

Glottal inverse filtering and its application in automatic classification of diseases

Paavo Alku

Aalto University, Finland

Department of Information and Communications Engineering

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1. Introduction

Basics of glottal inverse filtering (GIF)

- (a) Production of (voiced) speech is modelled by three processes:
- (1) Glottal flow: excitation
 - (2) Vocal tract: prominent physiological filter with resonances (i.e. formants)
 - (3) Lip radiation: conversion of flow in mouth into pressure in free field

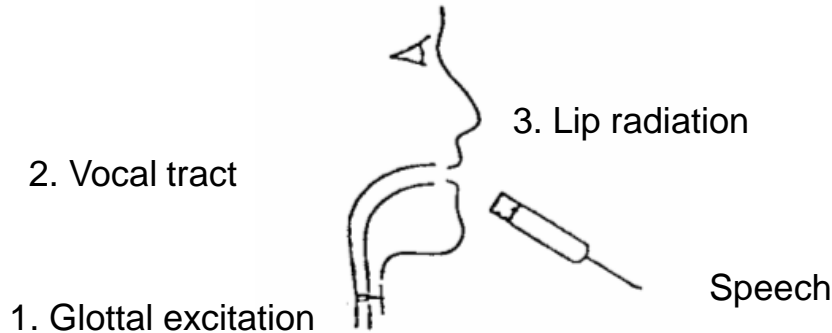


Fig. 1. Production of speech.

- (b) Filtering processes (vocal tract, lip radiation) are estimated and represented typically by digital filters. Lip radiation is modelled by a fixed high-pass filter, whereas modelling of the vocal tract is more challenging and calls for adaptive methods.
- (c) Glottal excitation is estimated by cancelling the effects of the vocal tract and lip radiation by filtering speech through the inverses of the filters.

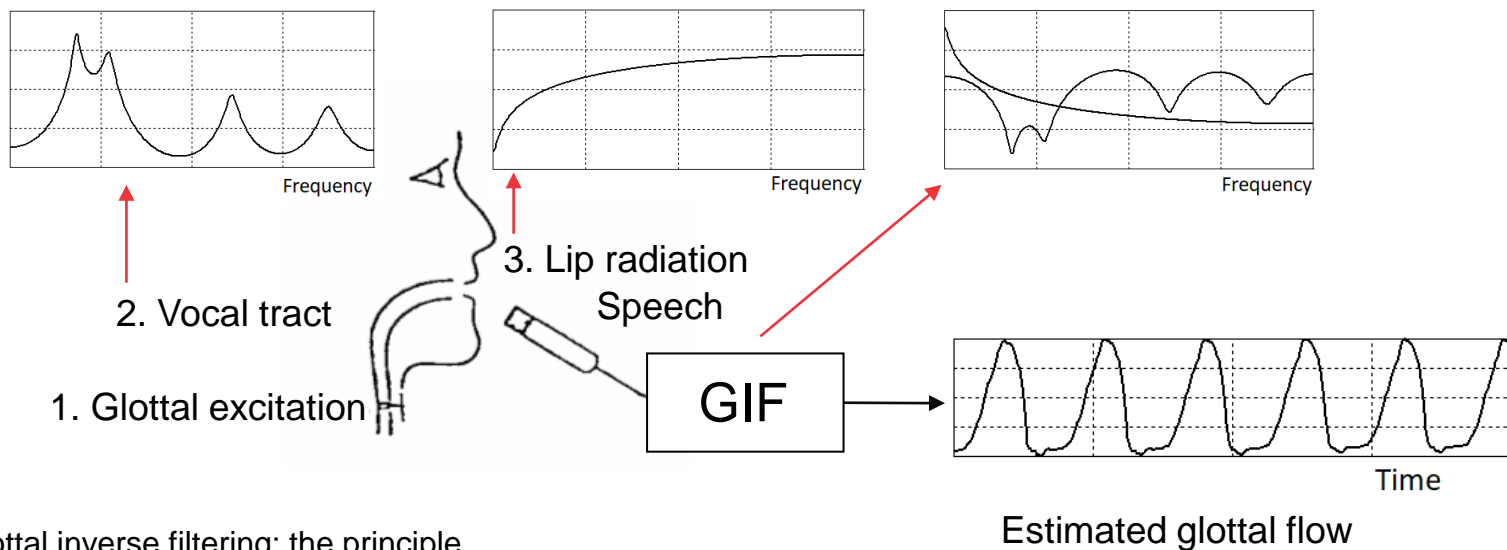


Fig. 2. Glottal inverse filtering: the principle.

- In the current talk, we will focus on the inverse filtering scenario shown in Fig. 2 that is based on using as input the speech pressure signal recorded outside the mouth.
- Inverse filtering can also be computed using the oral flow input recorded with a mask (Rothenberg, 1973) and this approach has been used in many studies (e.g. Sundberg, 2017; Sundberg *et al.*, 2005).
- The use of free-field input enables applying inverse filtering in biomarking state of health from speech recordings conducted in real-life situations (e.g. from spontaneous conversations).

Benefits of inverse filtering

- Provides a **non-invasive** method to estimate the origin of voiced speech.
- Reveals **valuable information** about the generation of several essential acoustical cues (e.g. F0, phonation type) that are used in speech communication. Differently from other techniques such as electroglottography this information corresponds to **real acoustical** phenomenon (air flow) that takes place when speech is produced.
- Can be used in **technical applications** such as in automatic classification of disorders and in speech synthesis.

Drawbacks of inverse filtering

- Estimation **accuracy** sometimes not satisfactory (e.g., for high-pitched speech).
- Some GIF methods need **user adjustments** => Estimation results might be biased by the user.
- Calls for high-quality **recording equipment**.
- Many GIF methods are based on linear source-tract models => Non-linear phenomena in speech production (e.g. interaction between source and tract) cannot be modelled.

Voice source analysis is typically conducted in two stages

(1) The inverse filtering stage

- Input: pressure signal recorded by microphone
- Output: time-domain waveform of the estimated glottal excitation

(2) The parameterization stage

- Input: time-domain waveform of the estimated glottal excitation
- Output: numerical value(s) that captures the most essential information embedded in the glottal excitation waveform

2. Glottal inverse filtering methods

- The idea of GIF was proposed in Miller (1959).

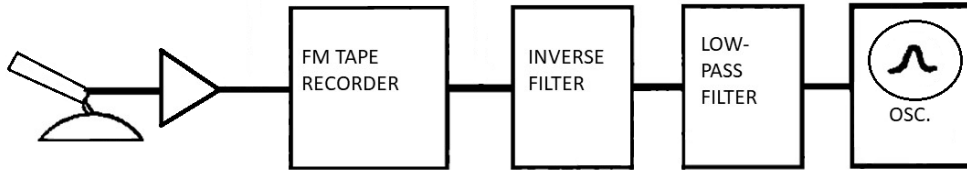


Fig. 3. Schematic of the experimental GIF setup used in Miller (1959).

- Other early experiments using analog techniques (e.g. Fant 1961; Lindqvist-Gauffin 1965; Rothenberg, 1973)
- First GIF experiments based on digital signal processing were conducted by Oppenheim and Schafer (1968) and Nakatsui and Suzuki (1970).
- Many GIF methods have been proposed in the past four decades, examples:
 - Closed phase analysis (Strube, 1974; Wong *et al.*, 1979)
 - Iterative adaptive inverse filtering (IAIF) (Alku, 1992)
 - Simultaneous inverse filtering and model matching (Fröhlich *et al.*, 2001)
 - Zeros of z-transform (Bozkurt *et al.*, 2005)
 - Autoregressive model with an exogenous input (Fu and Murphy, 2006)
 - Complex cepstrum based decomposition (Drugman *et al.*, 2011)
 - **Quasi-closed phase analysis** (Airaksinen *et al.*, 2014)
 - State-space modelling optimized by Kalman filtering (Sahoo and Routray, 2016; Cortes *et al.*, 2022) or the expectation-maximization algorithm (Alzamendi and Schlotthauer, 2017)
 - Quadratic programming (Airaksinen, Bäckström and Alku, 2017)
 - Modified IAIF (Mokhtari *et al.*, 2018)
 - Deep neural network –based analysis (Narendra *et al.*, 2019; Langheinrich *et al.*, 2022)

3. Glottal parameters

- Glottal inverse filtering maps a time-domain speech waveform to a time-domain glottal flow estimate.

=>

The estimated time-domain waveform is expressed using glottal parameters (*i.e.* numerical values) that aim to capture the most essential information embedded in the glottal excitation waveform.

- Glottal parameters are used both in fundamental research of voice production and also in machine learning –based classification studies (as will be described in Section 5).
- Many glottal parameters have been developed both using time-domain and frequency-domain approaches.

Examples of **time-domain** glottal parameters: (1) based on extracting critical time instants: open quotient, speed quotient (Timcke *et al.*, 1958), closing quotient (Monsen and Engebretson, 1977), normalized amplitude quotient (Alku *et al.*, 2002), (2) based on matching the estimated flow (or its derivative) with artificial waveforms (e.g. the Liljencrants-Fant model) (Strik and Boves, 1992).

Examples of **frequency-domain** glottal parameters: H1-H2 (Titze and Sundberg, 1992); harmonic richness factor (Childers and Lee, 1991), parabolic spectral parameter (Alku *et al.*, 1997)

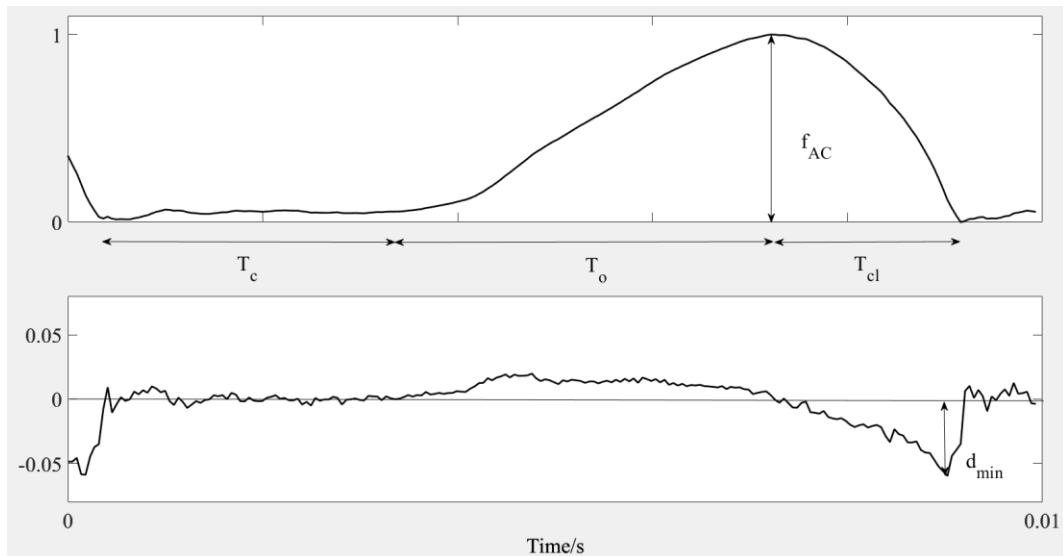


Fig. 4. Glottal flow pulse (upper panel) and its derivative (lower panel).

An example of a time-domain glottal parameter (closing quotient): $CIQ = T_{cl} / (T_c + T_o + T_{cl})$

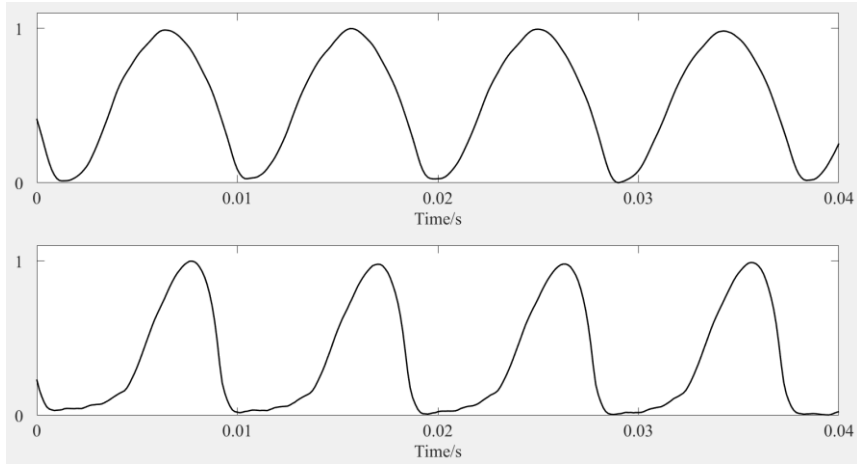


Fig. 5. Time-domain glottal flow pulseform in breathy phonation (upper panel) and in pressed phonation (lower panel).

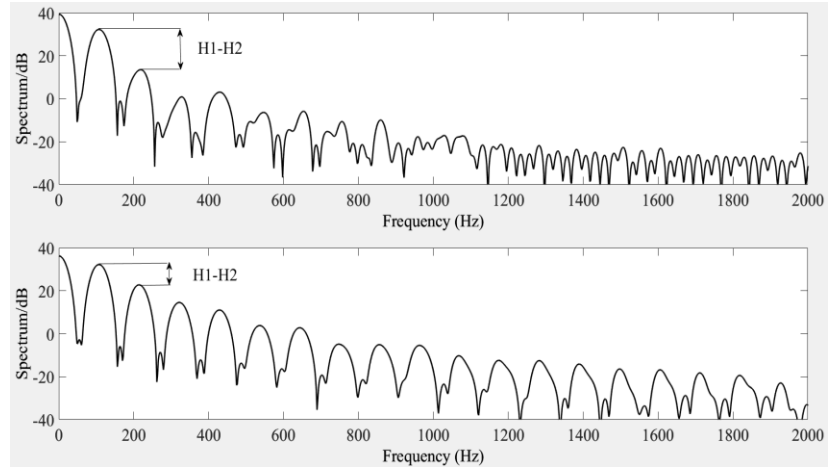


Fig. 6. Glottal flow spectrum in breathy phonation (upper panel) and in pressed phonation (lower panel).

An example of a frequency-domain glottal parameter (level difference at F_0 and $2F_0$): H1-H2

4. Automatic machine learning -based biomarking of health from speech

- Speech is produced by the human speech production mechanism and therefore it contains acoustical cues of the speaker's state of health.
- Signal processing and machine learning (ML) can be used to automatically biomark state of health from speech. In this talk, the technology is called "Speech-based biomarking of health":

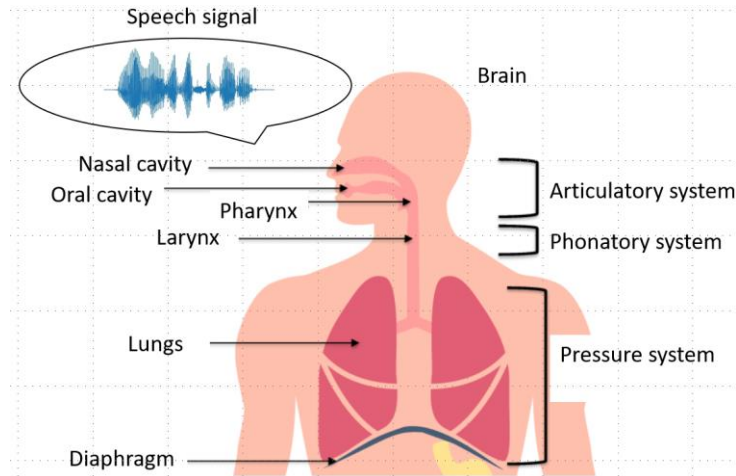


Fig. 7. Organs affecting acoustical cues embedded in speech

Typical machine learning tasks studied

- The **binary classification problem**: detection of speakers with, for example, spasmodic dysphonia from healthy controls
- The **multiclass classification problem**: classification of speakers with different diseases (e.g. healthy vs. hyperfunctional dysphonia vs. vocal fold paresis) or classification of speakers with different levels of disease severity (e.g. healthy vs. mild dysarthria vs. severe dysarthria)

This presentation focuses on the binary classification problem. (1) Two technologies (the classical pipeline approach, the end-to-end approach) are first generally described in this section. (2) Section 5 presents two examples of studies where automatic ML-based detection of diseases has been investigated using inverse filtering.

4.1 The classical pipeline approach

- Two separate parts: feature extraction and classifier
- Speech microphone signals are expressed in a compressed form using **features** such as mel-frequency cepstral coefficients (MFCCs) (Davis and Mermelstein, 1980).
- A machine learning (ML) **classifier** (e.g. support vector machine, SVM, Cortes and Vapnik, 1995) is trained to distinguish, for example, speech produced in disease “X” from speech produced by healthy speakers.

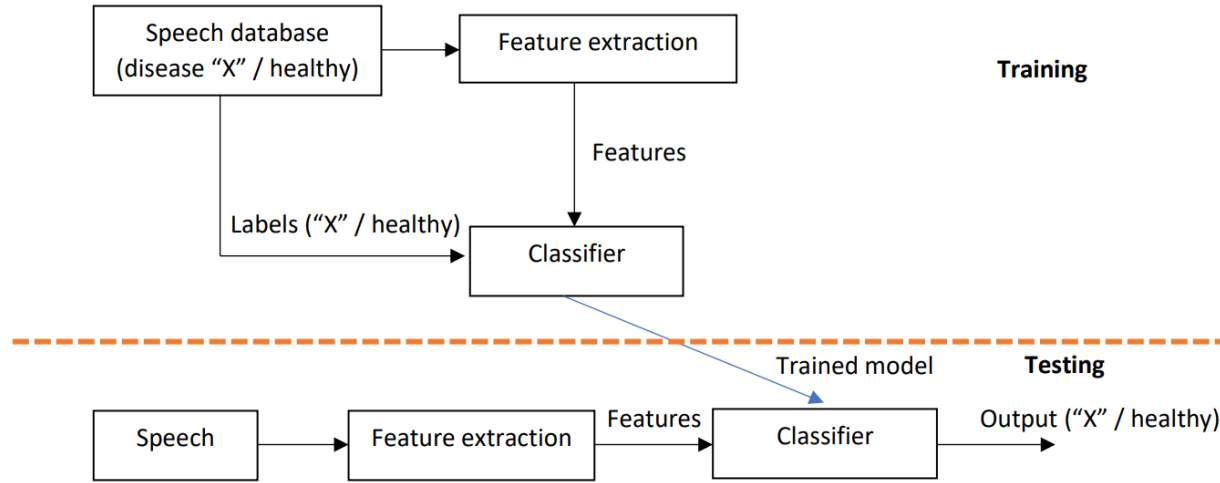


Fig. 8. A general structure of a detection system based on the traditional pipeline approach. Speech database includes labelled speech signals (disease "X" vs. healthy). Classifier can be, for example, SVM.

The support vector machine (**SVM**) classifier

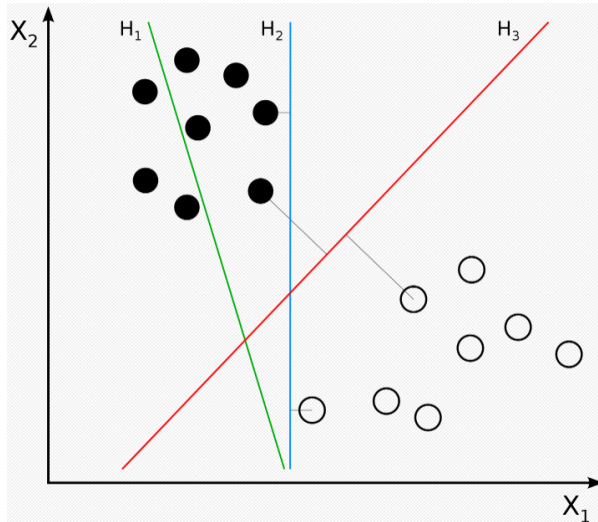


Fig. 9. **Training** data in two classes (back circles: disease "X"; white circles: healthy) in a 2-dimensional speech feature space. SVM defines H_3 , which separates the classes with the maximal margin.

- **Test samples** are mapped into that same space and predicted to belong to a category based on which side of the gap they fall.
- Because the two classes in the original, low-dimensional feature space are not necessarily linearly separable, SVM implicitly maps the data to a higher-dimensional space using a **kernel** function.

4.2 The end-to-end approach

- Detection is computed directly from the time-domain input speech waveform (or from spectrogram) using deep learning networks (typically convolutional neural nets, CNNs).
- No separate feature extraction and classification stages: they are replaced with a single network structure.

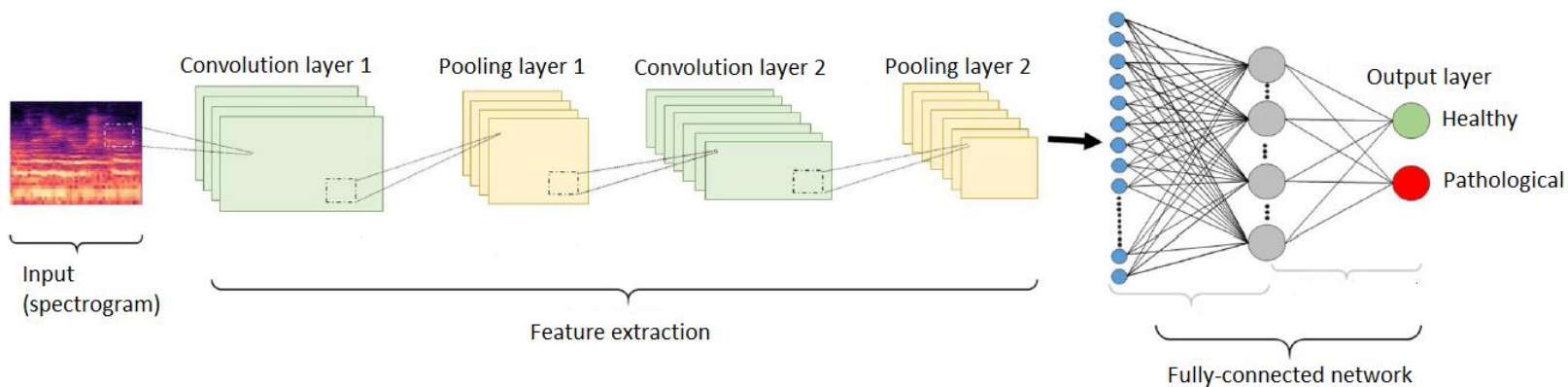


Fig. 10. An example of a CNN-based deep learning classification system (binary detection between “healthy” and “pathological” voice) (modified from Kaushik *et al.*, 2021).

5. Machine learning studies in automatic classification of diseases using glottal inverse filtering

- Automatic ML-based classification of diseases from speech has been widely studied in recent years.
- Most studies use existing feature sets, such as openSMILE (Eyben *et al.*, 2010), that are extracted from speech pressure signals.
- Glottal features have been used in some studies, for example:
 - Classification of nodules in children (Szklanny and Wrzeciono, 2019)
 - Pathology classification (Wu *et al.*, 2021; Gomez-Vilda *et al.*, 2009; Kadiri and Alku, 2020; Tirronen *et al.*, 2023)
 - Detection of Parkinson's disease (Novotny *et al.*, 2020; Vasquez-Correa *et al.*, 2021; Narendra *et al.*, 2021; Liu *et al.*, 2023;
 - Detection of Covid-19 (Deshmukh *et al.*, 2021)
 - Detection of depression (Ooi *et al.*, 2012; Simantiraki *et al.*, 2017)
- Let us study next two of our investigations where glottal features have been used in automatic ML-based detection of diseases from speech.

5.1 Reddy, Helkkula, Keerthana, Kaitue, Minkkinen, Tolppanen, Nieminen, Alku. The automatic detection of heart failure using speech signals. *Comp. Speech Lang.* 69, article no. 101205, 2021.

- Binary detection: heart failure (HF) vs. healthy
- Speech data (Finnish): 20 patients, 25 healthy controls (recorded by the team at Helsinki University Central Hospital)
- System architecture: a classical pipeline system (with different classifiers and features)
- Study goal: can the detection of HF be improved by using **glottal** features?

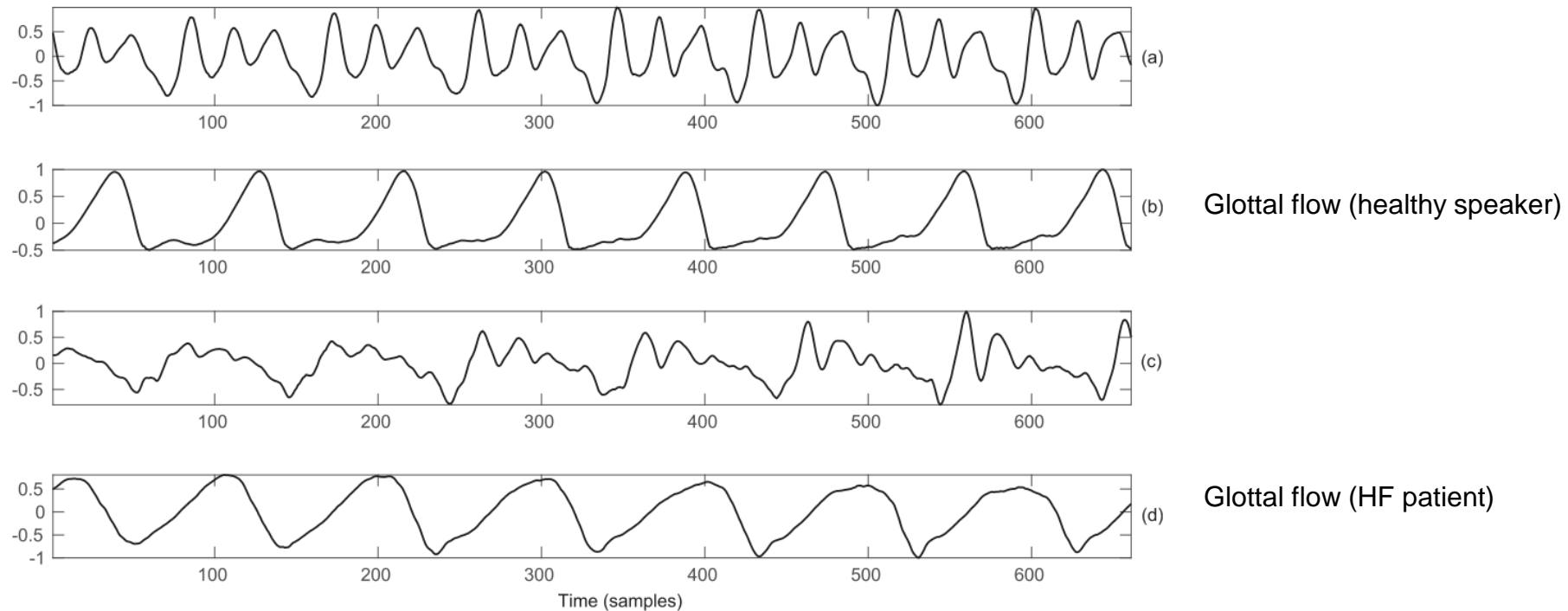


Fig. 11. Speech signal (a) and the estimated glottal flow (b) of a healthy speaker. Speech signal (c) and the estimated glottal flow (d) of an HF patient.

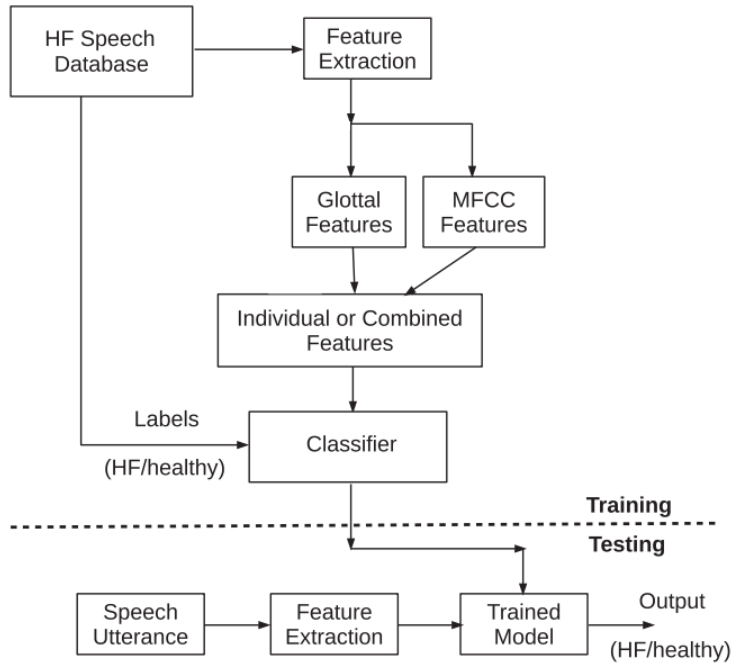


Fig. 12. The classical pipeline method utilized to detect HF from speech.

Baseline: MFCC features and SVM classifier

The best system: combined glottal and MFCC features and neural net classifier

Classifier	MFS (104)	GFS (192)	MFS + GFS (296)	MFS + GFS with feature selection (85)
SVM	76.26	65.59	75.52	77.15
ET	68.07	64.15	64.80	72.29
AdaBoost	76.54	68.85	73.04	79.23
FFNN	77.02	71.03	75.34	81.51

Table 1. Detection accuracy (in %) for four different classifiers with different feature sets. MFS: the mel-frequency cepstral coefficient set, GFS: the glottal feature set. The length of the feature vector is given in parenthesis.

5.2 Narendra, Alku: Glottal source information for pathological voice detection. IEEE Access 8(1): 67745–67755, 2020.

- Binary detection experiments: dysarthric vs. healthy (the UA-Speech database and the TORGO database) and dysphonic vs. healthy voices (the UPM database).
- Note: dysarthria in this article is due to ALS and CP. For our similar studies on Parkinson's disease, see Liu *et al.*, 2023 & Narendra, Schuller and Alku, 2021.
- Study goal: to investigate the use of the estimated glottal flow in detection of pathological voice by comparing the classical pipeline approach to the end-to-end approach.
- System architectures:
 - a classical pipeline system (with the SVM classifiers and different features)
 - an end-to-end system (using either the raw voice signal or the estimated glottal flow)

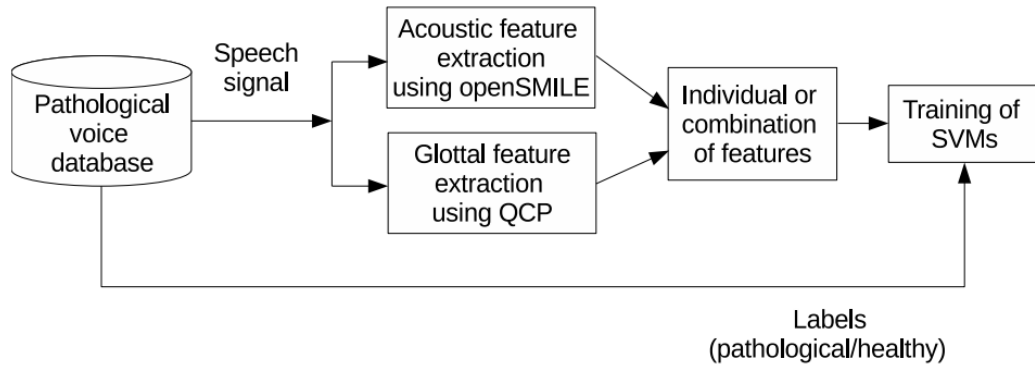


Fig. 13. The classical pipeline system (training stage).

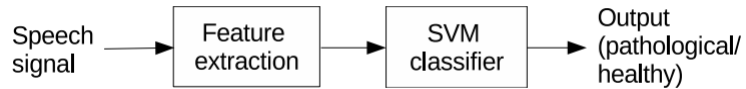


Fig. 14. The classical pipeline system (test stage).

Feature set	UA-Speech			TORGO			UPM		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
openSMILE-1	76.65	73.76	79.54	78.24	72.94	83.54	70.73	78.49	62.98
openSMILE-2	86.99	82.35	91.63	80.62	73.73	87.52	72.50	77.61	67.84
Glottal-1	73.56	76.47	70.65	67.17	71.22	63.12	63.17	67.08	59.27
Glottal-2	68.74	69.36	68.12	66.93	71.55	62.17	64.63	65.85	63.41
openSMILE-1 + Glottal-1	81.01	82.55	79.48	79.62	73.21	86.03	73.39	79.54	67.24
openSMILE-2 + Glottal-1	91.88	92.56	91.21	82.12	79.02	85.22	75.61	79.11	72.20
openSMILE-1 + Glottal-2	80.02	81.93	78.12	80.63	72.59	88.68	74.17	80.05	68.29
openSMILE-2 + Glottal-2	91.19	91.57	90.82	81.35	76.83	85.87	76.83	80.81	73.36

Table 2. Classification results obtained using the classical pipeline systems with the openSMILE and glottal features for the three pathological voice databases

Reading instructions:

- openSMILE-1 and openSMILE-2: widely used acoustic feature sets (no inverse filtering)
- Glottal-1 and Glottal-2: glottal feature sets (based on inverse filtering)
- UA-Speech, TORGO, UPM: databases of pathological speech
- accuracy, sensitivity, specificity: widely used metrics (optimal value: 100%)

6. Summary and conclusions

- Glottal inverse filtering (GIF) enables non-invasive estimation of the voice source from microphone speech signals.
- Many GIF methods and glottal parameters have been developed during past decades, and new GIF methods have been proposed recently.
- The QCP method (Airaksinen *et al.*, 2017) is available as MATLAB code and as implementation in the Aalto Aparat GIF tool (Alku *et al.*, 2017).
- GIF has been used in fundamental research, but the topic was handled in the current presentation mainly from the point of view speech-based biomarking of health that uses machine learning (ML) classifiers.
- GIF can be used with ML in biomarking of health both in (1) classical pipeline classifiers (in feature extraction) and (2) in end-to-end classifiers (as an alternative input to the speech signal).

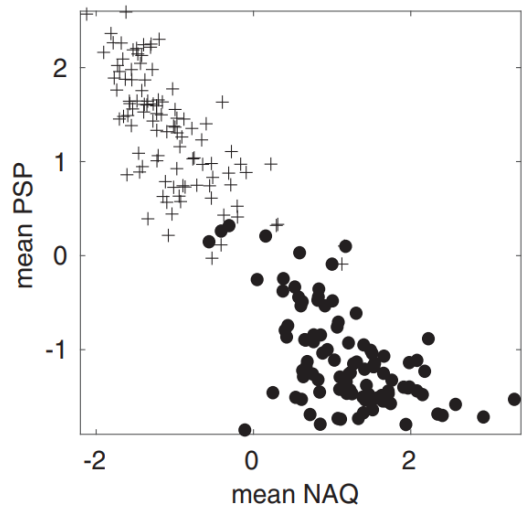
- Adding glottal features to widely used speech features (e.g. MFCCs, openSMILE) has been shown to improve detection accuracy in several recent biomarking studies.

=> Glottal features *per se* are not necessarily best features for biomarking but they include complementary information about phonation that has been shown to improve existing speech features.

- In speech-based biomarking of health, deep learning –based end-to-end approaches are popular today. Therefore, the computation of glottal (and other) features might sound less attractive. However, the following issues justify the use of glottal features.

(1) Glottal features provide better explainability compared to deep learning –based end-to-end systems (“black boxes”).

(2) Since voice source information is embedded in the speech signal, this information should be able to be extracted by non-linear end-to-end networks without using GIF. However, end-to-end networks are data hungry and they cannot necessarily be trained properly in the area of pathological voice, where little training data is typically available.



Glottal parameters used:

NAQ (normalized amplitude quotient, Alku *et al.*, 2002): a measure of relative glottal closing phase length. Large value: breathy phonation, small value: pressed phonation.

PSP (parabolic spectral parameter, Alku *et al.*, 1997): a measure of spectral tilt. Large value: small tilt, small value: large tilt.

Fig. 15. An example demonstrating dysarthric speech of two severity levels. The speech signals are expressed in a 2-dim space spanned by two glottal parameters for low disease severity (filled circles) and for high disease severity ('+' marks). (Narendra and Alku, 2020). Both parameters were z-score normalized (mean=0; std=1).

- Out latest biomarking studies have addressed other than GIF-related topics such as exemplar-based sparse representations in detection of Parkinson's disease (Reddy and Alku, 2023), wavelet scattering features (*e.g.* Keerthana *et al.*, 2024) and pre-trained models (*e.g.* Tirronen, Kadiri and Alku, 2023; Javanmardi, Kadiri and Alku, 2024).

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