Minkowski Metrics and Phylogenetic Inference

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\section*{ABSTRACT}

The mapping of putative ancestral character states onto extrinsic phylogenetic trees has been used to test a wide variety of evolutionary hypotheses about the timing, ordering, rates, and correlates of character-state changes. In addition, character-mapping is an integral part of the process of finding the "best" tree for a set of terminal taxa. We consider a framework for testing hypotheses about the timing, ordering, rates, and correlates of character-state changes in a systematic probability distribution function from Uniform through Gaussian to Dirac. In the context of phylogenetic inference, such distributions are used as models of the evolution of character-state changes along branches. The minimum change ("linear parsimony"), based on Manhattan distance, and minimum squared-change ("squared-change parsimony") are special cases of this application. However, we show that combinations of special cases in their proper context within this family. The evolutionary model under the squared-change metric is a Brownian walk. Branch changes are independent, but each Minkowski metric specifies a unique random walk (e.g., a Cauchy walk under the linear parsimony metric).

\section*{MINKOWSKI METRICS}

\subsection*{Random Walks}

- If consecutive branch changes are independent, then movement along the branches of any tree (from Fig. 2 to Fig. 5) corresponds to a random walk through a character space (Fig. 6). The general class of random walks for k = 2 is a Lévy walk.
- The total area of morphospace that a set of diversifying taxa can explore is potentially greater for small k than for large k.
- Special cases:
  - "Linear parsimony" (k = 1) corresponds to a Cauchy random walk.
  - "Squared-change parsimony" (k = 2) corresponds to a Brownian (Gaussian) random walk.

\subsection*{Mapping Character States onto an Extrinsic Tree}

- An extrinsic tree is one determined by data or hypothesis outside of the current analysis, and is assumed to be a "true" tree.
- Given an extrinsic tree (topology + branch lengths) and a set of character values for the terminal taxa, hypothetical ancestral character states may be optimally "mapped" onto the nodes of the tree (Fig. 6). Character-mapping is common to comparative studies of character evolution.
- Current methods use optimality criteria based on minimizing Minkowski metrics.
- "Linear parsimony" mappings minimize the sum of absolute branch changes (k=1).
- "Squared-change parsimony" and "maximum likelihood" mappings minimize the sum of squared branch changes (k=2).
- The nature of the mapping is conveniently controlled by varying k.
- For small k, the effect of the root and side branch changes is minimized.
- For large k, the effect of the extrinsic branch lengths is dominated.
- Various diagnostics (Fig. 6) can be used to judge the quality of the mapping.

\subsection*{Random Walks}

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\subsection*{Weighting Branch Lengths}

- Total tree length is the sum of the weighted branch lengths.
- Weighting by reciprocal branch lengths allows us to map the extrinsic tree as closely as possible for any particular weighting, and it also influences the reconstructed branch lengths in an unbiased manner for any k.

\subsection*{Conclusions}

- Current methods for selecting the best tree (most "parsimonious") tree and for mapping ancestral character states onto trees are based on either Manhattan or Euclidean metrics.
- Manhattan and Euclidean metrics are special cases for k = 1 and k = 2, respectively, of the general family of Minkowski metrics.
- The "maximum-likelihood" method usually applied to tree fitting and mapping corresponds to k = 2. However, maximum likelihood inference can in principle be applied to any Minkowski distribution.
- Both the determination of the optimal k for a set of data and the optimal mapping of ancestral character states onto a character tree depend on choice of k, and various diagnostics can be used to assess the quality and the results.
- It has often been noted that "maximum-likelihood" trees correspond to an evolutionary model of a Brownian (Gaussian) random walk. However, all tree fittings and mappings correspond to some model of random walk to the extent that branch changes on the tree are independent (e.g., a Cauchy random walk for linear parsimony).