

Fingerprint 1:

	1	2	3	4	5	6	7	8	9
w	[-2.5]	[1.0, 1.5]	[2.5]	[5.0]	[-2.5]	[4.5]	[4.0]	[4.5]	[-2.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-3.5	-0.5	-1	5	NaN
2.0	-2.5	-2.5	2.5	0.5	-4	-1.5	4	NaN	NaN
3.0	-4	1.5	-1	0	-5	3.5	NaN	NaN	NaN
4.0	0	1.5	-1	0	0	0	NaN	NaN	NaN
5.0	-3.5	-2.5	-2.5	4	NaN	NaN	NaN	NaN	NaN
6.0	0	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
7.0	-5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

The Fingerprint Algorithm: Detecting and Quantifying Similarity in Fiddle Tunes

Fingerprint 2:

	1	2	3	4	5	6	7	8	9
w	[-2.5]	[1.5]	[0.0]	[1.5]	[-2.5]	[1.5]	[-0.5]	[-1.0]	[-2.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-4	0.5	-1.5	5	NaN
2.0	-2.5	-2.5	2.5	0	-3.5	-1	3.5	NaN	NaN
3.0	-4	1.5	-1.5	0.5	-5	4	NaN	NaN	NaN
4.0	0	-2.5	-1	-1	0	NaN	NaN	NaN	NaN
5.0	-4	-2	-2.5	4	NaN	NaN	NaN	NaN	NaN



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NATIONALES
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Overview

- Background
 - Why is a similarity algorithm necessary for this repertoire?
 - Why use a database of fiddle tunes from Quebec?
 - Existing initiatives
 - General characteristics of the repertoire
- How does the fingerprint algorithm work?
- Results
- Challenges, next steps

Overview

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Background



- In Montreal in the 1920s and 1930s, fiddlers, accordionists and harmonica players recorded over 1000 sides of instrumental dance tunes for commercial labels.
- These 78s offer the first large-scale musical documentation of a working-class repertoire then popular in the home, on stage and on radio.

Images source: The Virtual Gramophone,
<http://www.collectionscanada.gc.ca/gramophone/index-e.html>

Background



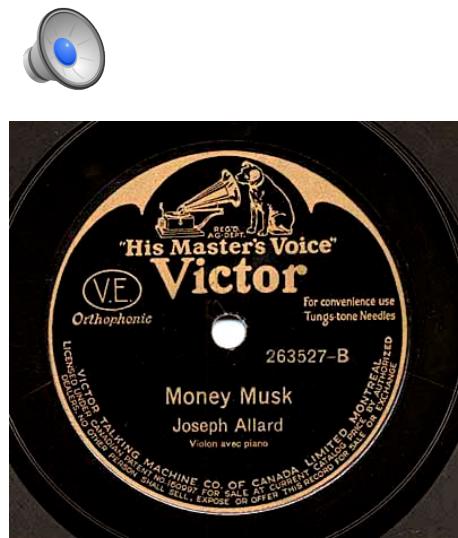
- The musical contents of these recordings remain largely unexamined. The only detailed musicological study of this repertoire (Duval 2012) is limited to a subset of metrically irregular tunes.
- This project proposes a computer-aided approach to parsing this repertoire. Specifically, it proposes an algorithm that searches not only for identical but also for similar melodic phrases, and quantifies that similarity.

Why is a similarity algorithm necessary for this repertoire?

- Frequent melodic and rhythmic variation: certain tunes were recorded multiple times (usually by different artists) and these settings are often quite varied
 - Occasionally we can identify these as variants because they share a common title, as for the tune “Money Musk”
 - However, this is not the case for most variants



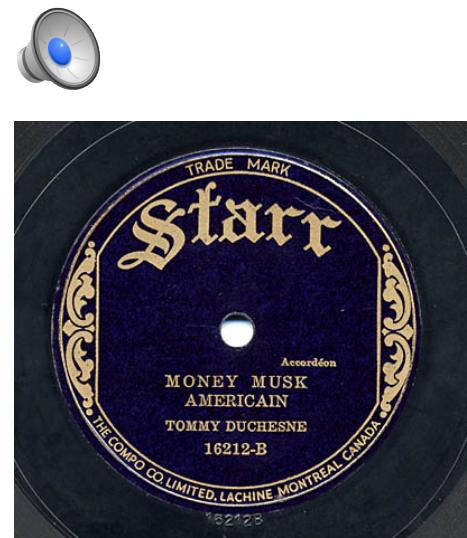
1927



1928



1934



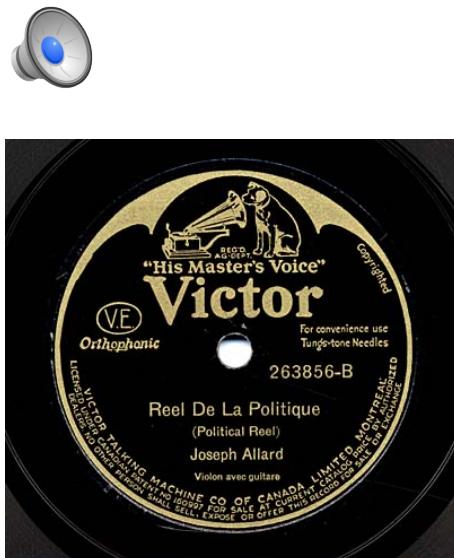
1938

Why is a similarity algorithm necessary for this repertoire?

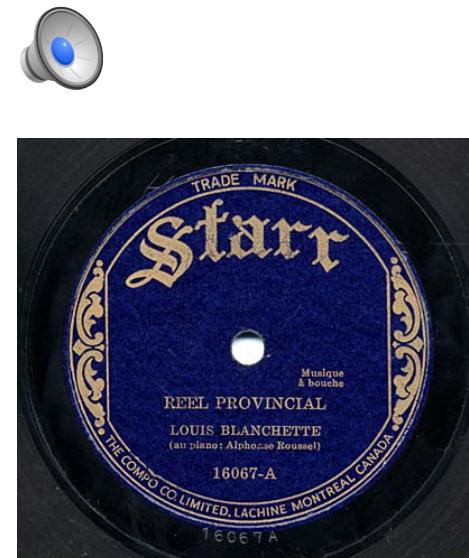
- Non-standardized titles
 - Many tunes are variants of common Scottish, Irish and American tunes but were not recorded under the usual titles
 - Ex.: three variants of the Scottish song “My Love She’s But A Lassie Yet”
- The only way to identify these as variants is to compare the melodies.



1928



1931



1937

Why is a similarity algorithm necessary for this repertoire?

- This repertoire is too large for one person to hold all the melodies in his/her head at once. As a result, identifying variants is something like searching for a needle in a haystack.
 - Given a tune, this algorithm will search for tunes that are similar and quantify that similarity.



Why use a database of fiddle tunes from Quebec?

- Many examples of melodic and rhythmic variation => a diverse set of test cases
 - The many recordings of “Money Musk” (from 1920s to the present) serve as an encyclopedia of variation techniques and may be used to generate comparison and analysis functions.
- Ease of use: the tunes are monophonic, relatively short and often follow standard forms (AB, AABB, ABC, ABCD, etc.)
- Unique incipits: the first two bars of a tune are nearly always enough to identify the tune
- Availability: many of these tunes are accessible via the Virtual Gramophone (Library and Archives Canada). Nearly all have been catalogued by Labbé (1995).



Some existing initiatives

Global Chant Database (<http://globalchant.org>): searches for a given string of notes in a database of over 24,000 chant incipits. Returns exact matches and transpositions occurring at the beginning of a chant, and instances of the interval pattern within melodies.

Early American Secular Music Index (<http://www.colonialdancing.org/Easmes/Index.htm>): Searches for a given string of notes in a database of over 75,000 items. However, there is no actual search engine (to my knowledge). Rather, the user selects an incipit “of interest” or a series of “stress notes” (the first notes of consecutive bars) from a web page listing all of the options.

Scottish Music Index (<http://www.scottishmusicindex.org>): Searches for a numerical theme code in a database of over 12,000 such codes. Each code is a numerical representation (by scale degree) of the strong beats of the first two bars of a tune. The database contains theme codes for most printed Scottish tunes from the eighteenth century to the early twentieth century.

Traditional Tune Archive (<http://tunearch.org/wiki/TTA>): This wiki is currently under construction. It uses the same theme code system as the Scottish Music Index. The search function will not find partial strings (“11H6” will only return tunes in 3/4, not tunes in 4/4 that begin with this string).

Some existing initiatives

TunePal (<http://tunepal.org/tunepal/index.php>) : This is an excellent tool for identifying Irish tunes from audio sources. The program uses the MATT2 tools developed by Bryan Duggan (PhD thesis, 2009). TunePal translates audio into symbolic notation (a simplified setting in ABC) and compares that to a database of over 24,000 Irish tunes, also in simplified ABC notation. The database is “crowd-sourced” from several dozen online sites that contain ABC transcriptions of tunes (mostly Irish tunes).

TunePal uses an edit distance algorithm to compare tunes. This is very effective if the unknown tune is an exact or near-exact match to a tune in the database. However, a variant with significant melodic alterations may not register. In addition, TunePal does not identify transpositions. Note that TunePal looks for exact or similar strings of ABC anywhere in the tune, regardless of metrical placement.

- I have used TunePal to identify several common Irish and American tunes that were recorded in Montreal under new names.

Note that Duggan (2009:65-78) includes a thorough review of existing (in 2009) methods for detecting melodic similarity.

General characteristics of the repertoire

- Transposition is common and tonal centers are sometimes ambiguous.
- Each tune has two or more strains (A, B, C, etc.). These must be treated independently.
- Metrical placement matters: notes that fall on strong beats are more essential to the identity of a strain than notes that fall on weak beats.
- The first two bars serve as a unique identifier for many strains: a “fingerprint.”
- Poor audio quality and piano / percussion accompaniment preclude the use of automated transcriptions for the early commercial recordings.

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 - Existing initiatives
 - General characteristics of the repertoire
- **How does the fingerprint algorithm work?**
- Results
- Challenges, next steps

How does the fingerprint algorithm work?

Given a database of MusicXML files, where each file is one strain, the algorithm generates a numerical “fingerprint” for each file and then compares these fingerprints using a series of functions.



		Fingerprint 2:								
		1	2	3	4	5	6	7	8	9
w	0.0	[-2.5] 0	[1.0, 1.5] 0	[2.5] 0	[5.0] 0	[-2.5] 0	[4.5] 0	[4.0] 0	[4.5] 0	[-2.5] 0
0.0	0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-3.5	-0.5	-1	5	NaN	
2.0	-2.5	-2.5	2.5	0.5	-4	-1.5	4	NaN	NaN	
3.0	-4	1.5	-1	0	-5	3.5	NaN	NaN	NaN	
4.0	0	-2	-1.5	-1	0	NaN	NaN	NaN	NaN	
5.0	-3.5	-2.5	-2.5	4	NaN	NaN	NaN	NaN	NaN	
6.0	-4	-3.5	2.5	NaN	NaN	NaN	NaN	NaN	NaN	
7.0	-5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN	
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	

Col. 1: Interval from the first strong beat to each successive strong beat

Col. 2: Interval from the second strong beat to each successive strong beat

Col. 3: Interval from the third strong beat to each successive strong beat

Interval from each strong beat to the following weak beat note(s)

etc.

How does the fingerprint algorithm work?

A musical score for a single melodic line. The key signature is one sharp, indicating G major. The time signature is common time (indicated by a 'C'). The melody consists of eighth and sixteenth notes. It begins with a descending eighth-note pattern (F#-E-G), followed by a sixteenth note (D) and a quarter note (B). This is followed by a sixteenth-note pattern (G-A-B-C) and a quarter note (F#). The melody continues with a sixteenth-note pattern (E-F#-G-A) and a quarter note (D). The score ends with a sixteenth-note pattern (B-C-D-E) and a quarter note (B). The music is written on five horizontal lines.

“Money Musk”

A musical score for 'The Star-Spangled Banner' in G major (one sharp) and common time. The vocal line consists of eighth and sixteenth notes. Measures 10-12 are shown, starting with a half note followed by a quarter note. The vocal line continues with eighth and sixteenth-note patterns. The piano accompaniment is indicated by a bass staff with a bass clef and a treble staff with a treble clef, both in common time.

Boivin 1974, A strain

How does the fingerprint algorithm work?

The image shows two musical staves. The top staff is labeled "Allard 1928, A strain" and the bottom staff is labeled "Boivin 1974, A strain". Both staves are in G major (one sharp) and have a common time signature. The notation consists of quarter notes and eighth notes. Red double-headed arrows between the staves indicate matched strong beats. Orange double-headed arrows indicate non-matched but corresponding strong beats. A purple arrow points from the text "missing strong beats on weak beats" to a position where a red double-headed arrow is missing.

- assume that the first strong beats of both fingerprints correspond (i.e., align) and match (i.e., they are the same pitch)
- search for additional **matched strong beats**
- identify **non-matched but corresponding strong beats**
- search for **missing strong beats on weak beats**

How does the fingerprint algorithm work?

Allard 1928, A strain

Boivin 1974, A strain

"Money Musk"

- assume that the first strong beats of both fingerprints correspond and match
- search for additional **matched strong beats**
- identify **non-matched but corresponding strong beats**
- search for **missing strong beats on weak beats**
- search for **matched weak beats on matched strong beats** and on **non-matched strong beats**

Two more functions: contour and reversal

Two more functions: **contour** and **reversal**

- search for identical and similar contour **on consecutive non-matched strong beats** and on **associated weak beats**

The image shows two musical staves side-by-side for comparison. The top staff is labeled "Allard 1928, A strain" and the bottom staff is labeled "Lajoie 1951, E strain (transposed from C major)". Both staves are in G major (one sharp) and show a similar melodic line.

Annotations highlight specific features:

- Identical SB contour:** Indicated by a blue box and arrow pointing to a segment where the melody moves from S7 to S8 (minor 3rd) and S7 to W7 (major 2nd).
- Similar WB contour:** Indicated by a blue box and arrow pointing to a segment where the melody moves from S7 to S8 (minor 3rd) and S7 to W7 (minor 2nd).
- Contour and Reversal:** Vertical double-headed arrows indicate pitch movements between notes. Red arrows point upwards, green arrows point downwards, and orange arrows indicate pitch reversals (e.g., from a note down to a note up).
- Textual annotations:** "Allard 1928, A strain" and "Lajoie 1951, E strain (transposed from C major)" are printed below their respective staves.

Two more functions: contour and reversal

- check for **strong-beat reversal on consecutive non-matched strong beats**,
and then check if associated weak beats are also reversed



Allard 1928, B strain
"Money Musk"

Joyal 1956, B strain (transposed from A major)

Truncation

Truncation

Truncation: discard the first full beat (strong beat plus weak beats) of each fingerprint and assume that the **second strong beat matches**.

Continue until the number of truncations exceeds 50% of the number of strong beats in the shorter fingerprint.

The algorithm outputs the comparison results from all of these truncations and selects the best result.

Ex. 5

Truncate

Arthur-Joseph Boulay, Gigues pot-pourri (1923), 1st tune, A strain

Arthur-Joseph Boulay, Reel à quatre (1929), A strain

Correspondences for fingerprints of different lengths

Establish a one-to-one correspondence between as many **matched strong beats** as possible.

Identify as many **corresponding but non-matched strong beats** as possible.

Ex. 4

The image shows two musical staves. The top staff is labeled "Boivin 1974, A strain" and the bottom staff is labeled "Soucy 1927, G strain (transposed from A major)". Both staves have a treble clef and a key signature of one sharp. The music consists of eighth-note patterns. Red double-headed arrows at the beginning of each staff indicate a correspondence between the first two notes. Red arrows point from notes in the top staff to notes in the bottom staff, establishing a one-to-one correspondence between strong beats. An orange arrow points from a note in the top staff to a note in the bottom staff, indicating a corresponding but non-matched strong beat.

How do the functions work?

- Matched and non-matched strong beats
- Matched weak beats on matched and non-matched strong beats
- Functions
 - Strong beat displaced to weak beat
 - Matched weak beats on matched strong beats
 - Matched weak beats on non-matched strong beats
 - Identical or similar contour on strong beats
 - Identical or similar contour extends to weak beats
 - Reversal of strong beats
 - Reversal extends to weak beats

Matched and non-matched strong beats

	Fingerprint 1:									
	1	2	3	4	5	6	7	8	9	
w	[-3.5]	[-2.0]	[-3.5]	[2.0]	[-3.5]	[-2.0]	[1.0]	[2.0]	[-3.5]	
0.0	0	0	0	0	0	0	0	0	0	
1.0	-1.5	1.5	-1	1	-1.5	-1	1.5	1	Nan	
2.0	0	0.5	0	-0.5	-2.5	0.5	2.5	Nan	Nan	
3.0	-1	1.5	-1.5	-1.5	-1	1.5	Nan	Nan	Nan	
4.0	0	0	-2.5	0	0	Nan	Nan	Nan	Nan	
5.0	-1.5	-1	-1	1	Nan	Nan	Nan	Nan	Nan	
6.0	-2.5	0.5	0	Nan	Nan	Nan	Nan	Nan	Nan	
7.0	-1	1.5	Nan	Nan	Nan	Nan	Nan	Nan	Nan	
8.0	0	Nan	Nan	Nan	Nan	Nan	Nan	Nan	Nan	
	Fingerprint 2:									
	1	2	3	4	5	6	7	8	9	
w	[-3.5]	[-2.0]	[0.0]	[4.5]	[-3.5]	[-2.0]	[0.0]	[3.5]	[-3.5]	
0.0	0	0	0	0	0	0	0	0	0	
1.0	-1.5	-2	0	3.5	-1.5	-1	0	2.5	Nan	
2.0	-3.5	-2	3.5	2	-2.5	-1	2.5	Nan	Nan	
3.0	-3.5	1.5	2	1	-2.5	1.5	Nan	Nan	Nan	
4.0	0	0	1	1	0	Nan	Nan	Nan	Nan	
5.0	-1.5	-1	1	3.5	Nan	Nan	Nan	Nan	Nan	
6.0	-2.5	-1	3.5	Nan	Nan	Nan	Nan	Nan	Nan	
7.0	-2.5	1.5	Nan	Nan	Nan	Nan	Nan	Nan	Nan	
8.0	0	Nan	Nan	Nan	Nan	Nan	Nan	Nan	Nan	

Allard 1928, A strain Boivin 1974, A strain

Matched weak beats on matched strong beats

Question: Given a matched strong beat, do the corresponding weak beats also match?

Solution: Given a matched strong beat “SX” in one fingerprint that corresponds to strong beat “SY” in another, compare the elements of “SX => WX” with those of “SY => WY”.

If WX and/or WY contain multiple elements, look for 1) the number of elements in common and 2) whether or not those common elements are in the same order in both. Each of these outputs is worth 50% of the total.

Maximum output per strong beat: 1 (“nan” = non-matched strong beat)

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9=> W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

matched
strong beat

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9=> W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

= ?

Matched weak beats on matched strong beats

		1	2	3	4	5	6	7	8	9
	w	[-3.5]	[-2.0]	[-3.5]	[2.0]	[-3.5]	[-2.0]	[1.0]	[2.0]	[-3.5]
0.0	0.0	0	0	0	0	0	0	0	0	0
1.0	1.0	-1.5	1.5	-1	1	-1.5	-1	1.5	1	NaN
2.0	2.0	0	0.5	0	-0.5	-2.5	0.5	2.5	NaN	NaN
3.0	3.0	-1	1.5	-1.5	-1.5	-1	1.5	NaN	NaN	NaN
4.0	4.0	0	0	-2.5	0	0	NaN	NaN	NaN	NaN
5.0	5.0	-1.5	-1	-1	1	NaN	NaN	NaN	NaN	NaN
6.0	6.0	-2.5	0.5	0	NaN	NaN	NaN	NaN	NaN	NaN
7.0	7.0	-1	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Fingerprint 2:		1	2	3	4	5	6	7	8	9
	w	[-3.5]	[-2.0]	[0.0]	[4.5]	[-3.5]	[-2.0]	[0.0]	[3.5]	[-3.5]
0.0	0.0	0	0	0	0	0	0	0	0	0
1.0	1.0	-1.5	-2	0	3.5	-1.5	-1	0	2.5	NaN
2.0	2.0	-3.5	-2	3.5	2	-2.5	-1	2.5	NaN	NaN
3.0	3.0	-3.5	1.5	2	1	-2.5	1.5	NaN	NaN	NaN
4.0	4.0	0	0	1	1	0	NaN	NaN	NaN	NaN
5.0	5.0	-1.5	-1	1	3.5	NaN	NaN	NaN	NaN	NaN
6.0	6.0	-2.5	-1	3.5	NaN	NaN	NaN	NaN	NaN	NaN
7.0	7.0	-2.5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN



Allard 1928, A strain

Boivin 1974, A strain

Matched weak beats on non-matched strong beats

Question: Given a non-matched strong beat, do the corresponding weak beats match?

Solution: Given a non-matched strong beat “SX” in one fingerprint that corresponds to strong beat “SY” in another, add “S1 => SX” and “SX => WX”. Compare that result to “S1 => SY” plus “SY => WY”. If they are the same, then weak beat X is the same note as weak beat Y.

If WX and/or WY contain multiple elements, look for 1) the number of elements in common and 2) whether or not those common elements are in the same order in both. Each of these outputs is worth 50% of the total.

Maximum output per strong beat: 1 ("nan" = matching strong beat)

non-matched
strong beat

$$+ \quad = \quad + \quad ?$$

Matched weak beats on non-matched strong beats

Yellow + Yellow = Blue + Blue ?

Fingerprint 1:

	1	2	3	4	5	6	7	8	9
w	[-3.5]	[-2.0]	[-3.5]	[2.0]	[-3.5]	[-2.0]	[1.0]	[2.0]	[-3.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	1.5	-1	1	-1.5	-1	1.5	1	NaN
2.0	0	0.5	0	-0.5	-2.5	0.5	2.5	NaN	NaN
3.0	-1	1.5	-1.5	-1.5	-1	1.5	NaN	NaN	NaN
4.0	0	0	-2.5	0	0	NaN	NaN	NaN	NaN
5.0	-1.5	-1	-1	1	NaN	NaN	NaN	NaN	NaN
6.0	-2.5	0.5	0	NaN	NaN	NaN	NaN	NaN	NaN
7.0	-1	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Fingerprint 2:

	1	2	3	4	5	6	7	8	9
w	[-3.5]	[-2.0]	[0.0]	[4.5]	[-3.5]	[-2.0]	[0.0]	[3.5]	[-3.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-2	0	3.5	-1.5	-1	0	2.5	NaN
2.0	-3.5	-2	3.5	2	-2.5	-1	2.5	NaN	NaN
3.0	-3.5	1.5	2	1	-2.5	1.5	NaN	NaN	NaN
4.0	0	0	1	1	0	NaN	NaN	NaN	NaN
5.0	-1.5	-1	1	3.5	NaN	NaN	NaN	NaN	NaN
6.0	-2.5	-1	3.5	NaN	NaN	NaN	NaN	NaN	NaN
7.0	-2.5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN



Allard 1928, A strain

Boivin 1974, A strain

Strong beat displaced to weak beat

Question: Has a non-matched strong beat note been displaced to the corresponding weak beat in the other fingerprint?

Solution: Given a non-matched strong beat “SX” in one fingerprint that corresponds to strong beat “SY” in another, add the values “S1 => SX” and “SX => WX” and compare to “S1 => SY”. If they are the same, then weak beat X is the same note as strong beat Y. Note that X=Y if the two fingerprints are of the same length.

Output: “1” for each strong beat displaced to a weak beat. “0” for a non-matched strong beat without displacement. “nan” for matched strong beats.

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9 => W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

non-matched
strong beat

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9 => W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

$$+ = ?$$

Strong beat displaced to weak beat

+ =



Allard 1928, B strain



Joyal 1956, B strain (transposed from A major)



Fingerprint 1:									
	1	2	3	4	5	6	7	8	9
w	[-2.5]	[1.0, 1.5]	[2.5]	[5.0]	[-2.5]	[4.5]	[4.0]	[4.5]	[-2.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-3.5	-0.5	-1	5	NaN
2.0	-2.5	-2.5	2.5	0.5	-4	-1.5	4	NaN	NaN
3.0	-4	1.5	-1	0	-5	3.5	NaN	NaN	NaN
4.0	0	-2	-1.5	-1	0	NaN	NaN	NaN	NaN
5.0	-3.5	-2.5	-2.5	4	NaN	NaN	NaN	NaN	NaN
6.0	-4	-3.5	2.5	NaN	NaN	NaN	NaN	NaN	NaN
7.0	-5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Fingerprint 2:									
	1	2	3	4	5	6	7	8	9
w	[-2.5]	[1.5]	[0.0]	[1.5]	[-2.5]	[1.5]	[-0.5]	[-1.0]	[-2.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-4	0.5	-1.5	5	NaN
2.0	-2.5	-2.5	2.5	0	-3.5	-1	3.5	NaN	NaN
3.0	-4	1.5	-1.5	0.5	-5	4	NaN	NaN	NaN
4.0	0	-2.5	-1	-1	0	NaN	NaN	NaN	NaN
5.0	-4	-2	-2.5	4	NaN	NaN	NaN	NaN	NaN
6.0	-3.5	-3.5	2.5	NaN	NaN	NaN	NaN	NaN	NaN
7.0	-5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

non-matched
strong beat

Identical or similar contour on strong beats

Question: Given two consecutive non-matched strong beats, check for identical or similar contour.

Solution: Given non-matched strong beats “SX” and “SX+1” corresponding to “SY” and “SY+1”, compare “SX => SX+1” to “SY => SY+1”. If they have the same value, the contour is identical. If the values are either +.5 or -.5 apart, there is a similar contour. (The half-step difference allows for the figure to start on a different scale degree.) The algorithm also compares consecutive similar contours to determine if they are similar in the same direction (i.e. +.5 or -.5).

Output: 1 for an identical contour, .5 for a similar contour, 0 for consecutive non-matched strong beats with no matched contour, “nan” for everything else (matched strong beats or non-consecutive non-matched strong beats)

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9=> W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

consecutive
non-matched
strong beats

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9=> W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

= +/- 0.5 ?

Identical or similar contour extends to weak beats

Question: Given an identical or similar contour, as above, do the corresponding weak beats also have an identical or similar contour?

Solution: If SX and SY each only have 1 weak beat, compare “SBX => WBX” to “SBY => WBY”. If they are identical, the weak beat contour is identical. If the values are either +.5 or -.5 apart, there is a similar contour.

Note: If SX and/or SY has multiple weak beats, the algorithm will check for identical contour (1 or more of the same weak beats, appearing in the same order). It does not check for similar contour in this case.

Output: 1 for an identical contour [.5 for a similar contour].

consecutive
non-matched
strong beats
with identical or
similar contour

 =  +/- 0.5 ?

Reversal of strong beats

Question: Given two consecutive non-matched strong beats, are they in fact matched strong beats that have been reversed?

Solution: Given non-matched strong beats “SX” and “SX+1” corresponding to “SY” and “SY+1”, does “S1 => SX” equal “S1 => SY+1” and “S1 => SY” equal “S1 => SX+1”? If both are true, then the strong beats are reversed.

Output: “1” if reversed, “0” if non-matched and not reversed, “nan” for everything else (matched strong beats or non-consecutive non-matched strong beats)

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9 => W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

consecutive
non-matched
strong beats

	1	2	3	4	5	6	7	8	9
w	S1 => W1	S2 => W2	S3 => W3	S4 => W4	S5 => W5	S6 => W6	S7 => W7	S8 => W8	S9 => W9
0	S1 => S1	S2 => S2	S3 => S3	S4 => S4	S5 => S5	S6 => S6	S7 => S7	S8 => S8	S8 => S9
1	S1 => S2	S2 => S3	S3 => S4	S4 => S5	S5 => S6	S6 => S7	S7 => S8	S8 => S9	
2	S1 => S3	S2 => S4	S3 => S5	S4 => S6	S5 => S7	S6 => S8	S7 => S9		
3	S1 => S4	S2 => S5	S3 => S6	S4 => S7	S5 => S8	S6 => S9			
4	S1 => S5	S2 => S6	S3 => S7	S4 => S8	S5 => S9				
5	S1 => S6	S2 => S7	S3 => S8	S4 => S9					
6	S1 => S7	S2 => S8	S3 => S9						
7	S1 => S8	S2 => S9							
8	S1 => S9								

$$\text{[yellow box]} = \text{[yellow box]} \quad \text{and} \quad \text{[blue box]} = \text{[blue box]} \quad ?$$

Reversal of strong beats

= **=**

The musical score shows two measures of music for a single melodic line. The first measure consists of six eighth-note pairs, with the second pair highlighted by a yellow arrow pointing to the second note. The third pair is highlighted by a blue arrow pointing to the first note. The second measure begins with a single eighth note, followed by a sixteenth-note rest, then a sixteenth note, and finally a sixteenth-note rest.

Allard 1928, B strain

Joyal 1956, B strain (transposed from A major)

consecutive
non-matched
strong beats

Reversal extends to weak beats

Question: Given two consecutive non-matched strong beats that are reversed (as above), are the weak beats also reversed?

Solution: Does “ $SX \Rightarrow WX$ ” equal “ $SY+1 \Rightarrow WY+1$ ”? If so, one of the weak beats is reversed. Does “ $SX+1 \Rightarrow WX+1$ ” equal “ $SY \Rightarrow WY$ ”? If so, the other weak beat is reversed.

If WX and/or WY contain multiple elements, look for 1) the number of elements in common and 2) whether or not those common elements are in the same order in both. Each of these outputs is worth 50% of the total.

Maximum output per strong beat: 1

consecutive
non-matched
strong beats that
are reversed

$$\boxed{\hspace{1cm}} = \boxed{\hspace{1cm}} ?$$

 =  ?

Overview

- Background
 - Why is a similarity algorithm necessary for this repertoire?
 - Why use a database of fiddle tunes from Quebec?
 - Existing initiatives
 - General characteristics of the repertoire
- How does the fingerprint algorithm work?
- **Results**
- Challenges, next steps

Results: The similarity measure

The algorithm combines the results of these comparison functions into a single “similarity measure” with a maximum value of 100.

The similarity measure is currently weighted as follows:

- 80% Number of matched strong beats OR
- 50% Displaced strong beats, reversals, contour (these all replace matched strong beats)
- 20% Number of matched weak beats

The result is slightly higher if the matched strong beats are predominantly in the first half of each fingerprint.

The result is adjusted slightly if the two fingerprints are not the same length.

Results

	Best Result:								
	1	2	3	4	5	6	7	8	9
Strong Beat Comparison	[0.0, 0, 0]	[-1.5, 1, 1]	[nan, 2, 2]	[nan, 3, 3]	[0.0, 4, 4]	[-1.5, 5, 5]	[-2.5, 6, 6]	[nan, 7, 7]	[0.0, 8, 8]
Displacement Comparison (Strong-Weak)	NaN	NaN	1	0	NaN	NaN	NaN	0	NaN
Weak Beats Comparison (Matched Strong)	[1.0, 1.0]	[1.0, 1.0]	NaN	NaN	[1.0, 1.0]	[1.0, 1.0]	[0, 0]	NaN	[1.0, 1.0]
Weak Beats Comparison (Mismatched Strong)	NaN	NaN	[1.0, 1.0]	[1.0, 1.0]	NaN	NaN	NaN	[1.0, 1.0]	NaN
Contour Comparison (Strong)	NaN	NaN	0	NaN	NaN	NaN	NaN	NaN	NaN
Contour Comparison (Weak)	NaN	NaN	0	NaN	NaN	NaN	NaN	NaN	NaN
Reversal Comparison (Strong)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Reversal Comparison (Weak)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Shorter FP Length	9	9	9	9	9	9	9	9	9
Longer FP Length	9	9	9	9	9	9	9	9	9
Number of Truncations	0	0	0	0	0	0	0	0	0
Best Similarity Measure:	75.0								

The image shows two musical staves side-by-side. The top staff is labeled "Allard 1928, A strain" and the bottom staff is labeled "Boivin 1974, A strain". Both staves are in G major (one sharp) and show a similar sequence of notes. Colored double-headed arrows highlight specific note differences between the two versions. Red arrows point from Allard's staff to Boivin's staff at measures 1, 2, 4, 5, 6, and 8. Green arrows point from Boivin's staff to Allard's staff at measures 1, 2, 4, 5, 6, and 8. Orange arrows point from Allard's staff to Boivin's staff at measures 3 and 7. A purple arrow points from Allard's staff to Boivin's staff at measure 3.

Results (out of 59 strains of “Money Musk”)

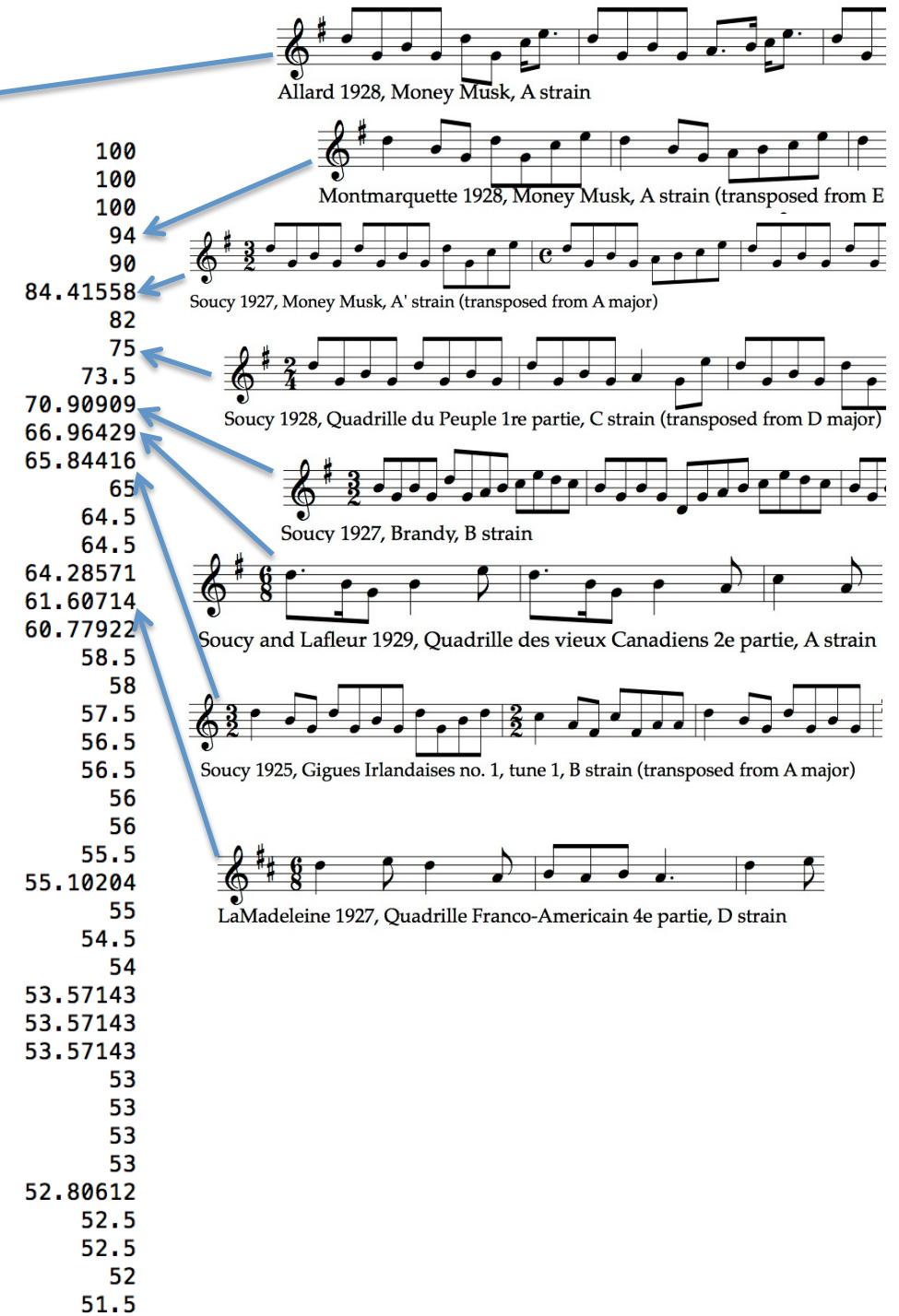
```
>>> db.rankings_for("Allard_1928_MoneyMusk_A.xml")
Boulay_1923_GiguesPotPourri_2ndTune_A.xml
Soucy_1927_MoneyMusk_A.xml
Soucy_1927_MoneyMusk_F.xml
Duchesne_1938_MoneyMuskAmericain_A.xml
Picard_1930_MoneyMusk_C.xml
Potvin_1980_MoneyMusk_E.xml
Joyal_1956_MoneyMusk_A.xml
Picard_1930_MoneyMusk_A.xml
Montmarquette_1928_MoneyMusk_A.xml
Potvin_1980_MoneyMusk_B.xml
Boivin_1974_MoneyMusk_E.xml
Soucy_1927_MoneyMusk_D.xml
Duchesne_1934_MoneyMusk_A.xml
Boivin_1974_MoneyMusk_C.xml
Lajoie_1951_MoneyMusk_C.xml
Potvin_1980_MoneyMusk_C.xml
Joyal_1956_MoneyMusk_D.xml
Richard_1975_MoneyMusk_A.xml
Soucy_1927_MoneyMusk_A1.xml
Montmarquette_1928_MoneyMusk_C.xml
Lajoie_1951_MoneyMusk_A.xml
Lajoie_1951_MoneyMusk_E.xml
Boivin_1974_MoneyMusk_A.xml
Duchesne_1934_MoneyMusk_E.xml
Duchesne_1934_MoneyMusk_D.xml
Lajoie_1951_MoneyMusk_F.xml
Lajoie_1951_MoneyMusk_B.xml
Boulay_1923_GiguesPotPourri_2ndTune_B.xml
Richard_1975_MoneyMusk_B.xml
Allard_1928_MoneyMusk_B.xml
Joyal_1956_MoneyMusk_C.xml
Soucy_1927_MoneyMusk_B.xml
Duchesne_1934_MoneyMusk_B.xml
Duchesne_1938_MoneyMuskAmericain_B.xml
Boivin_1974_MoneyMusk_B1.xml
```

100
100
100
98
98
96
96
96
94
92
90
90
88
86
85
85
84.41558
82
79
77
75
59
57.4026
55
53
53
50.5
50
49.5
47.5
47.5
47.5
47.5
45.5

Allard 1928, A strain
Picard 1930, C strain (transposed from C major)
Potvin 1980, E strain (transposed from F major)
Boivin 1974, C strain
Lajoie 1951, C strain
Soucy 1927, Money Musk, A' strain (transposed from A major)
Lajoie 1951, A strain (transposed from C major)
Lajoie 1951, E strain (transposed from C major)
Boivin 1974, A strain
Duchesne 1934, E strain (transposed from D major)
Duchesne 1934, D strain (transposed from A major)
Allard 1928, B strain (transposed from G major)

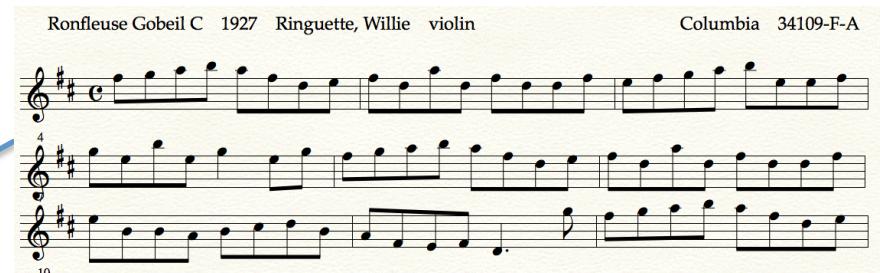
Results (out of 652 strains recorded 1923-1929)

```
>>> db.rankings_for("Allard_1928_MoneyMusk_A.xml", 50)
Boulay_1923_GiguesPotPourri_2ndTune_A.xml
Soucy_1927_MoneyMusk_A.xml
Soucy_1927_MoneyMusk_F.xml
Montmarquette_1928_MoneyMusk_A.xml
Soucy_1927_MoneyMusk_D.xml
Soucy_1927_MoneyMusk_A1.xml
Montmarquette_1928_MoneyMusk_C.xml
Soucy_1928_QuadrilleDuPeuple1rePartie_C.xml
Soucy_1929_GigueATiGus_B.xml
Soucy_1927_Brandy_B.xml
SoucyLafleur_1929_QuadrilleDesVieuxCanadiens2ePartie_A.xml
Soucy_1925_GiguesIrlandaisesNo1Tune1_B.xml
Allard_1928_ReelDuVoyageur_B.xml
Soucy_1928_GigueEcossaise_B.xml
Soucy_1929_GigueATiGus_D.xml
LaMadeleineA_1929_QuadrilleDesSeigneurs2ePartie_D.xml
LaMadeleine_1927_QuadrilleFrancoAmericain4ePartie_D.xml
Soucy_1927_Brandy_B1.xml
Allard_1928_ReelDuPendu_B.xml
Allard_1929_ReelDeMonMaton_C.xml
Boulay_1929_ReelAQuatre_A.xml
LaMadeleine_1929_ReelDuCordonnier_A.xml
Allard_1929_ReelDuCordonnier_A.xml
Soucy_1927_ReelDesPompiers_B.xml
Boulay_1929_SetCanadianDeQuebec3ePartie_B.xml
Soucy_1927_ReelDesMillionaires_A.xml
Ringuette_1927_ValseCharmante_B.xml
LaMadeleine_1928_QuadrilleDesBucherons5ePartie_A.xml
Boulay_1923_GiguesPotPourri_1stTune_B.xml
Soucy_1927_LeCasseReel_C.xml
Allard_1929_CotillonAHuit_B.xml
Soucy_1927_QuadrilleLaurier2ePartie_A.xml
Allard_1929_ReelDuJournalier_A.xml
Ringuette_1927_ReelDesNoces_A.xml
Soucy_1927_LeCasseReel_B.xml
Soucy_1927_LAsDePique_B.xml
Boulay_1923_GiguesPotPourri_2ndTune_B.xml
Daignault-LaMadeleine_1928_EnFaisantLaTourDeLaMontagne_A.xml
Boulay_1923_GiguesPotPourri_1stTune_A.xml
Gauthier_1926_ReelOpera_D.xml
LaMadeleine_1928_QuadrilleDeMatane2ePartie_A.xml
LaMadeleine_1928_QuadrilleDesBucherons3ePartie_B.xml
```



Results (out of 652 strains recorded 1923-1929)

```
>>> db.rankings_for("Ringuette_1927_RonfleuseGobeil_C.xml")
Soucy_1929_GigueDesVieuxSouliers_C.xml
Soucy_1927_ReelDeLaPolice_A1.xml
Allard_1929_BreakdownDuNuit_B.xml
Soucy_1927_LaPleureuse_B.xml
Soucy_1927_ReelDeLaPolice_A.xml
Soucy_1925_GiguesIrlandaisesNo2Tune3_A.xml
LaMadeleine_1928_QuadrilleDesBucherons2ePartie_B.xml
Gauthier_1926_ReelAHuit_B.xml
Soucy_1929_GigueDesTricoteuses_B1.xml
Soucy_1925_GiguesIrlandaisesNo2Tune2_B.xml
Allard_1929_ReelDuCultivateur_B.xml
Allard_1928_ReelDuPendu_B1.xml
LaMadeleineA_1929_MarcheDeQuebec_A.xml
Gauthier_1926_ReelAQuatre_B.xml
LaMadeleine_1928_QuadrilleDesBucherons5ePartie_A.xml
...
SoucyLafleur_1929_QuadrilleDesVieuxCanadiens5ePartie_B.xml
Soucy_1928_BouleDeNeige_A.xml
Allard_1929_ReelDesMontagnes_A.xml
Soucy_1927_LeReveDuDiable_A.xml
Soucy_1928_ReelDesVieuxGarcons_A.xml
Boulay_1929_SetCanadianDeQuebec2ePartie_A.xml
Allard_1929_ReelDuChauffeur_A.xml
Soucy_1928_CotillonNational-doubletime_B1.xml
Soucy_1928_CotillonNational-doubletime_B.xml
Soucy_1926_SetAmericain1rePartie_A.xml
Soucy_1929_SetDuCanada1rePartie_A.xml
Boulay_1928_QuadrilleDeBerthier3ePartie_A.xml
Soucy_1927_SetCanadianFrancais3ePartie_B.xml
Boulay_1926_ReelsCanadiens1rePartie_B.xml
Allard_1929_ReelDuSemeur_B.xml
```



83	
78	
76.5	
62	
62	
61	Gigue des vieux souliers C 1929 Soucy, Isidore violin Starr 15635-A 31393568
59	
58	
58	
58	
57	
57	
56.25	
56	
55.5	
18	
18	
18	
17.81818	
17.5	
17.5	
16.5	
16.07143	
16.07143	
15	
15	
14.5	
13.39286	
13.39286	
12.5	

Overview

- Why French-Canadian fiddle tunes?
Which French-Canadian fiddle tunes?
- How does the fingerprint algorithm work?
- Results
- Challenges, next steps

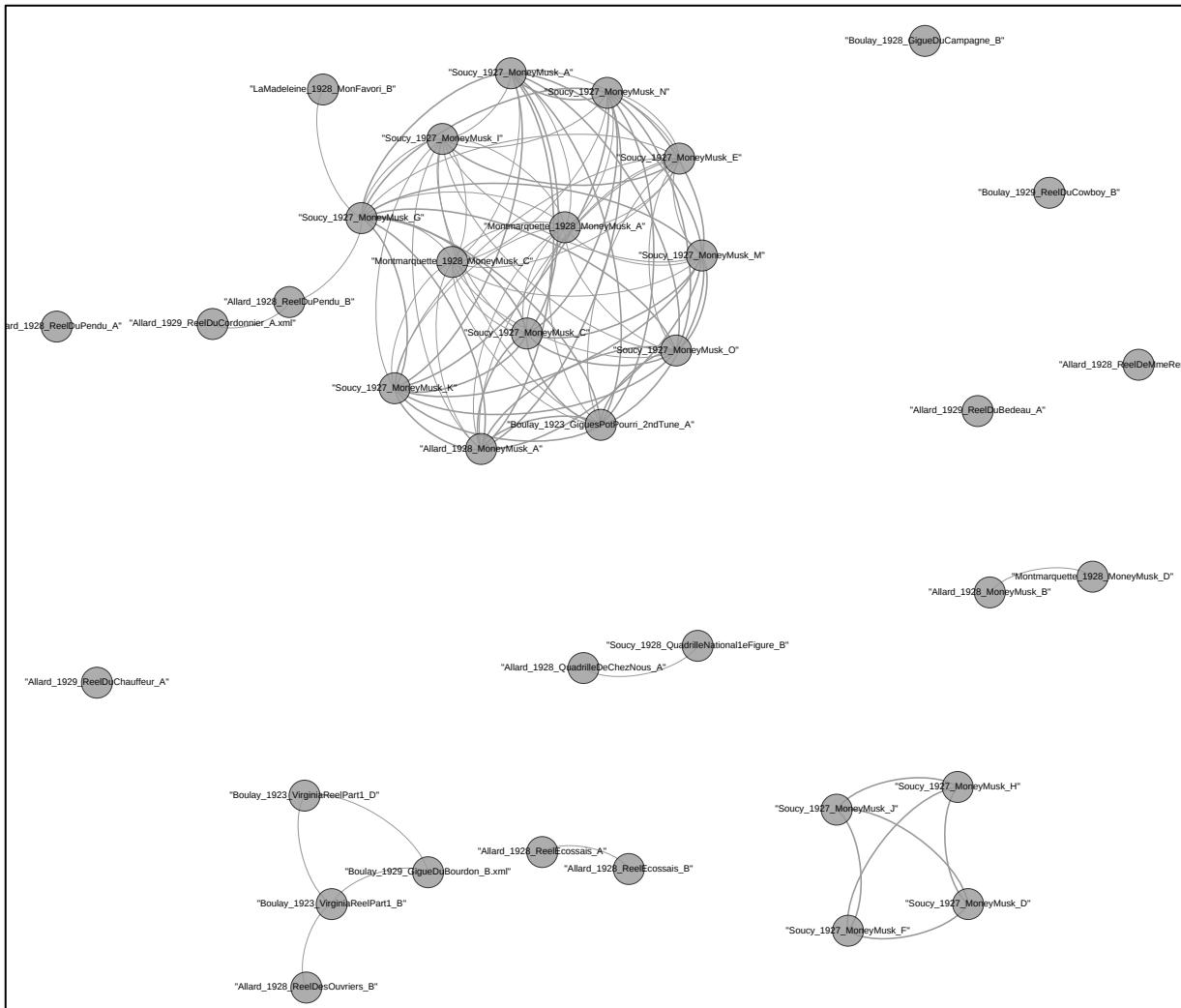
Challenges

- Human error
 - Errors in transcription
 - Incorrect placement of the first two barlines in metrically irregular tunes
- Comparison errors
 - Incorrect correspondences for fingerprints of different length: the correspondence function should only allow extension.
 - Incorrect fingerprint length when bars 1 and 2 are in different meters.
 - What if unequal truncations would give a better match? (see “human error” #2)
 - 4/4 vs. 6/8: perhaps add double-time settings of duple meter tunes?
- Should the algorithm use more than the first two bars of a strain?
 - Perhaps combine this algorithm with a “first pass” algorithm based on edit distance?

Next steps

- Refine calculation of similarity measure
 - user-entered?
- Automate the preparation of the XML files (currently done by hand)
 - remove pickups
 - remove grace notes, chords, articulation markings
 - realize all repeats, including first and second endings
 - split file into strains and name accordingly
 - create doubletime versions of 4/4 files?
 - double-stops? rests?
- User interface
 - share this algorithm with researchers studying other repertoires of fiddle tunes (British Isles, elsewhere in North America)
- How might we adapt this algorithm to other repertoires?
- Graphic display of results

Creating a visual representation



Sample visualization of 36 strains using Gephi (Yifan Hu layout). This mapping shows edges between all strains with a similarity measure of 10 or more (old weighting system). Edge thickness is proportional to similarity measure.

Fingerprint 1:

	1	2	3	4	5	6	7	8	9
w	[-2.5]	[1.0, 1.5]	[2.5]	[5.0]	[-2.5]	[4.5]	[4.0]	[4.5]	[-2.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-2.5	-0.5	-1	5	NaN
2.0	-2.5	-2.5	2.5	0.5	-4	-1.5	4	NaN	NaN
3.0	-4	1.5	-1	0	-5	3.5	NaN	NaN	NaN
4.0	0	-2	-1.5	-1	0	NaN	NaN	NaN	NaN
5.0	-3.5	2.5	2.5	4	NaN	NaN	NaN	NaN	NaN
6.0	-4	-3.5	2.5	NaN	NaN	NaN	NaN	NaN	NaN
7.0	-5	1.5	NaN	NaN	NaN	NaN	NaN	NaN	NaN
8.0	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Thank you!

Questions? Comments? Suggestions?

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Fingerprint 2:

	1	2	3	4	5	6	7	8	9
w	[-2.5]	[1.5]	[0.0]	[1.5]	[-2.5]	[1.5]	[-0.5]	[-1.0]	[-2.5]
0.0	0	0	0	0	0	0	0	0	0
1.0	-1.5	-1	-1.5	4	-4	0.5	-1.5	5	NaN
2.0	-2.5	-2.5	2.5	0	-3.5	-1	3.5	NaN	NaN
3.0	-4	1.5	-1.5	0.5	-5	4	NaN	NaN	NaN
4.0	0	-2.5	-1	-1	0	NaN	NaN	NaN	NaN
5.0	-4	-2	-2.5	4	NaN	NaN	NaN	NaN	NaN



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