**TraitRELAX – A codon model for associating phenotypic traits with altered selective patterns of sequence evolution**

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**Phenotype associations with selective patterns**

- Phenotypic organismal traits are often associated with shifts in the pattern of selective forces operating on protein-coding genes
- Here, we propose a novel model for the identification of trait-related changes in the strength of selection operating on coding sequences

**The RELAX model**

- **Site level:** Allow different selective regimes ($\omega$) in different sequence sites
  - $\omega_0 < 1 \rightarrow$ purifying
  - $\omega_0 \approx 1 \rightarrow$ neutral
  - $\omega_0 > 1 \rightarrow$ positive

- **Branch level:** Allow different selection intensity ($k$) in different branches

**Joint Likelihood Framework**

$M_C, M_S$ – Character trait model and RELAX

$D_C, D_S$ – Character trait data and coding sequence data

$T$ – A phylogeny

$L = P(D_S, D_C|T, M_C, M_S) = P(D_C|T, M_C) P(D_S|T, D_C, M_C, M_S)$

Felsenstein’s pruning Algorithm

Character history is unknown → Integration over all possible histories

**Results**

- **Sensitivity & Specificity**
  - Poison digestion & Drug metabolism genes
  - Mating-system & Reproductive genes

**Conclusions**

- The power and accuracy of TraitRELAX increase with data size
- TraitRELAX is superior to standard codon models such as RELAX

**References:**
3. Minin and Suchard Phil. Trans. R. Soc. B 2008