

Title: Validation of a novel model predicting efficiency of CRISPR genome editing in Atlantic salmon

Keywords/Stikkord: Atlantic Salmon

CRISPR

Machine learning

Thesis type/Oppgavetype: Master

Credits/Stp: 60

Language/Språk: English

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Description:

CRISPR based genome editing is a powerful tool that now enables us to introduce precise cuts in genomes of a wide range of species. However, the efficiency with which these cuts are made varies dramatically between specific genomic sequence contexts. There were several attempts to come up with generalized models that predict the efficiency of the edit introduced by a Cas9 CRISPR nuclease. One of the best current models is a machine learning algorithm trained on empirical datasets generated in human and mouse cells. This model is widely used in design of CRISPR experiments, but reduced correlation between predicted and observed cutting efficiency was observed in cells from many species, especially those from aquatic animals. To enable efficient genome editing experiments in Atlantic salmon we are generating an new experimental dataset that will allow us to retrain the model to generate better estimates of cutting efficiency. The project will involve experimental evaluation of how well this new salmon-specific model predicts the probability of successful edits in cell from Atlantic salmon as well as other aquatic species. To achieve this the student will design and score using both the new and the old models a set of guides targeting several genes in salmon and human cells. These guides will be used in CRISPR based gene knockout experiments where empirical efficiency of genome editing will be determined by sequencing the genomic region of the cut. These sequencing results will allow us to compare the performance of both models across different species and to determine if our new model provides us with an improved way of design CRISPR based genome editing experiments in Atlantic salmon.

Project and/or collaborators: PetriFish

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