

Conclusions and Future Work

Conclusions

Approximate Simulations of Dynamical Graph Grammars using the DGG Modeling Library

- An approximation of the exact simulation algorithm has been designed using the novel Expanded Cell Complex (ECC) and improved by making use of a semi-online match data structure with incremental updates.
- A new modeling library DGGML and a graph library YAGL have been developed.
 - The building blocks of DGGML each have their own unique contribution.
- Conducted three experiments for the CMA DGG, observing long-time behaviors of cytoskeletal network-like formation and localized alignment in the simulated array, and the approximate algorithm outperforming the exact.
- In the PCMA we explored the effects that different face shapes and boundary conditions have on local and global alignment.
 - In the case of a square face shape, we find the evidence to indicate array orientation may be multi-modal.
 - In the case of a rectangular face shape, we find that different boundary conditions may reorient the array mainly between the long and short axes.
 - The periclinal CMA DGG demonstrates the flexibility and utility of DGGML and highlights its viability to be used as a computational means of testing, screening or inventing hypotheses to explain emergent phenomena.