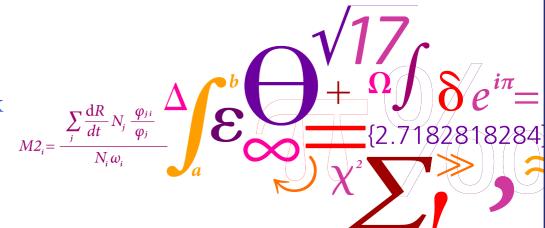


# Welcome to Fish stock assessment: SAM and TMB

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## DTU Aqua

National Institute of Aquatic Resources

# Preliminary agenda

## Day 1: Intro and basics

- ICES presentation (30m)
- Intro (what is TMB, what is SAM)
- First simple TMB example
- Parameters
- Data
- Basic parametric assessment model (study basic model implementation, add small improvements)

## Day 2: SAM basic use and foundation

- Ways to run SAM (basic sam, web, R, git)
- Multivariate normal distribution
- Intro to random effects

## Day 3: Processes in SAM

- Recruitment & Survival (a) Explain, (b) Implement, (c) Study SAM configuration
- Fishing mortality (a) Explain, (b) Implement, (c) Study SAM configuration

## Day 4: Observations in SAM

- Catches, total catches, Biomass indices
- Surveys, tagging, missing, and correlations

## **Day 5: Validation and forecast**

- Validating assessment models (e.g. observation and process residuals, leave out, retrospective, simulation, prediction based, jit)
- Forecast scenario options

# Time and place

#### Time:

Monday 12 Oct. 2020 — Friday 16 Oct. 2020 each day from 9—17:30 (CET)

#### Place:

By your computer<sup>a</sup>

<sup>&</sup>lt;sup>a</sup>Consider sitting together during exercises — where it is safe and where more participants are joining from the same institute

# Format adapted for online course

- Course is a mixture of lectures and exercises
- Each day the lecture parts are recorded for participants in different time zones<sup>a</sup>
- On days 2-6 the time from 16-17:30 is dedicated to questions mainly from participants in other time zones<sup>b</sup>
- All participants are welcome to join all parts.

- Questions can be asked at all times by interrupting please do!
- Questions can also be asked by writing in the chat box

#### This will be difficult — but we will do our best

<sup>&</sup>lt;sup>a</sup>The plan is that the participants in very different time zones view the lectures and work on the exercises offline and then join and ask questions online the following day

<sup>&</sup>lt;sup>b</sup>Notice that we are available on Saturday for questions regarding Friday's exercises

# Prepare for course by installing:

Basic R: Follow the instructions for your platform here https://cran.r-project.org/

TMB including R-tools: Follow the instructions on https://github.com/kaskr/adcomp/wiki/Download. Notice that on win and mac you need to install R-tools. Pay close attention to the instructions.

**devtools:** Install the package devtools by typing the following in your R:

> install.packages('devtools')

**Test installation** Type the following lines to test that it is all working:

- > devtools::install\_github('fishfollower/SAM/stockassessment')
- > library(stockassessment)
- > example(sam.fit)
- > fit
- > #Should output: SAM model: log likelihood is -145.5167 Convergence OK

## See you soon

- If all went well you should be setup to run all examples and exercises needed in the course
- If you got strange error messages, then please contact an@aqua.dtu.dk or olavbr@nr.no
- Special requests or questions w.r.t. the agenda please don't hesitate to ask.
- Looking forward to "seeing" you all soon.

# Appendix: Linear regression in TMB - 1

Run the following example, where each line is explained below, to prepare yourself for the TMB syntax ahead of the course.

- 10 observations are assumed to follow a linear regression model:
- Copy the following lines to a plain text file named linreg.dat

```
1 x y  
-1 1.4  
3 0 4.7  
4 1 5.1  
5 2 8.3  
6 3 9.0  
7 4 14.5  
8 5 14.0  
9 6 13.4  
10 7 19.2  
11 8 18
```

linreg.dat

- Two columns of paired (x, y) observations
- The model we want to fit is  $y_i = \alpha + \beta x_i + \varepsilon_i$ , where  $\varepsilon_i \sim \mathcal{N}(0, \sigma^2)$  all independent.

## Appendix: Linear regression in TMB - 2

• Copy the following lines to a plain text file named linreg.cpp

```
#include <TMB.hpp>
 2
    template < class Type >
    Type objective_function < Type >:: operator() ()
 5
 6
      DATA_VECTOR(x)
 7
      DATA_VECTOR(y);
 8
 9
      PARAMETER (alpha);
      PARAMETER (beta);
10
11
      PARAMETER (logSigma);
12
      vector < Type > pred = alpha + beta * x;
13
      Type ans = - sum (dnorm (y, pred, exp(logSigma), true));
      ADREPORT (pred);
14
15
16
      return ans;
17
```

## linreg.cpp

- The first five lines are obligatory syntax
- lines 6 and 7 reads data from R data object (names must match)
- lines 9-11 reads parameters from R parameter object (names must match)
- line 12 calculates the linear prediction (line 14 reports it back to R)
- line 13 calculates negative log likelihood and line 16 returns it.

# Appendix: Linear regression in TMB - 3

• Try to run the following lines in R

```
dat <-read.table("linreg.dat", header=TRUE)</pre>
 1
    library(TMB)
    compile("linreg.cpp")
 4
    dyn.load(dynlib("linreg"))
 6
7
    data <- list(x=dat$x,y=dat$y)</pre>
    parameters <- list(</pre>
      alpha=0,
10
      beta=0,
11
      logSigma=0
12
13
    obj <- MakeADFun(data,parameters,DLL="linreg")</pre>
14
15
    obj$fn()
16
    obj$gr()
    system.time(opt <- nlminb(obj$par,obj$fn,obj$gr))</pre>
17
18
    rep <- sdreport(obj)</pre>
```

- line 1 reads the data from the text file into R
- lines 3-5 loads TMB, compiles the function we defined and links it into our R-session.
- lines 3-5 loads TMB, compiles the function we defined and links it into our R-session.
- lines 7-12 defines two lists one with data objects and one with initial values for the model parameters.
- lines 14 defines the model object from the data list, parameter list, and the negative log likelihood function
- line 15 evaluates the function value (at the initial parameters)
- line 16 evaluates the function gradient (at the initial parameters)
- line 17 optimizes w.r.t. the model parameters
- line 18 gives summary of model results