Prediction and assessment of retail hake freshness during storage

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Introduction

Objective
To develop tools to monitor and predict fish quality and variability based in:

- Dynamic mathematical models of SSO growth
- Expected fish-to-fish variability
- Relationship between SSO concentration and standard Quality Sensory Methods (QSM)

Why?
- Fish quality degradation leads to losses of around 30-50% of fish catches.
- Fish freshness has a direct impact on market price

Final Model

Bacterial growth model [1]

Two spoilage bacterial groups: Pseudomonas (Ps), Shewanella (Sh)

\[ \frac{dN}{dt} = \mu N \left( 1 - \frac{N}{N_{\text{max}}} \right) \]

Growth rate: square-root model [2]

\[ \sqrt{\mu} = \alpha (T - T^*) \]

Initial conditions

\[ N(t = 0) = N_0 \]

Relation QIM/Bacterial concentration [3]

\[ QIM = \text{nint}(10^{lQ}) - 1 \]

\[ lQ = \alpha \log_{10}(N_{Ps}) + \beta \log_{10}(N_{Sh}) \]

Methods

Experimental scheme

- 3 exps with constant storage temperature (1, 5 and 7 C°) for initial parameter estimation
- Three-four specimen analyzed per sampling time
- After initial estimation, one optimally designed experiment (with variable temperature)
- 1 experiment (3 C°) for validation

Model building loop to ensure predictive capabilities.

Parameter estimation from experimental data

Core predictions (Monte-Carlo Method) Fish-to-fish variability

Optimal Experimental Design (OED) to reduce uncertainty

Results

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<th>Time [days]</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
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<tbody>
<tr>
<td><strong>Experts</strong></td>
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<td>E</td>
<td>A</td>
<td>B</td>
<td>B</td>
<td>NA</td>
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<td>(E-E)</td>
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<td>(E-A)</td>
<td>B</td>
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Conclusions

- Development of a dynamic model for fish quality prediction including fish-to-fish variability
- Storage temperature is the only stress variable considered although others could be included in the methodology
- Different catching methods/effect of evisceration were analyzed. No significant differences were detected within the inherent fish-to-fish variability [3]