**Suggested processes to extract incubation behavior from temperature measurements in uniparental shorebirds.**

The suggested process includes a series of procedures adapted to a particular type of dataset, particularly MSR temp loggers with 5s recordings and TTn with 1min recordings. The processes that are described below were suggested to be as simple and as universal as possible, with the preservation of relatively good model performance. In particular cases, change of parameters, inclusion of another sensor measurements, or changing the post-processing methods may help to improve the model outputs, but at costs of extreme time consumption and methodological complexity. Thus, I suggest to run this relatively simple process on the whole set of nests, then separate nests with no, or only small number of extraction errors which can be then repaired manually. Model parameters can be then adjusted individually for the subset of nests where performance of basic models will be poor.

The core model used for the extraction is one-dimensional two-state Hidden Markov Models (hereafter HMM) with unsupervised learning via Baum-Welch algorithm. Model predictions are then provided by Viterbi’s algorithm. Briefly, HMM is a machine-learning method which may be used for prediction of the unknown (“hidden”) state (here “incubation bout”/”incubation break”) from known (observed) time-series (here mainly temperature measurements from the nest). An assumption of the HMM is “conditional stationarity” of analyzed time series, that is that measurements representing particular state (e.g. incubation break) should come from approximately same probability distribution (below mentioned models uses the approximation by the normal distribution). This is the reason why the observed time series ussually cannot enter the model directly, but have to be “stationarized” (e.g. differences taken). This is the main reason for the inclusion of “preprocessing”, that is that single or multiple data transformation.

Briefly, suggested procedure (below more in detail) starts with converting the within-nest temperatures to the temperature differences, and then dividing it to the two variables: “**tdfn**” with only negative differences (and 0 for all other values), and “**tdfp**” with only positive differences (and 0 for all other values). Then, HMM is run for both variables. **The “tdfn” model usually well predicts vaste majority of incubation breaks, while “tdfp” model predicts steep temperature increases after the parent’s return and may be later used to searching the ends of long incubation breaks.** **Thus, “tdfn” model is used for prediction of the incubation behaviour, while “tdfp” model can be then used for it’s correction.**

In many cases (high quality datasets), the prediction by the “tdfn” model is sufficient itself. However, there are also relatively common errors, which should be repaired during “postprocessing” stage of the suggested procedure. The first type of problems arises from the fact that the used model is usually very sensitive in predicting even very short incubation breaks. While this is positive for high quality datasets with clear signal, it might be a problem in datasets of poorer quality, or taken in turbulent environment. In these datasets we frequently observe small frequent temperature fluctuations, which are (very probably) not connected to the departure and arrival of the incubating bird. Such temperature measurements might be either recognised and smoothed before fitting of the model (which would require to adjust the smoothing method and parameters specifically to the particular dataset), or the problem can be solved by the correction of the model prediction. In this case, I suggest to proceed as follows: a) delete very short incubation bouts (i.e. <1min), unless the temperature increase during this bout is not highly improbable without true bird arrival (i.e. >99% quantile of positive differences measured during breaks); and b) delete incubation gaps associated with very small temperature decrease (i.e. <1°C).

Another problem arises from the early end of long incubation breaks. This occurs especially because as within-nest temperature converges to the ambient temperature, it’s changes becomes to be too small to be detected (note, that suggested algorithms works with temperature differences, not with it’s absolute value). The correction in this case may be done using the second (“tdfp”) model. This works well, because the within-nest temperature rise after the end of long break (i.e. >10 min) associated with big (i.e. <-7°C) temperature drop is ussually steep and clearly identifiable.

Further are described particular suggested processes for MSR and TTn data respectively, together with the list of parameters that need to be set. These parameters are also highlighted within text in bold.

MSR data extraction summary

1. Preprocessing
   1. delete temperatures “-46°C “(logger errors)
   2. take difference with **lag=1**.
   3. From the differences, two separate variables for models are than prepared:
   4. “tdfn”
      * set differences >0 to 0
      * smooth resulting time series by moving averages with **window=10**, left-centered.
   5. “tdfp”
      * set differences <0 to 0
      * smooth resulting time series by moving averages with **window=10**, left-centered.
2. Model
   1. Separate two-state HMMs are estimated for “tdfp” and “tdfn” respectively.
   2. Take and save Viterbi-based predictions from both models.
3. Postprocessing: In many cases (optimal data quality), the prediction of “tdfr” model itself provide sufficient quality prediction, and may be used without any other corrections. In other cases, the subsequent series of steps is suggested.
   1. Delete incubation bouts shorter than **1** minute **(sbout\_length)**, unless the temperature increase within one step (i.e. 5 sec) is not **>0.1**°C **(ib\_max )**. This treshold might be replaced by some quantile from tdfp during predicted incubation breaks, but in most cases this value is ok. Note, that tdfp has been smoothed previously. Also, this step is better to proceed at the end of the postprocessing (after c.).
   2. Calculate temperature drop during incubation breaks and delete incubation breaks with temperature drop (calculated as a sum of “tdfn” during the gap) > -**1**°C **(sgap\_drop)**.
   3. Find incubation breaks, longer than ~**7** min **(5 - 10) (lgap\_length)**, during which the temperature drop (see above) is deeper, than **-7**°C **(-10 - -5) (lgap\_drop)**. These will be further called “long breaks”. Then define predicted break-ends from the “tdfp” HMM. In order to make the model prediction less sensitive calculate maximum “tdfp” value within each such “break-end”, and don’t use those “break-ends” below **25**% quantile of maximal values **(sstop\_max)**. Then take each “long break” and stop it at the beginning of the first subsequent “break-end”.
   4. Further corrections may be done manually.

TTn data extraction summary

1. Preprocessing
   1. delete temperatures “-46°C” (logger errors)
   2. take difference with lag=1
   3. From the differences, two separate variables for models are than prepared:
   4. “tdfn”
      * set differences >0 to 0
      * smooth resulting time series by moving averages with window=3, left-centered, but then shift 2 cells to right.
   5. “tdfp”
      * set differences <0 to 0
      * smooth resulting time series by moving averages with window=3, left-centered, but then shift 2 cells to right.
2. Model
   1. Two-state HMMs is estimated for “tdfn”. “Tdfp” may be used itself, without model prediction.
   2. Take and save Viterbi-based predictions from the model.
3. Postprocessing: In many cases (optimal data quality), the prediction of “tdfr” model itself provide sufficient quality prediction, and may be used without any other corrections. In other cases, the subsequent series of steps is suggested.
   1. Delete incubation bouts of predicted length **1** minute **(sbout\_length)**.
   2. Calculate temperature drop during incubation breaks and delete incubation breaks with drop temperature drop (calculated as a sum of “tdfn” during the gap) > -**1**°C **(sgap\_drop)**.
   3. Find incubation breaks, during which the temperature drop (see above) is deeper, than **-7**°C **(-10 - -5) (lgap\_drop)**, regardless of its length. These will be further called “long breaks”. Than calculate **85**% quantile of non-zero values of “tdfp”. Finally take each “long break” and stop it at the first subsequent measurement, when value of “tdfp” is above the 85% quantile **(sstop\_max)**.
   4. Define all measurements with temperature difference >**0.5**°C **(ib\_max )** as incubation bout. This treshold might be replaced by some quantile from tdfp during predicted incubation breaks, but in most cases this value is ok. Note, that here is worked with unsmoothed differences, not with “tdfp”.
   5. Further corrections may be done manually.

Parameters that need to be set and suggested values.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | Definition | Suggested for MSR | Suggested for TTn |
| lag | Lag of the differences taken | 1 | 1 |
| window | Width of the smoothing window for the “tdfp” and “tdfn” | 10 | 3 |
| sbout\_length | Length of the incubation bout, until which the bout will be deleted, as very probably false-positive | 12(i.e. 1 min.) | 1 |
| ib\_max | Minimal value of “tdfp”, for which incubation bout is predicted in any case | 0.1°C | 0.5°C |
| sgap\_drop | Minimal acceptable drop during predicted incubation break | 1°C | 1°C |
| lgap\_length | Length of incubation break, which is during postporcessing taken as “long break” | 90 (i.e. 7.5 min.) | NA |
| lgap\_drop | Temperature drop during incubation break, which is during postporcessing taken as “long break” | -7°C | -5°C |
| sstop\_max | Criterion to find the end of long incubation breaks, based on the “tdfp”. Meanings are different between loggers (see above). | 0.25 | 0.85 |

Together with this protocol is provided:

* Directory “tools” with “tools.R” script loading all libraries and user-made fuctions needed to run analyses and several functions in separate scripts.
* HMM\_unip\_incub.R script to run the above described processes.
* Two folders of actograms:
  1. “hmm\_t” compare the final prediction after postprocessing (green bars + temerature measurements in red/yellow) with the model predictions without any postprocessing (black bars).
  2. “inc\_ref” compare final prediction after postprocessing (green bars + temerature measurements in red/yellow) with the MB method (black bars).

example of vizualization:



*Red line – temperature within nest (yellow, if predicted break), orange is the temperature near the nest, light blue is the “tdfn” and deep blue the “tdfp” transformed variables. Green bars are predicted incubation bouts after HMM and postprocessing, black bars are incubation bouts predicted by MB method (here), or by HMM without postprocessing (in “hmm\_t” folder).*