

A simple method for determining pulse width as a substitute for RR interval: A  
brief technical guide

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Funding for this research was supported by a grant from the Morris Animal  
Foundation/Human-Animal Bond Research Initiative Grant #D15HA-030 awarded to Robin L.  
Gabriels Psy.D.

Clinical Trial Registration Information: Wellness Effects of Animal-assisted Activities  
With Autism Spectrum Disorder Youth in a Specialized Psychiatric Hospital;  
<http://clinicaltrials.gov>; NCT03369769.

## PULSE INTERVAL ANALYSIS

### Abstract

Photoplethysmography (PPG) provides cheap, simple access to pulsatile intervals which correspond to heart beats. However, it often provides a signal which is significantly degraded, and requires cleaning. Manual correction is time consuming, automated correction often fails to deal with unusual features within the signal. This paper briefly presents a simple method of template matching PPG-derived heart beats for use in heart rate variability analyses.

*Keywords:* photoplethysmography, RR intervals

## PULSE INTERVAL ANALYSIS

### **Introduction**

The two most common methods for assessing heart rate are measuring electrical potential across the chest or the physical/vascular pulse signal. These are, respectively, the electrocardiogram (ECG) or the photoplethysmogram (PPG). Both methods are commonly used in a variety of research and consumer devices and are often both described non-specifically as measuring 'heart rate.' ECG measures an absolute difference between two electrodes and returns a consistent signal (i.e., most hearts provoke a signal of about 1 millivolt, with a range almost always between 0.5 mV and 1.5mV). However, PPG measures a relative signal – it takes local fluctuations in blood just under the skin and measures how much they fluctuate relative to the instantaneous signal. The value of this signal may be anywhere on a wide continuum and depends on the specific device and how it is attached to the person one wishes to measure. As a consequence, these devices require a windowing algorithm, which place the relative signal within dynamics limits to maximise the visibility of the signals. This approach works well at rest, but the slightest movement can produce strong fluctuations in the relative local signal, and push it outside the measurement window.

In sensitive or active populations, there are a variety of ways to produce the above fluctuations, and thus measurements suffer from a variety of errors. Individuals may hypersensitive to any skin-attached device, which results in picking, adjusting, or pressing the device, the device may be attached incorrectly or partially, and any movement may introduce noise, or drastically change the pulsatile waveform's height or width. Strong movement or physical activity may destroy the measured signal entirely. In addition, the signal parameters

## PULSE INTERVAL ANALYSIS

may change between participants – PPG signals are more idiosyncratic than ECG signals. Some common morphologies can be seen below.

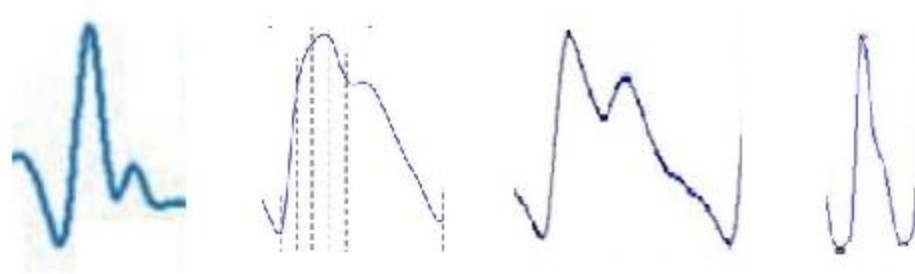


Figure 1: Morphological differences between recordings from various sources of PPG pulse wave recordings. The second minor ‘dip-and-peak’ complex (the diacritic notch and diastolic peak respectively) varies considerably between recordings, as does the sharpness of the main peak, and the placement of the initial ‘dip’.

Calculating heart rate variability, the fluctuations in beat-to-beat intervals of the heart, which predict the state of the nervous system, requires accurate beat-to-beat interval estimates, therefore PPG systems are often problematic – much of the data can be destroyed during collection through no fault of the experimenter or participant. It should be noted here that device manufacturers do not mention these sorts of limitations, they are generally discovered by researchers after they purchase and use PPG-based heart rate measurements.

Despite these challenges, several automated techniques exist to retrieve signals from such messy records. These (a) remove noise (b) extract features of the pulsatile waveform (c) assign points within each cardiac cycle to act as markers, and (d) calculate the distance between these

## PULSE INTERVAL ANALYSIS

points as heart rate. There are several dozen published methods just for peak detection alone at present, ranging from simple to sophisticated, which are offered in a variety of commercial and non-commercial software packages (Scholkmann, Boss, and Wolf 2012). Unfortunately, these packages are often tested on a single, reasonably clean dataset and will not generalise well. The idiosyncrasies of the signals between subjects, the tendency for the PPG signal to show slurred or double peak, and the frequent destruction of the PPG shape by even a small amount of noise can persist. And, of course, no method will retrieve data from a destroyed recording, and ambulatory recordings of PPG invariably involve long periods of missing data. This is not ideal, but nor is it fatal to measuring heart rate variability, as some techniques are tolerant to missing data (Table 1). As these methods are the most commonly reported, it is still possible to measure HRV even with moderately degraded data.

TECHNIQUE	REQUIREMENTS	NOTES
HR	Beats in any order	Stable in ~10-15 seconds
SDNN	Beats in any order	Stable in ~30 seconds
RMSSD	3 consecutive beat sections	Stable in ~30 seconds
Frequency Domain	~75% beats present	Use LSP

Table 1: methods of analysis which are tolerant of missing data. HR = heart rate; SDNN = standard deviation of normal to normal intervals; RMSSD = root mean square of successive differences; LSP = Lomb-Scargle Periodogram (Clifford and Tarassenko 2005).

## PULSE INTERVAL ANALYSIS

The solution we rely on at present is a semi-automated procedure which, after any form of beat detection is performed, returns a simple visualisation of the data, collapses it into a single panel which allows the user to compare the morphologies of all the beat-to-beat intervals detected (accurate or otherwise), and allows the user to exclude those beats which do not display the appropriate, and sometimes unpredictable, morphologies. This procedure is anything but complex. However, once the user has sufficient familiarity, it retains enough flexibility and usability to simultaneously plot and clean several hours worth of messy BVP data within a single procedure.

The algorithm is described visually in the panels corresponding to the steps below.

## PULSE INTERVAL ANALYSIS

### Procedure

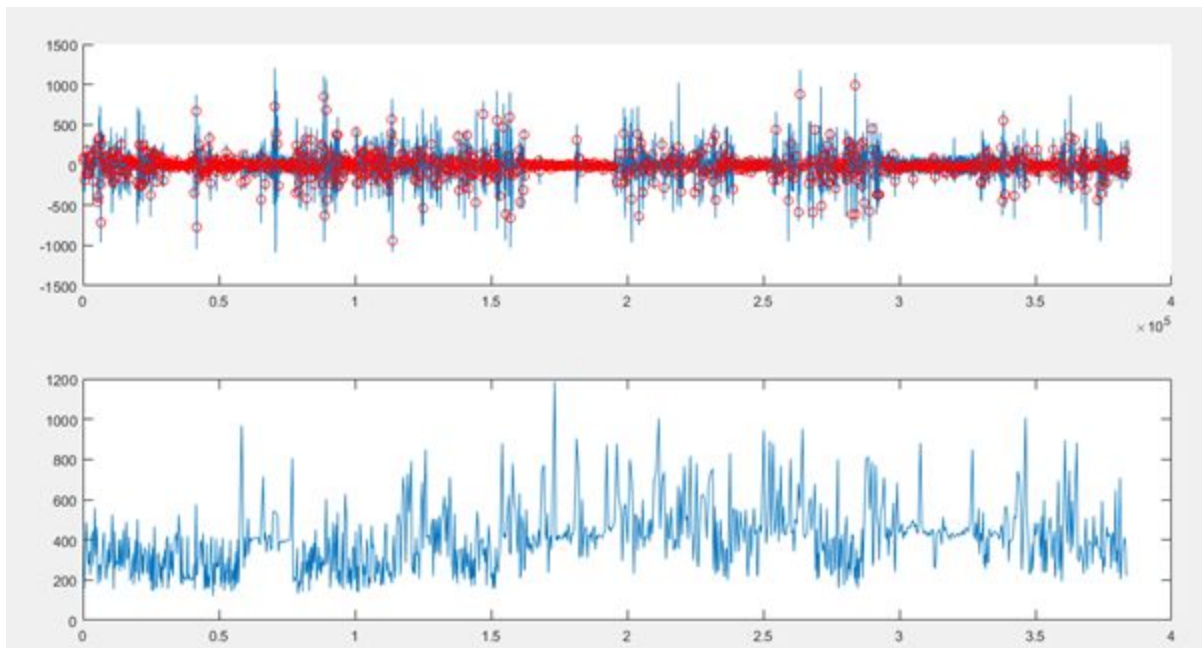


Figure 2: The top panel describes a raw BVP signal where the first derivative was subject to the AMPD algorithm in binned sections, with the raw BVP signal in blue and the detected points in red. The first derivative peak, corresponding to the point of maximum acceleration on the systolic face, is preferred over other morphological features (Clifford and Tarassenko 2005; Heathers 2013). The bottom panel describes the messy resultant series of beat-to-beat intervals. Most beat lengths (y-axis) are from 200 to 400 milliseconds –far too short to be an accurate heartbeat. However, there are clean periods of this heartbeat which allows us to retrieve a section where the geometry of a ‘good’ BVP signal is preserved. A ‘clean’ period is described with consistent 500ms beats from  $3e5$  to  $3.2e5$  on the x-axis, which is selected by marking the start and end points from the bottom panel.

## PULSE INTERVAL ANALYSIS

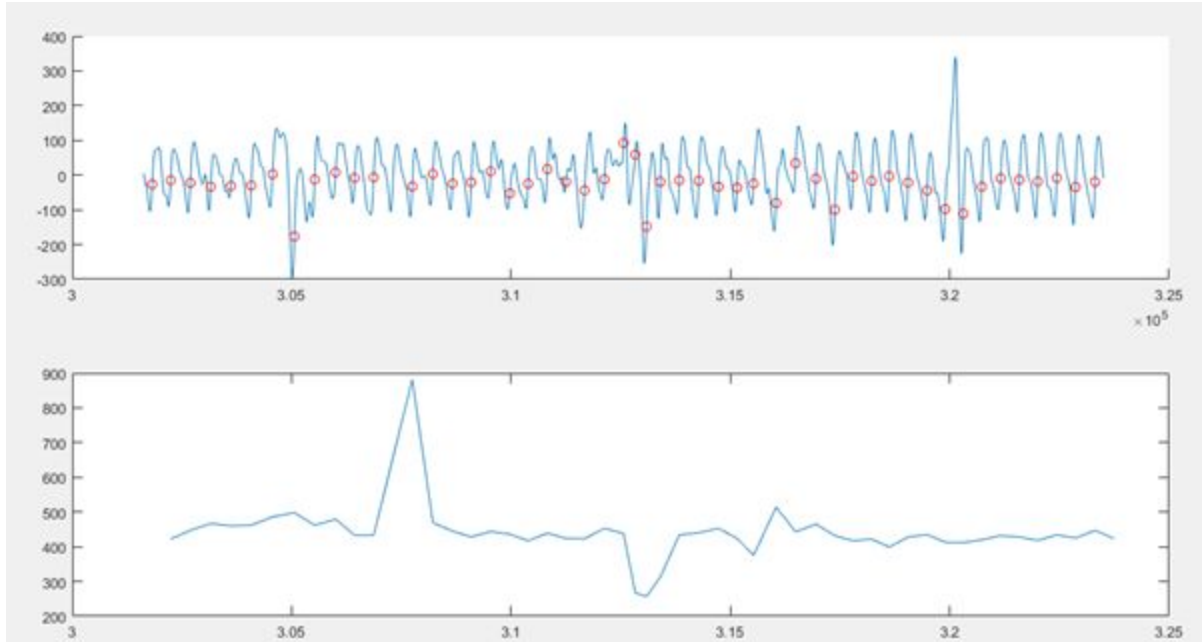


Figure 3: the top panel illustrates just the selection from the top panel of Figure 2, where reasonably accurate beat detection has occurred. The bottom panel describes the same. At this point, beat markings which are obvious erroneous in three sections at  $3.075 \times 10^5$ ,  $3.13 \times 10^5$  and  $3.16 \times 10^5$  are selected and removed. The remaining marked beats in red now exclusively describe correctly-identified systolic waveforms. These waveforms are normalised (0 at the nadir, and 1 at the peak) and averaged together to form a template.



## PULSE INTERVAL ANALYSIS

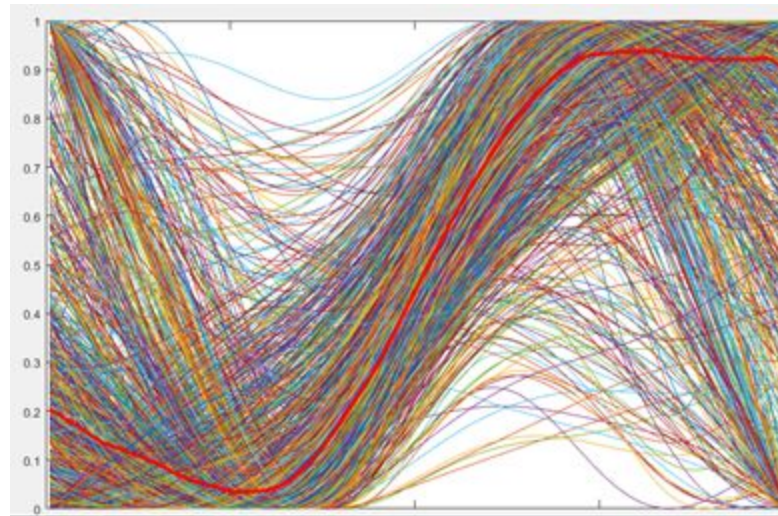
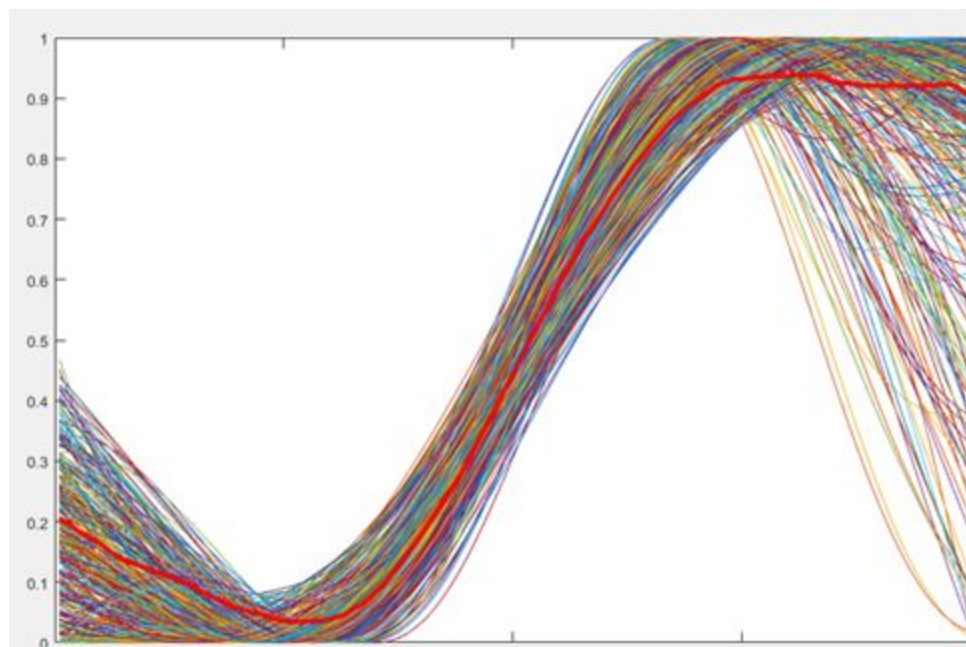


Figure 4: every single interval around each detected beat plotted, showing the template curve in heavy red. Beats with the incorrect morphology can be clearly seen as deviating from the template.



## PULSE INTERVAL ANALYSIS

Figure 5: single graph points are selected and all beats below or above (the function provides both) are removed. This is best done sequentially, to reveal the underlying nature of the correct beats. The above is partially cleaned; some aberrant beats still remain.

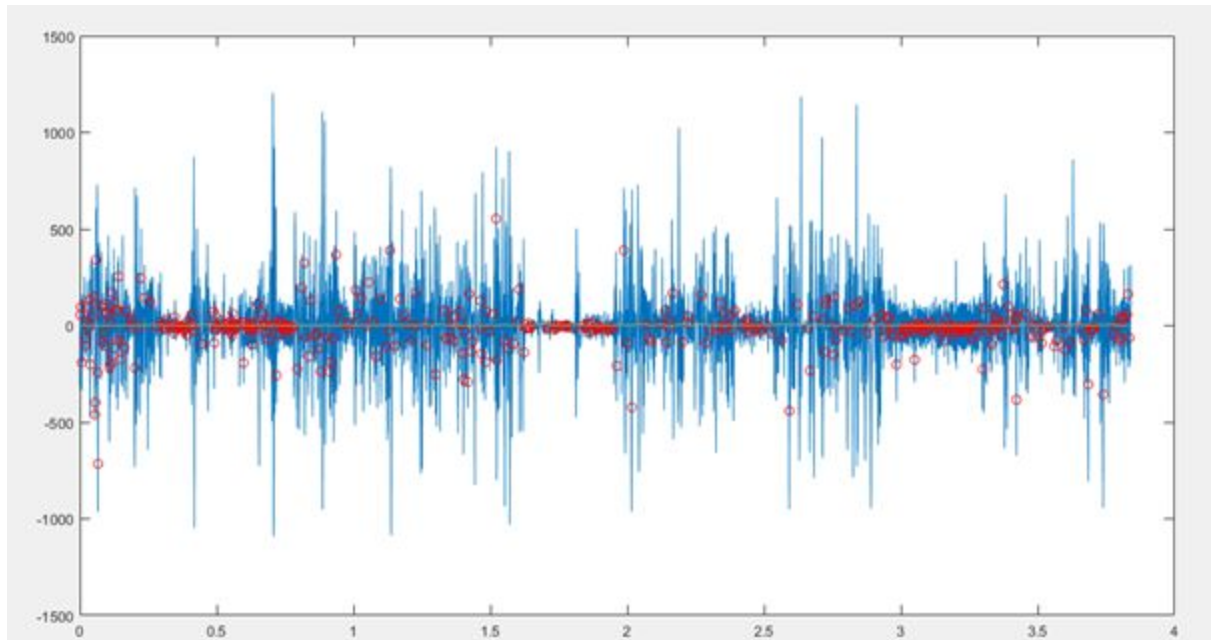


Figure 6: This illustrates Panel 1 again, but this time only beats which correspond to accurate morphology are retained. Areas with little noise (i.e., with a low signal profile) are overwhelmingly preferred.

The beats in the above should return heart rate and SDNN in almost all cases, and RMSSD if degradation is not severe, as well as usability metrics (i.e. the approximate number of beats included calculated from the average heart rate vs. the entire analysis period).

## PULSE INTERVAL ANALYSIS

### Discussion

This ‘template matching’ procedure, while not yet established more broadly against test signals with baseline accuracy, performed extremely well according to visual inspection of the relevant data. It requires several improvements for widespread use. First, a properly controllable UI to remove the piecemeal functions. Second, some basic rejection methods at the step above corresponding to Figure 5. Third, to include an additional function to assess relative accuracy. If these additions are made, they will be included as this document is updated over time.

For any given use of a method like this, it is important that every time the method is deployed on a novel dataset to establish its *relative accuracy*. For instance, a clean record can be gradually degraded (i.e. removing 1%, 5%, 10%, 20% of the data at random) and the effect on the overall accuracy determined by resampling. Populations with high amounts of beat-to-beat change over shorter records will see greater relative inaccuracy. If this is known before a study begins in full, a determination of how this reduced accuracy - inevitable in any approximate method - will decrease the experimental power.

This pathway was developed to determine heart rate from PPG measurements taken from children on the autistic spectrum during a human-animal interaction. This is a difficult population to instrument at measure; these participants were both hypersensitive and physically active, and are likely to derange data features normally handled by less robust algorithms. However, in this and many similar populations, a watch or fingerclip-based heartrate monitor may be the only tolerable option, rather than a chest-mounted ECG or similar device attached directly to the torso. Watch-based devices containing both PPG measurement and accelerometers

## PULSE INTERVAL ANALYSIS

are popular, if not laboratory-accurate, and if the data can be properly conditioned, they may provide a solution to expanding physiological measurement into difficult-to-access populations.

### Code

All functions in Matlab R2016b. The below calls an implementation of the Automatic Multiscale Peak Detection algorithm located here: <https://github.com/mathouse/AMPD-algorithm>

```
% CLEAN SECTIONS WITH AMPD

for sect=1:n_sect,

    panel=trim_BL((30*new_hz*(sect-1)+1):(30*new_hz*sect));
    d_panel=diff(panel);

    tic;
    c=ampd(d_panel);
    toc;

    if sect > 1,
        c=30*new_hz*(sect-1)+c;
    end

    beatsack=[beatsack;c'];

end

% FINDING A REASONABLE SECTION

pts=trim_BL(beatsack);

ax1=subplot(2,1,1);
hold on; plot(trim_BL); scatter(beatsack,pts,'r');

x_locs=beatsack(2:end);
RR_locs=diff(beatsack);

ax2=subplot(2,1,2);
plot(x_locs,RR_locs);

linkaxes([ax1,ax2],'x')
```

## PULSE INTERVAL ANALYSIS

```
% SNIP GOOD BIT

[snip,~]=getpts();

close all

[ind1, ~] = find(x_locs >= snip(1) & x_locs <= snip(2));

% REPLOT GOOD BIT

time_st=beatsack(ind1(1))-200;
time_end=beatsack(ind1(end))+200;

good_sect=x_locs(ind1);
good_RR_locs=RR_locs(ind1);

beat_trunc=beatsack(ind1);
beat_heights_trunc=pts(ind1);

ax2=subplot(2,1,2);
plot(good_sect,good_RR_locs);

ax1=subplot(2,1,1);
hold on; plot(time_st:time_end,trim_BL(time_st:time_end));
scatter(beat_trunc,beat_heights_trunc,'r');

linkaxes([ax1,ax2],'x')

% KILL BAD BEATS

[xkill,ykill]=getpts();

for qq=1:size(xkill,1),
    dist_mat1=(beat_trunc-xkill(qq));
    dist_mat2=(beat_heights_trunc-ykill(qq));
    sq_distances=dist_mat1.*dist_mat2;
    [xx,yy]=min(abs(sq_distances));
    beat_trunc(yy)=0;
    beat_heights_trunc(yy)=0;
end

beat_trunc=nonzeros(beat_trunc);
beat_heights_trunc=nonzeros(beat_heights_trunc);
```

## PULSE INTERVAL ANALYSIS

```
% POP GOOD BEATS
```

```
[xadd,yadd]=getpts();
```

```
beat_trunc=round([beat_trunc;xadd;]);
```

```
beat_heights_trunc=(beat_heights_trunc;yadd;);
```

```
[final_pts,Bsort]=sort(beat_trunc);
```

```
final_heights=beat_heights_trunc(Bsort);
```

```
final_mess_pts=diff(1000*(final_pts/new_hz));
```

```
close all; plot(final_mess_pts);
```

```
[x_rem,y_rem]=getpts();
```

```
final_mess_pts(final_mess_pts>y_rem)=0;
```

```
final_clean_pts=nonzeros(final_mess_pts);
```

```
sdnn_short=std(final_clean_pts);
```

```
close all;
```

```
% SIMPLE OUTPUT PLOT
```

```
plot(trim_BL); hold on; scatter(b_short,trim_BL(b_short),'ro');
```

## PULSE INTERVAL ANALYSIS

### References

- Clifford, Gari D., and Lionel Tarassenko. 2005. "Quantifying Errors in Spectral Estimates of HRV due to Beat Replacement and Resampling." *IEEE Transactions on Bio-Medical Engineering* 52 (4): 630–38.
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