

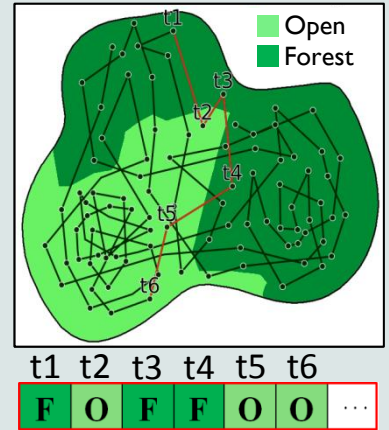
Background

A key aspect often neglected by movement ecologists is the *sequential* use of different habitats. We present a **tree-based method** with origins in molecular biology named **Sequence Analysis Methods (SAM)** to *Explore, Simulate, Classify* and *Visualize* sequential habitat use patterns.

Sequential Habitat Use

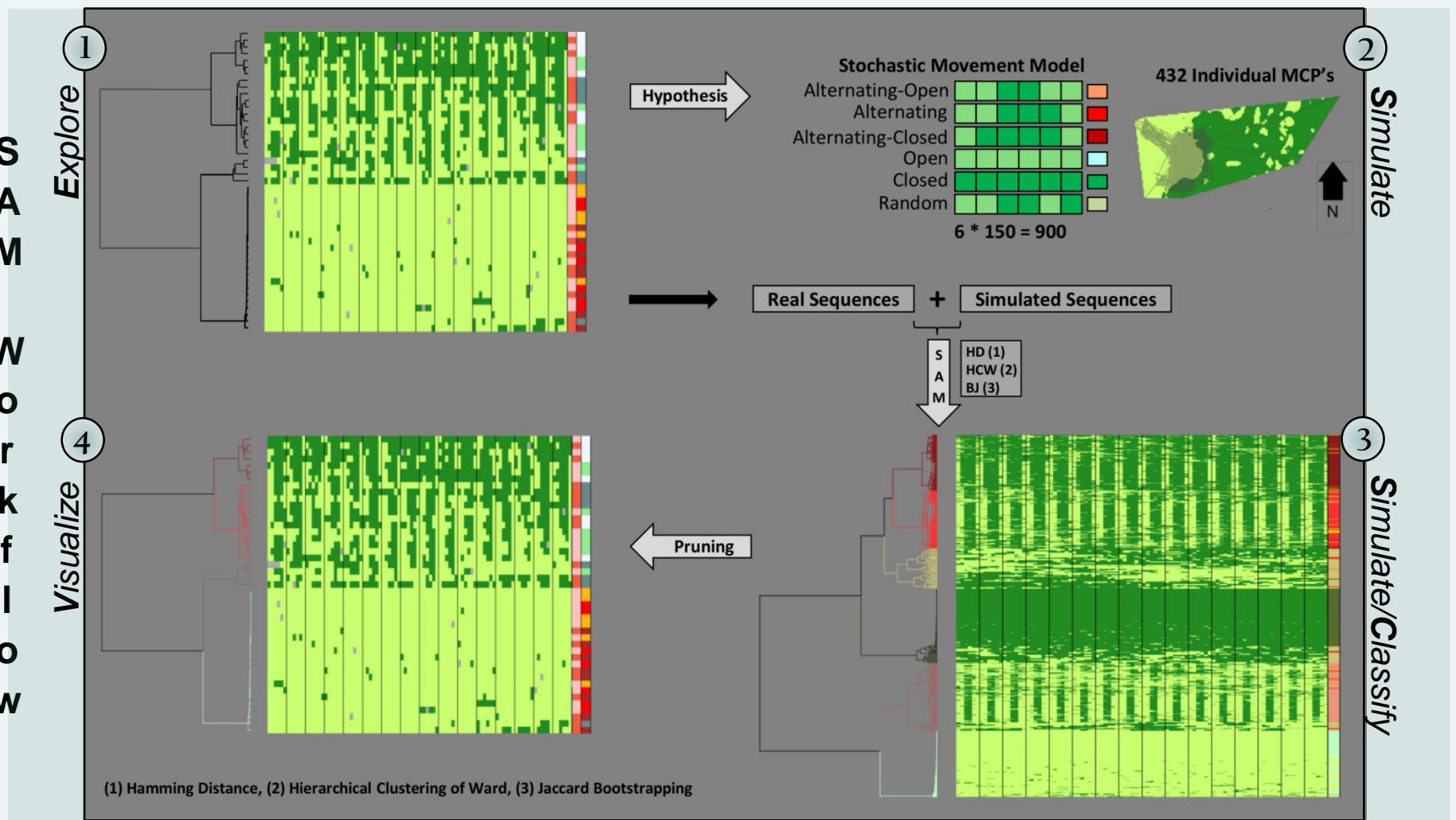
“Sequence of characters giving the habitat use of an animal for temporally ordered relocations extracted from spatial habitat layers, representing the animal’s surrounding landscape.”

Animal’s MCP



Workflow

- EXPLORE** biweekly sequences of habitat use by generating **exploratory trees** for each animal. Those trees are used to build hypotheses of expected patterns (P_e) of sequential habitat use.
- SIMULATE** P_e using stochastic movement rules to produce simulated trajectories within each animal's MCP, and generate individual level **simulation trees** (step 3).



- CLASSIFY:** Re-run SAM for real & simulated trajectories combined and generate **classification trees**.
- VISUALIZE:** Prune **classification trees** to visualize the classification of real sequences into P_e .

Conclusion

SAM allows to



sequential patterns of use.

Applicable to multiple species