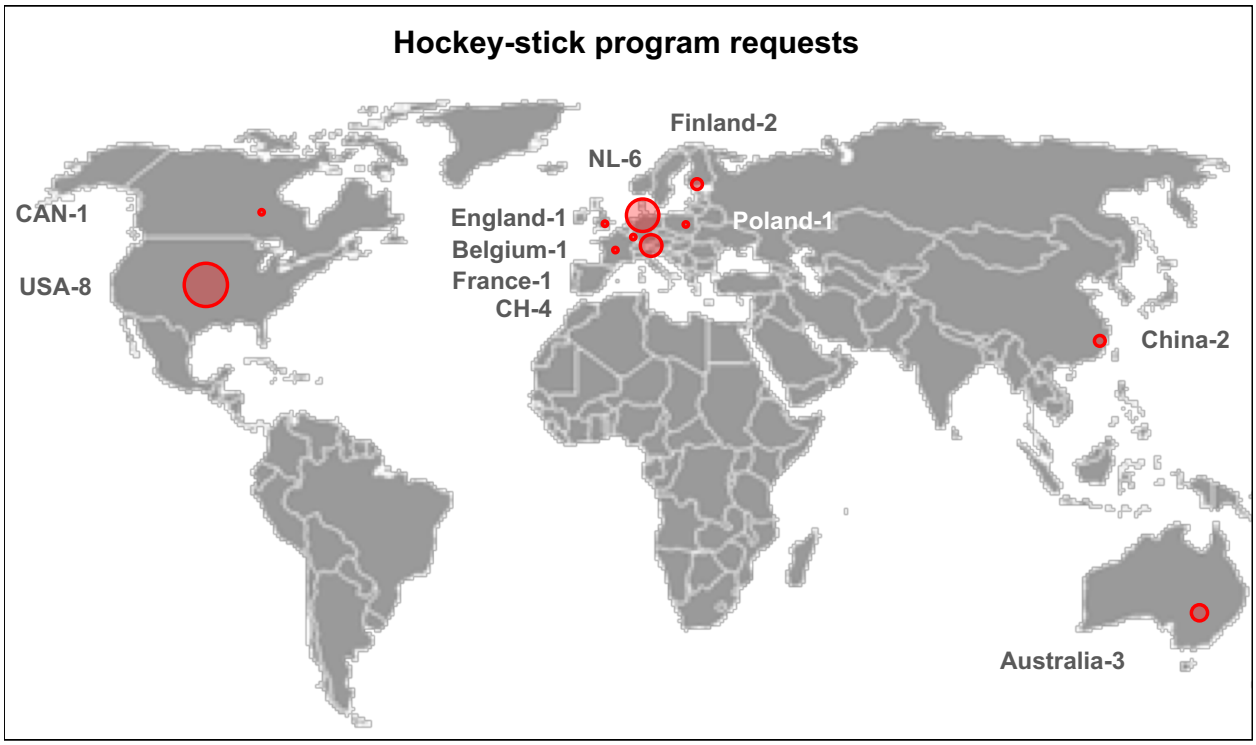
ALGORITHM-DETERMINED MELATONIN ONSET AND OFFSET

Dear colleagues,

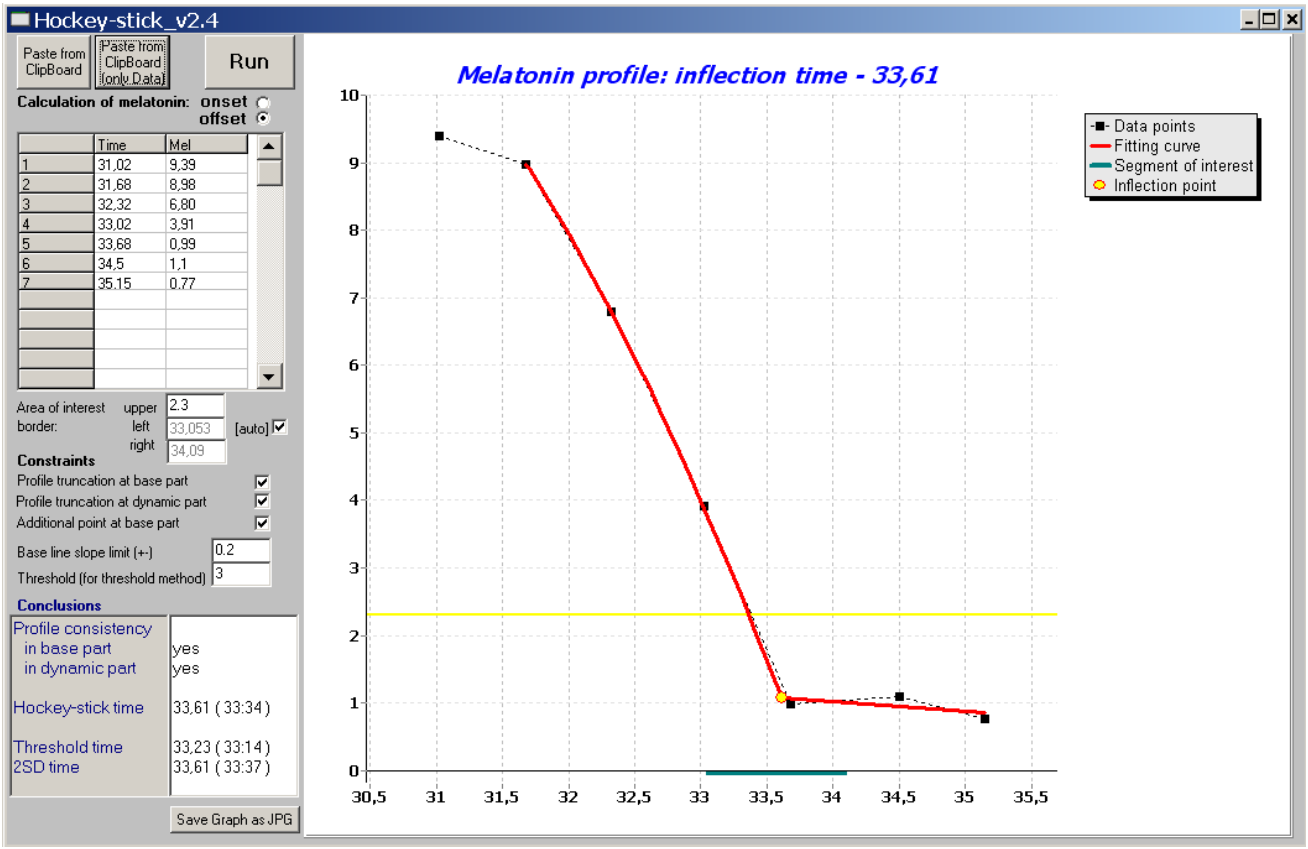
we launch a second (and probably the last) version of the hockey-stick program. The program determines salivary or blood **melatonin onset** (and **offset**) using a pairwise linear-parabolic function (looking like a **hockey stick**). The decision is an inflection point – the transition between a straight line and parabola branch. In addition, the program provides additional melatonin timing measures – "Threshold crossing time" and "2SD time" (to meet requirements of some users).

Since its initial publication in 2014 (Danilenko et al., Chronobiol Int 31:349-55), we have received 30 requests from around the world (see map) for the program, and the method has already been used in more than 10 studies published by independent centers.



What is new in version 2.0:
– in addition to melatonin onset, it can measure melatonin **offset**;
– the **left** and **right borders** of the area of interest (where the inflection point is supposedly located) are now modifiable (realised in version 1.6 already);
– corrected decision in the case when only one melatonin value constitutes the dynamic part;
– elimination of some previously identified **bugs**.

Hockey-stick v2.0 is freely available from: https://cloud.mail.ru/public/E3Dd/5iw38DSYy . The file size is 773 Kb. The program runs in Windows. The interface looks like this:



Basics for users

Copy/paste data: the method can be run even if there are only 3 or 4 melatonin data points for the profile. You can copy a large area of the data set, but only the values of the first and last column will be inserted into the program module; the separator in the values can be either a comma or a full stop.

Area of interest – a rectangle area, outlined by the program in which the inflection point is sought. During the fitting, the program "travels" across the points of a virtual grid with a step of 0.01 along each axis, chosing a point with the least sum of squares (orthogonal method).

The upper, left and right borders of the area of interest are interactively modifiable. By default, the upper border is set to 2.3 pg/ml since only less than 5% of salivary melatonin values exceed this threshold at baseline (daytime) [Molina & Burgess, Chronobiol Int, 2011, 28:714-8; Danilenko et al., Chronobiol Int, 2014, 31:349-55]. For blood values, this threshold should be increased to ~5 pg/ml.

The larger the area of interest, the longer the computation (usually no more than 1-10 seconds).

Constraints

Profile truncation at base part tab excludes from the computations any high (above the upper border of the area of interest) marginal baseline values, if they exist.

Additional point at baseline – automatically adds an additional point in the profile when only one data point constitutes the baseline part of the melatonin profile. It allows a more reasonable approximation.

Baseline is restricted to have a slope between -0.2 and 0.2. These limits were based on an assumption that melatonin concentration follows a "corridor" 0-2.3 pg/ml over ~11.5 daytime hours (2.3 / 11.5 = 0.2). In the case of low melatonin producers the slope constraints are recommended to be set to 0 interactively.

Threshold method level, pg/ml – the melatonin value applied in calculation of melatonin onset (or offset) by the threshold method. The default 3 pg/ml threshold may be changed interactively.

Conclusions

Profile consistency – a report on the profile consistency in baseline part and in dynamic part. "No" would indicate a diversity of the melatonin profile points, suggesting that the determined melatonin onset (or offset) may be unreliable; check after removing outliers. The conclusion window is blank when only one point constitutes the baseline or dynamic part.

Threshold time (other than hockey-stick method) – the time of melatonin onset (or offset) determined by linear interpolation when the melatonin profile segment crosses a fixed concentration level.

2SD time (other than hockey-stick method) – the time of melatonin onset (or offset) determined by linear interpolation when the melatonin profile segment crosses a "non-fixed" level – a mean of melatonin values comprising the baseline part of the profile (defined by the program) and the closest value in the dynamic part (if it is not higher than the baseline values), plus 2 standard deviations (SD) of the mean. 2SD time may be calculated with at least three values available, otherwise the conclusion window is blank.

A final note: the method is not designed to judge between two alternative decisions when, for some reason, melatonin levels rise (or decline) twice during a short period of time.

See also the article by Danilenko et al. (Chronobiol Int, 2014, 31:349-55) for more details.

Best regards,

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