Exploring epigenetics as a tool for population assessment and conservation in large marine predators

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Goals
- Identify exposures to pollutants in marine predators (focus on sharks and dolphins)
- Identify and understand age-related exposures
- Identify genes whose DNA methylation changes when exposed to pollutants
- Investigate inherited environmental changes to DNA methylation due to pollutant exposures

Research Methodology
- Create molecular aging tools needed for age-related evaluations of how pollutants affect species
- Find biomarkers of exposure to different pollutants using DNA methylation
- Identify genes where changes in DNA methylation occur with environmental changes

Results
- The BEAT-A model for estimating age in small cetaceans was created
- Used two of three genes investigated
- R²=0.778  Residual error=4.82 p=6.05X10⁻¹³

Future Research
- Age specific exposures are expected for dolphins and sharks
- An aging tool for sharks will be feasible once a reference genome is available
- Exposures to pollutants will produce unique DNA methylation markers that can be used to identify exposures
- Some of these marks will be heritable and affect subsequent generations

Figure 1. Bottlenose dolphins pictured at top, young of year lemon shark in tonic immobility bottom left, and myself collecting water samples in Bimini bottom right.

Figure 2. Calculating percent DNA methylation at CpG sites for age estimation

Figure 3. Histogram of ages used to calibrate the BEAT

Figure 4. The BEAT Graph: showing the fit of the model created

Table 1. Three genes were investigated for the creation of the BEAT. Showing # of CpG sites investigated per gene and how many were significantly correlated with age.

<table>
<thead>
<tr>
<th>Gene</th>
<th># of CpG sites</th>
<th># sign. Corr. To age</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene 1</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>Gene 2</td>
<td>4</td>
<td>3</td>
</tr>
<tr>
<td>Gene 3</td>
<td>6</td>
<td>3</td>
</tr>
</tbody>
</table>


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