Submodular Functions and Biodiversity Conservation

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Conservation biology

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Typically, individual species are the focus of attention, but this is not necessarily the best way to conserve diversity:

> *Although conservation action is frequently targeted toward single species, the most effective way of preserving overall species diversity is by conserving viable populations in their natural habitats, often by designating networks of protected areas.* Rodrigues et al. (2005)

Phylogenetic diversity

Phylogenetic diversity (PD) is a quantitative tool in measuring the biodiversity of a collection of species (Faith 1992).

For a subset Y of species, $PD(Y)$ is the evolutionary distance spanned by the species in Y.

- This distance is usually defined in reference to some phylogeny, but here we (initially) extend this with reference to a collection of 2-state characters.

Phylogenetic diversity on splits

A bipartition $\{A, B\}$ of a set X, where $|A|, |B| \geq 1$, is a split of X.

A split system Σ of X is a collection of splits of X.

Σ is weighted if there is a map $w : \Sigma \to \mathbb{R}^{\geq 0}$.

For a subset Z of X,

$$PD(Z) = \sum_{A|B \in \Sigma; A \cap Z, B \cap Z \neq \emptyset} w(A|B).$$

Phylogenetic diversity on splits

Example $w(ag|bcdef) = 1$, $w(abg|cdef) = 5$, $w(abefg|cd) = 2$, $w(a|-) = 1$, $w(b|-) = 3$, $w(c|-) = 1$, $w(d|-) = 2$, $w(e|-) = 3$, $w(f|-) = 2$, $w(g|-) = 2$

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If $Z = \{a, b, f\}$, then

$$\begin{aligned} PD(Z) &= ag|bcdef + abg|cdef + a|- + b|- + g|- \\ &= 1 + 5 + 1 + 3 + 2 = 12 \end{aligned}$$

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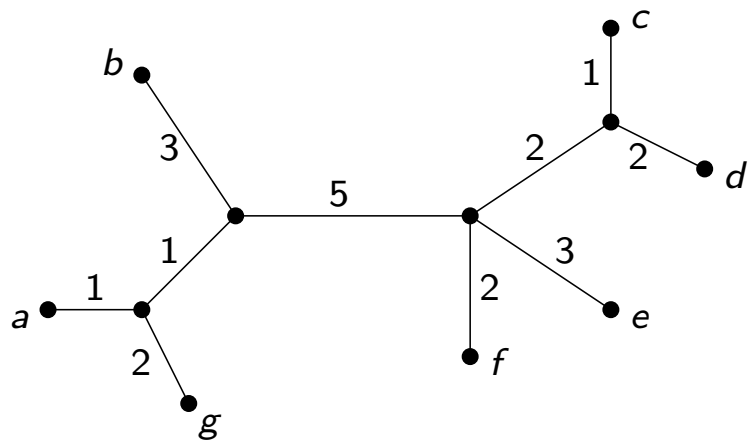

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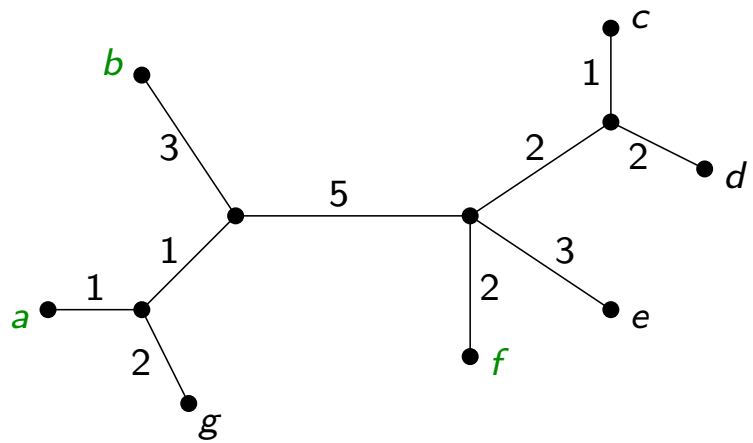

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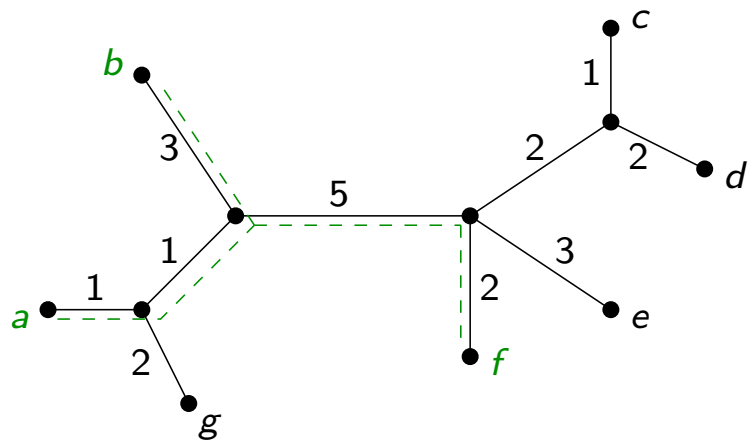

Phylogenetic diversity across reserves

For a weighted split system Σ of X and a collection $\mathcal{R}$ of protected reserves containing species in X, the phylogenetic diversity of a subset S of $\mathcal{R}$ is the PD score of the species contained within at least one reserve in S.

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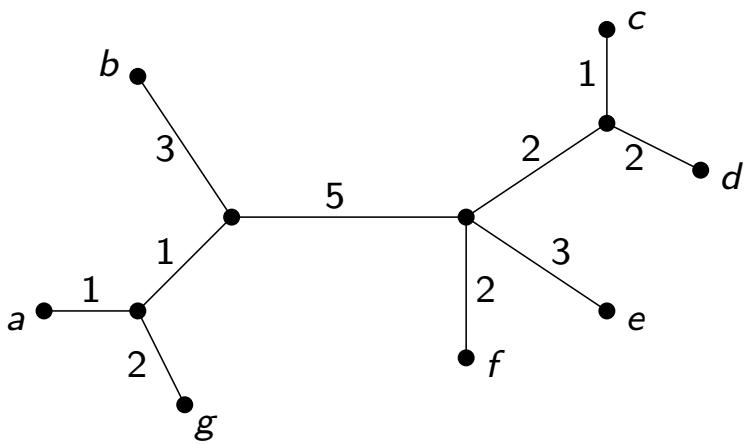

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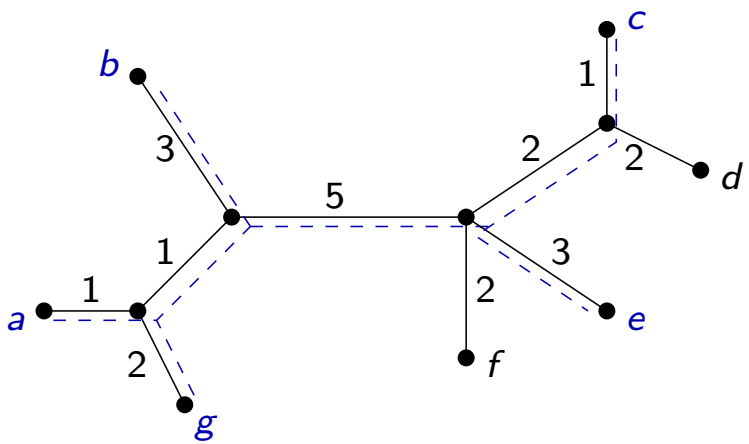

The problem

Budgeted Nature Reserve Selection (BNRS)

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Applications of using phylogenetic diversity across regions to make assessments in conservation planning include Moritz and Faith (1998), Rodrigues and Gaston (2002), Smith et al. (2000).

Budgeted Nature Reserve Selection

If $\mathcal{R}$ consists of all singleton subsets of X with each subset having unit cost and

- Σ is compatible, then BNRS is solvable in polynomial time (Pardi and Goldman, 2005; Steel, 2005).
- Σ is circular, then BNRS is solvable in polynomial time (Minh et al., 2009).
- Σ is affine, then BNRS is solvable in polynomial time (Spillner et al., 2008).

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However, if $\mathcal{R}$ consists of all singleton subsets of X with each subset having unit cost and Σ is arbitrary, then BNRS is NP-hard (Spillner et al., 2008).

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Theorem (Bordewich, S 2008)
If Σ is compatible, then there is a polynomial-time $\left(1-\frac{1}{e}\right)$-approximation algorithm for BNRS. Moreover, for any $\delta > 0$, BNRS cannot be approximated with an approximation ratio of $\left(1-\frac{1}{e}+\delta\right)$ unless P=NP.

- The algorithm returns a feasible solution whose score is at least $\left(1-\frac{1}{e}\right)$ (approx. 0.63) times the optimal score.

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The restriction to compatible split systems is redundant. In particular, we have

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Submodular functions

For a set E, a function $f : 2^E \to \mathbb{R}$ is submodular if, for all subsets $S, T \subseteq E$,

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Task: Find a subset S of E which maximizes f while keeping within budget B.

Approximation solution to OSF

ApproxFunction

1. Exhaustively find a feasible solution of size at most two that maximizes f. Call the resulting solution H_1.
2. For all subsets of E of size three,
   (i) Sequentially add elements of E that maximize the ratio of incremental f to cost while keeping within budget.
   (ii) Do this until no more elements can be added.

   Call the best solution H_2.
3. Output H_1 or H_2 depending on which has the bigger value.

Theorem (Sviridenko, 2004)
ApproxFunction is a polynomial-time $\left(1 - \frac{1}{e}\right)$-approximation algorithm for OSF.

A PD-based submodular function

Lemma Let Σ be a weight split system of X, let Q be a subset of X, and let $\mathcal{R}$ be a collection of subsets of X. Then the function $PD_{(Q,\Sigma)} : 2^{\mathcal{R}} \rightarrow \mathbb{R}^{\geq 0}$ defined for all subsets $\mathcal{R}'$ of $\mathcal{R}$, by the PD score of $Q \cup \bigcup_{R \in \mathcal{R}'} R$ is a submodular function.

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- Choosing E, f, c, and B to be $\mathcal{R} - Q$, $PD_{(Q,\Sigma)}$, c, and $B - c(Q)$, ApproxFunction is a polynomial-time $\left(1 - \frac{1}{e}\right)$-approximation algorithm for BNRS for when the selected set of reserves includes Q.

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- Choosing E, f, c, and B to be $\mathcal{R} - Q$, $PD_{(Q,\Sigma)}$, c, and $B - c(Q)$, ApproxFunction is a polynomial-time $\left(1 - \frac{1}{e}\right)$-approximation algorithm for BNRS for when the selected set of reserves includes Q.
- By running through each possible choice for Q, we get a polynomial-time $\left(1 - \frac{1}{e}\right)$-approximation algorithm for BNRS.

BNRS in the rooted setting

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Theorem (Bordewich, S 2008)
There is a polynomial-time $\left(1-\frac{1}{e}\right)$-approximation algorithm for rBNRS. Moreover, for any $\delta > 0$, rBNRS cannot be approximated with an approximation ratio of $\left(1-\frac{1}{e}+\delta\right)$ unless P=NP.

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Can we extend rBNRS while maintaining the property of a polynomial-time $\left(1-\frac{1}{e}\right)$-approximation algorithm for solving it?

rBNRS extensions

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2. It's unrealistic to expect a species probability of survival is zero if it is not contained in a selected region or, if it is contained in such a region, its probability of survival is one.
   - Allow for arbitrary survival probabilities.
3. PD assumes that features arise uniformly across a phylogeny and persist to be present in all descendant species. But features may disappear over time.
   - Allow for features to disappear.
     Once a feature is present, it has a constant and memoryless probability $e^{-\lambda}$ of surviving in each time step.

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$$PD_{(\lambda,\mathcal{T})}(X,p) = \int_{t\in\mathcal{T}} \mathbb{P}(t \to X)\mathrm{d}t,$$

where $(t \to X)$ denotes the event that a feature arising at point t on $\mathcal{T}$ survives to be present in a taxa in X which itself survives.

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Summing over a collection $\mathcal{P} = \{\mathcal{T}_1, \mathcal{T}_2, \ldots, \mathcal{T}_k\}$ of weighted trees, the PD of X on $\mathcal{P}$ is

$$PD_{(\lambda,\mathcal{P})}(X,p) = \sum_{j=1}^{k} w(\mathcal{T}_j) \int_{t\in\mathcal{T}_j} \mathbb{P}(t \to X)\mathrm{d}t.$$

rBNRS under the extended model

$\text{BNRS}_{(\lambda,\mathcal{P})}$

Instance: A collection $\mathcal{P}$ of weighted trees on X, a collection $\mathcal{R}$ of regions containing species in X, a cost of preservation for each region, a fixed budget B and, for all $(x, R) \in X \times \mathcal{R}$, probabilities $a(x, R)$ and $b(x, R)$, where $b(x, R) \geq a(x, R)$.

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Lemma The function $PD_{(\lambda,\mathcal{P})} : 2^{\mathcal{R}} \rightarrow \mathbb{R}^{\geq 0}$ is non-negative, non-decreasing, submodular, and computable in polynomial time.

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Theorem (Bordewich, S)

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