LSAR Click removal

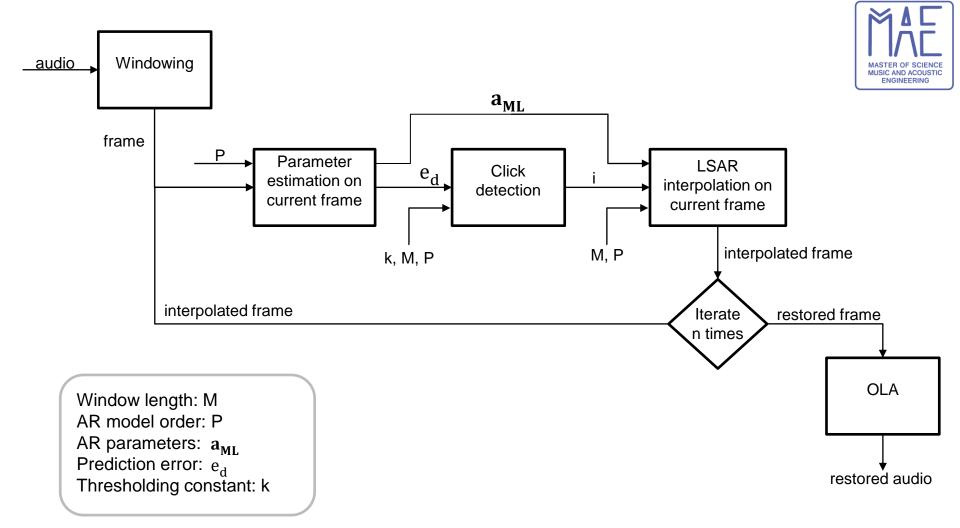


The algorithm is composed of 5 steps:

- Windowing
- 2. Parameter estimation
- 3. Click detection
- 4. LSAR interpolation
- Overlap and Add

Algorithm's characteristics:

- Input is drawn from a locally stationary AR process → windowing
 E.g., Hanning window of length M = 2048 and 50% overlap
- Steps from 2 to 4 can be iterated to improve performance



Parameter estimation



Using the Maximum Likelihood (ML) estimator

- Build the matrix G_x (see General linear model)
- \bullet Estimate the parameters a_{ML} by computing the pseudoinverse of G_{x}

 Compute the prediction error by filtering the corrupted signal with the prediction error filter

```
H_a = [1; -a_ml];
e_d = filter(H_a, 1, x);
```

Click detection



The prediction error is the sum of the innovation process of the AR model (which passes unfiltered) and the filtered clicks:

$$e_d(n) = e(n) + i(n)v(n) * h(n)$$

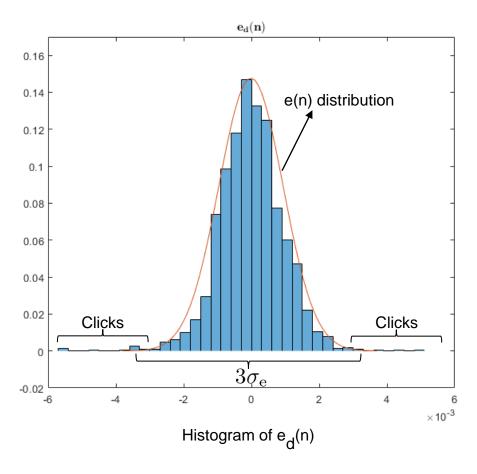
How to discriminate between the two?

- e(n) takes small values (Gaussian assumptions)
- clicks cause large error since the filter fails to predict

If we compute the standard deviation of e(n), we can tell when a sample of the prediction error is drawn from e(n) or not (i.e. it is a click!)

Standard deviation

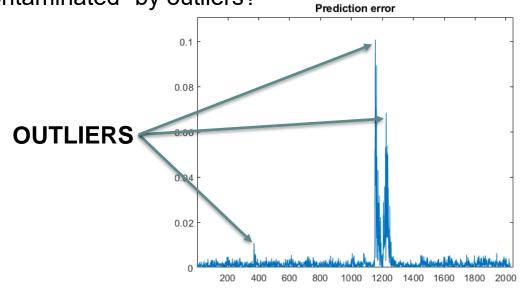




Click detection



Problem: how to compute the standard deviation of a Guassian process when it is "contaminated" by outliers?



Solution: use the **Median absolute deviation** (MAD), which is a robust measure of the variability of a process

Median absolute deviation



Given a sequence of samples $X = \{ X_1, X_2, ..., X_n \}$, the median absolute deviation is defined as

$$MAD = median(|X_i - median(X)|)$$

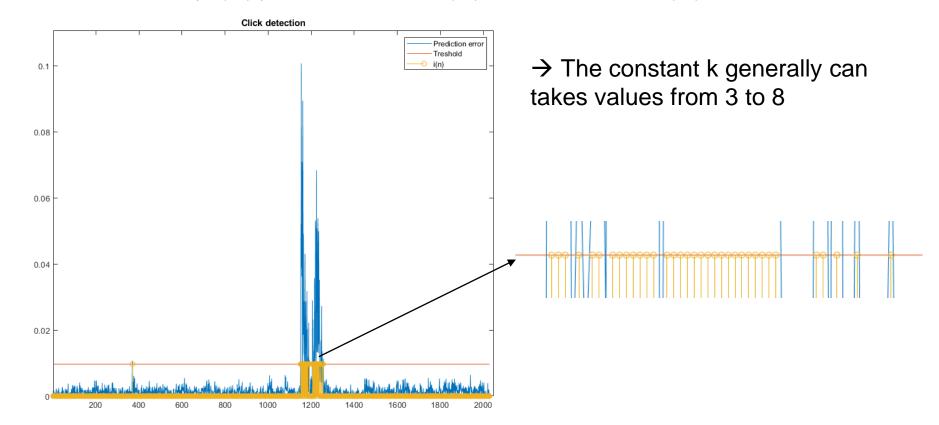
And it can been shown that for a Gaussian distribution (as in our case for e(n)) the following relation for the standard deviation holds:

$$\sigma \approx 1.4826 \times \text{MAD}$$

Thresholding



if
$$|e(n)| > k\sigma_e$$
 then $i(n) = 1$, else $i(n) = 0$



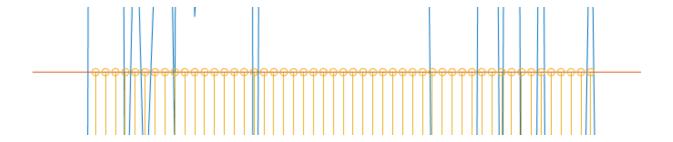
Grouping detections



Problem:

- to properly work, the LSAR interpolator needs at least P samples on the left and on the right
- Clicks trigger a full impulse response of the prediction error filter, thus an irregular behaviour afterward a click's peak in the prediction error
 detections are too close for the interpolator to work

Solution: group the detections in clusters by filling the gaps



LSAR interpolation



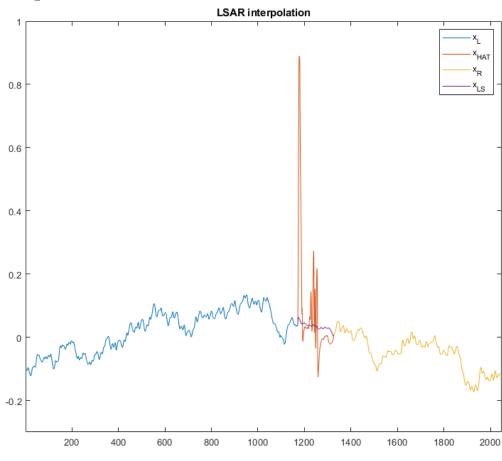
For each detected click:

- Build the relocation matrices U and K
- Build the matrix A (see linear model)
- ullet Compute $\hat{A}=AU$ and $ar{A}=AK$
- ullet Interpolate by computing the pseudoinverse of \widehat{A} :

$$x_ls = -pinv(A_hat)*A_sgn*x_sgn;$$

LSAR interpolation

$$P = 80$$

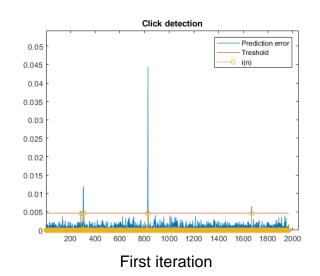


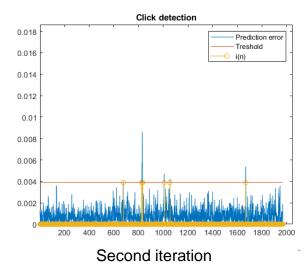


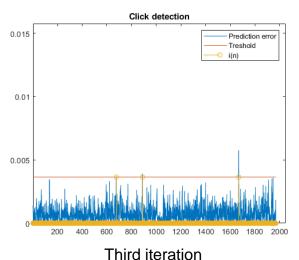
The importance of iteration



Clicks can be still classified as clicks even after interpolation

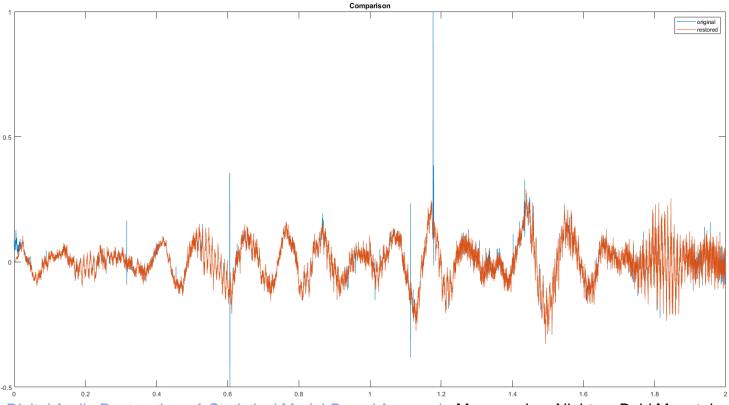






Results





<u>Digital Audio Restoration - A Statistical Model-Based Approach</u>. Mussorgsky - Night on Bald Mountain M = 2048 with 50% overlap, k = 3.5, P = 20, 5 iterations

Further improvements

- This implementation uses the function pinv() for computing the pseudoinverse of a m by n matrix. This function relies on the Singular Value Decomposition (SVD) which has complexity O(max(m, n)*min(m, n)^2), not exploiting the Toepliz structure of the system (Levinson-Durbin algorithm is O(m^2))
- Find a way to avoid grouping detections by rewriting relocation matrices that take into account gaps of length less than P samples
- Is there a way to dynamically choose the constant k by optimizing a metric?
- Is there a way to dynamically choose the number of iterations by optimizing a metric?

