks as a share of runtime



≈50,000 ticks: setup below 5%

100 years × daily steps:
>94% productive compute

CONUS forest simulation

Does GGap produce ecologically meaningful forests across a real continental domain?

GGap applies individual-tree ecology across CONUS using site-specific climate and species availability.

Initial CONUS study

0.5° grid to match E3SM land resolution
Forest masking leaves 1,424 sites
235-species pool with local availability
500 gaps/site × 1,000 Tree slots/gap
712 million Tree-agent slots
1,000 annual ticks from bare ground

Site-specific environmental inputs

NASA POWER / MERRA-2 climate
1991–2020 monthly means and variability
Shared ecological rules without site-specific tuning

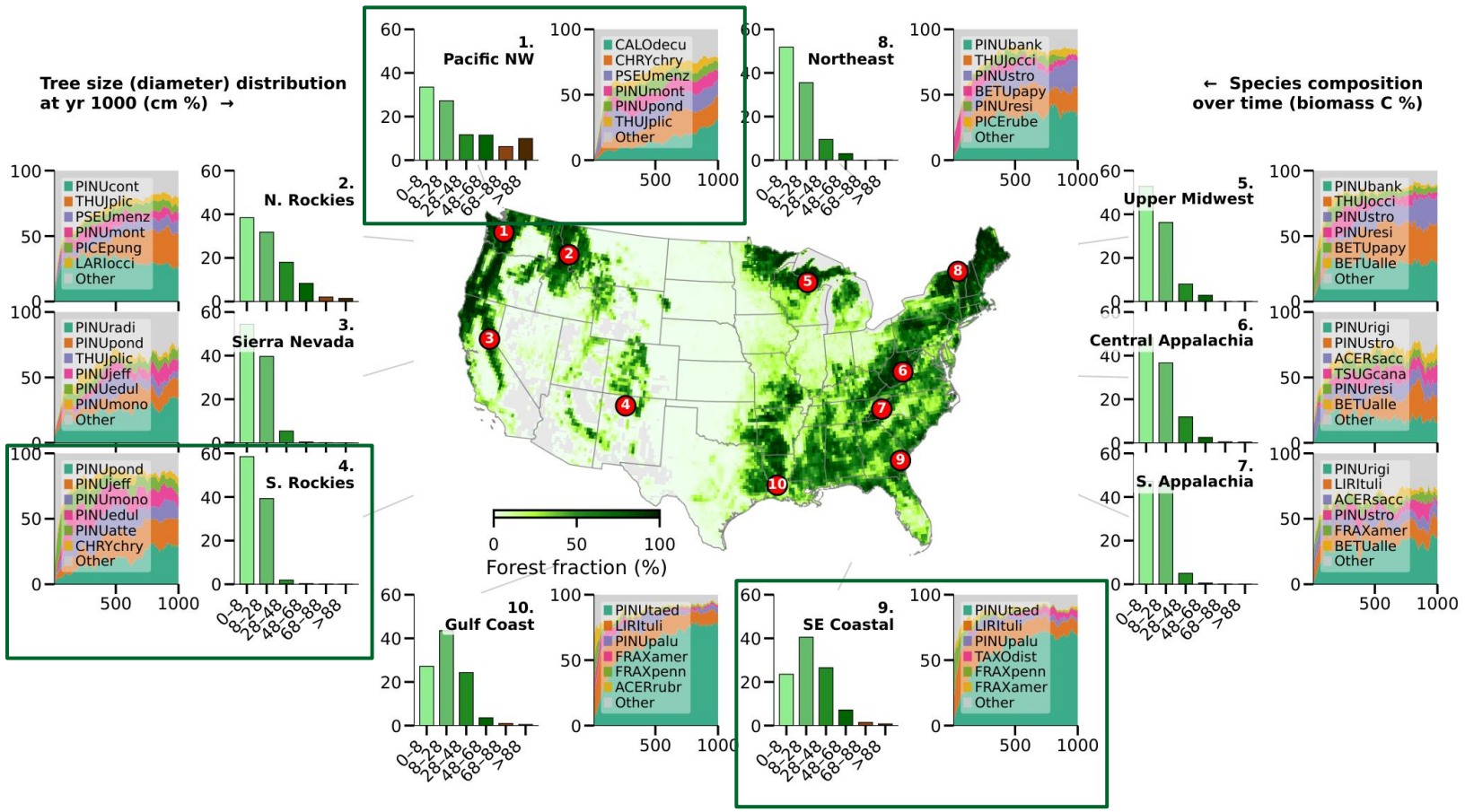
Compute-only execution on Frontier

20 Frontier nodes / 160 GPUs

112 s
Simulation loop
0.11 s per simulated year

170 s
Complete job
Initialization + setup

GGap's representative sites reproduce species and tree-size patterns consistent with observed regional forests.



1. Pacific Northwest

Mixed conifers with many medium and large trees.

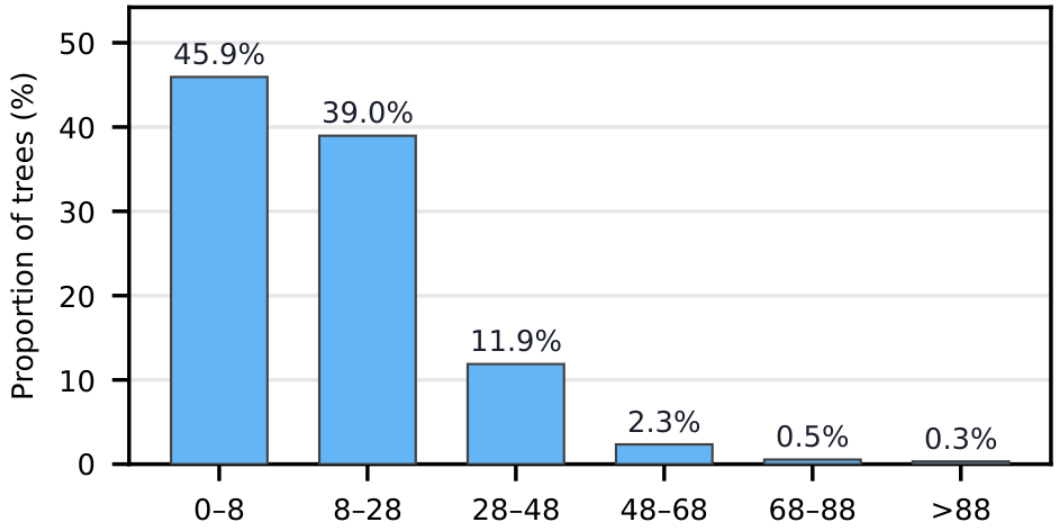
4. Southern Rockies

Dry climate limits growth, leaving mostly small stems.

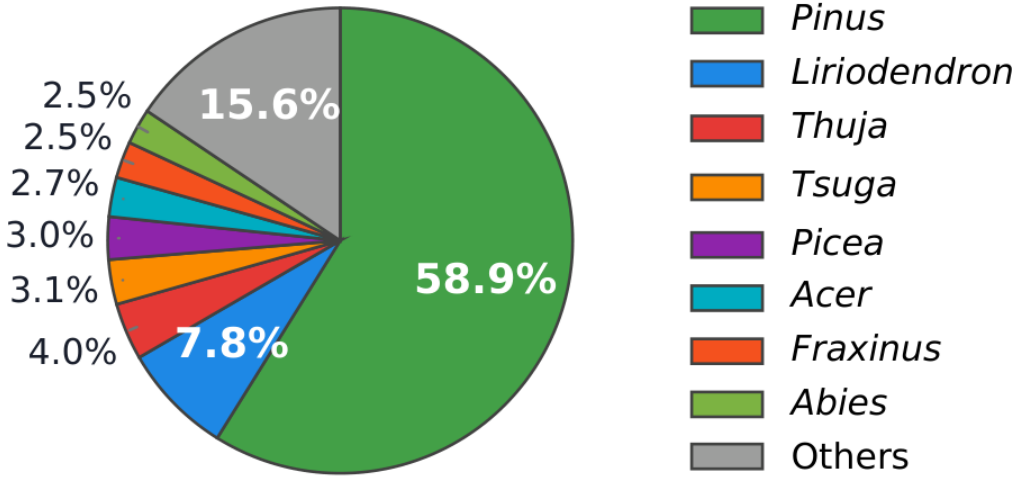
9. Southeast Coastal

Loblolly pine contributes ~80% of biomass carbon.

Aggregated CONUS tree sizes and genus biomass align with Forest Inventory and Analysis (FIA) observations.



(a) Size-class distribution



(b) Biomass carbon by genus

Small stems dominate tree counts

85% of stems are below 28 cm DBH.
Inverse-J form matches FIA size distributions.

Pinus dominates biomass carbon

Pinus contributes 59% of biomass carbon.
FIA also ranks Pinus first by wood volume.

Future work will improve SAGESim's runtime efficiency and GGap's predictive accuracy and Site–Site interactions.

SAGESim

Runtime development

GPU execution

Improve utilization for small workloads.
Reduce per-tick overhead.

Setup time

Reduce one-time initialization
and first-tick setup costs.

GGap

Ecological development

Quantitative validation and tuning

Broad patterns already agree qualitatively.
Measure errors against independent data,
then tune parameters where needed.

More types of Site–Site interaction

Add new Site–Site connections and rules
for spatial interactions, such as fire spread
and water exchange.

Continental forest dynamics can now be studied with individual-tree detail and explicit spatial interactions.

Demonstrated capability

GGap can support global forest studies

Computational capacity for moderate-resolution global domains with individual-tree detail.
20,480 sites at 96.2% weak-scaling efficiency.

GGap reproduces ecological patterns

Across CONUS, regional species composition, tree sizes and genus biomass patterns agree qualitatively with regional observations and FIA.

The scientific opportunity

Test aggregation assumptions against individual-tree forest dynamics.

Study how extreme events shape forest dynamics, response and recovery.

Couple with Earth system models to improve carbon and biomass predictions.

Acknowledgments

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