Evolving Four Part Harmony using a Multiple Worlds Model

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Keywords: Genetic Algorithms, Procedural Content Generation, Music.

Abstract: This application of the Multiple Worlds Model examines a collaborative fitness model for generating four part harmonies. In this model we have multiple populations and the fitness of the individuals is based on the ability of a member from each population to work with the members of other populations. We present the result of two experiments: the generation of compositions, given a static voice line, both in a constrained and unconstrained harmonic framework. The remaining three voices are evolved using this collaborative fitness function, which looks for a number of classical composition rules for such music. The evolved music is found to meet with the requirements placed on it by musical theory. Using the data obtained while running our experiments we observe and discuss interesting qualities of the solution space.

1 INTRODUCTION

A great variation of techniques have been used for the generation of music material. A large number of algorithms have been researched and explored in this particular application. This might be because music is, to a certain degree, quantifiable and abstract. There exists artificial intelligence systems that can produce very high quality music. (Cope, 1991) is focused on codifying music styles is very interesting and many more approaches are described by (Miranda, 2013). These algorithms can range from creating entire pieces of music, to solving specific problems (for example how to do a transition from a phrase A to a phrase B), to being a compositional aid and many more applications. Evolutionary algorithms have been a popular technique to use in this kind of application as this approach, based on the concept of random variation and selection, can efficiently search a large solution space. Notable works using this approach are (Dahlstedt, 2007) on evolving complete piano pieces, (Hoover et al., 2011) using interactive evolution of accompaniments, and (Miranda, 2003) in the evolution of music in artificial life societies.

The Multiple Worlds Model (MWM) (Brown and Ashlock, 2010) is an evolutionary approach which uses a multiple population approach with a collaborative fitness function between the populations. It uses multiple evolving populations acting upon the same target optimization, not unlike island models (Whitley et al., 1997). However, island models have the goal of providing a single solution to a problem and pass genetic traits to each other by an explicit migration step. The chromosomes in an island model are part of the same species as they breed amongst themselves. The multiple worlds model separates these populations on the genetic level, they are separate species under the biological species definition — they do not interbreed, due to biological infertility, or behavioral differences. The goal of the MWM is not to provide a single good solution, but a set of interacting solutions.

Previous examples of MWM have been demonstrated to split and join sets of iterated prisoners dilemma playing agents and produce new agents (Brown, 2012; Brown, 2013; Brown, 2014). (Ashlock and McEachern, 2011) used a MWM in order to simulate the biological networks produced by species of bacterium using game theory. Further, it has been used to model the splits in a radio station market based on the preferences of listeners in the demographic area (Brown, 2014). Each of the populations represents a radio playlist and fitness is defined by a set of listeners who change stations based on an enjoyment value. These studies of the MWM have been competitive, each of the species is fighting over food resources. This study has a collaborative aspect, with each of the species, a single musical voice, having to construct a which avoids conflict with other voices. Similar process of divergence are seen in roots, leaves, and seed structures of plants with a his-

Scirea, M. and Brown, J..
Evolving Four Part Harmony using a Multiple Worlds Model.
In *Proceedings of the 7th International Joint Conference on Computational Intelligence (IJCCI 2015) - Volume 1: ECTA*, pages 220-227
ISBN: 978-989-758-157-1

tory of coexistence (Tilman and Snell-Rood, 2014).

This process is known as Adaptive radiation. The properties of this species were first fully examined by (Lack, 1947) and were not used by Darwin's examinations due to a number of misclassifications in the species caused by poor record keeping (Sulloway, 1982). Finches were found to have large changes to their phenotypic traits in even short periods of time due to changes in food sources (Grant and Grant, 1979; Grant and Grant, 1982; Grant and Grant, 1983).

Furthermore, behavioural modification can also lead to specialization in food sources through a process of niche partitioning. Hanson in *Feathers* gives an anecdotal account of studying the behaviours of North American bird actions in a forest: "Nuthatches foraged mostly on the trunks, Chickadees dominated the main branches, and Kinglets spend their time flitting about in the side branches" (Hanson, 2011). The MWM aims to use such principles of inter-population competition with intra-population evolution to guide a process of partitioning into models.

The niche effect is intrinsic to MWM. It does not require an explicit calculation of phenotype distance, or a crowding measure, the novel method of fitness evaluation is implicitly making crowding undesirable. It has also been shown to increase the diversity of final solutions of the creation of multiple models (Brown, 2014). This diversity has been seen in studies of mixture vs. monoculture plants in (Zuppinger-Dingley et al., 2014), which examined the results of eight years of experimental growth in Jena, Germany. It showed there was an increased interspecific difference to those plants grown in mixture types compared ($P < 0.05$) and intraspecific distance within mixture types on traits was increased ($P = 0.101$). They attribute a difference in relative specific leaf area ($P = 0.073$) and height ($P = 0.074$) to specialization into a niche. While these findings where marginally significant correlations, the authors claim that these traits are representative of relevant niche dimensions, and that further study is warranted looking at the processes of change. (Tilman and Snell-Rood, 2014) examine this study, and the previous mentioned finch studies, to question if such studies can experimentally demonstrate a divergence of species.

This study examines the application of the adaptive radiation by the MWM on the creation of a four part harmony in which one of the voices is known. The remainder of this paper is organized as follows: Section 2 examines the problem of creating a four part harmony as an evolutionary process, with Section 3 explaining the compositional rules used by the generator. The Multiple World Model of evolutionary algorithm is examined in Section 4, with special attention

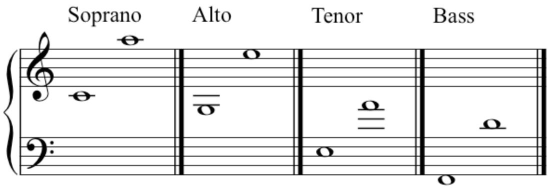

Figure 1: Ranges for the four voices used in four-part harmony.

to the collaborative model of fitness. Section 5 describes the experimental setting of the system used to demonstrate the method. The results of these experiments are examined in Section 6. Section 7 gives conclusions sets out further directions for this process.

2 FOUR PART HARMONY

Four-part harmony defines the category of music written for four voices (which could be singers or musical instruments) where the four parts produce a note for each chord in the piece. The four voices are generally called *soprano* (or *treble*), *alto* (*contralto* or *countertenor*), *tenor*, and *bass* (Boldrey, 1994). These voices all have some classically defined ranges (see figure 1), the origin of which comes from the limits of human singers: most singers have a vocal range of two octaves (McKinney, 1982), which means that most bass singers won't be able to reach the higher notes of a tenor or of a soprano. Typically the higher voice will perform a melody while the lower three will harmonize it, in our study any melody arising in the higher voice is going to be purely a by-product of evolution, as we do not interfere with its creation. Nonetheless, it's worth noting that this doesn't mean that interesting melodies cannot emerge.

This type of music (also called *chorale*) has slowly evolved from *Gregorian chant*, which was unison choir), becoming predominant in the Renaissance era, where its role as sacred music in Western Europe made it the main type of formally notated music. It has been explored by innumerable artists and later (Baroque and Classical music) accompanied by various types of instrumentation. Examples are Bach's *Mass in B minor*, Mozart's *Mass in C minor*, Haydn's *The Creation* and *The Seasons*. While all these works are thought to be for use in sacred ceremonies, the use of choirs (and chorale) soon after expanded to the concert stage, first examples of this tendency are Berlioz's *Te Deum* and *Requiem*, and Brahms's *Ein deutsches Requiem*.

We chose to explore the usage of evolutionary algorithms in creating this style of compositions as the composition style is commonly used as a teaching exercise for composers to learn to manage and create harmonies (Sessions, 1951). This exercise is particularly effective as the student must control both the horizontal and vertical dimensions of the texture. This strictly limited style of composition also provide us with a good benchmark to test the Multiple Worlds Model in the field of music generation.

We though it was interesting to consider each voice as a single individual, by using this assumption the MWM approach seemed a very interesting way to evolve cooperatively such compositions. These individuals are part of different populations that evolve at the same time, but without exchange of genetic material between them. We expected the populations (initialized randomly) to then achieve speciation, evolving in a way that the individuals from one population would evolve to "work well" with the voices belonging to the other populations.

3 SELECTED RULES FOR FOUR PART HARMONY

In this section we describe the rules of four-part harmony composition we decided to apply in this study, these are going to form the fitness function for the evaluation of the evolved individuals (see Section 4.3). We should note how the rules that we chose are just a subset of four-part harmony rules; many of the rules presented in various composition manuals are to be considered "guidelines" for "good" composition, so they can, in particular cases (stylistic, harmonic, or melodic reasons), be ignored (Schoenberg, 1978). The rules we chose consist of the *strongest* rules, the ones that should always, apart from extreme cases, be followed (Sessions, 1951).

Rule 1: for each beat each of the four voices plays one of the notes of a triad, with only one of the voices doubling a note one of the other voices are playing. This rule prevents usage of alterations, practically limiting the expression of chords to the diatonic triad appropriate for the degree considered (eliminating for example possible diminished chords). This rule would be considered "strong" mostly in a pedagogical context, but for this first study we believed it would be enough to consider the smaller problem space defined by this rule.

Rule 2: avoid *voice mixing*. By voice mixing we mean the situation where a higher voice plays a note lower in pitch than what a lower voice is playing. For example in the case where the soprano plays a C_4 while, at the same time, the alto plays a D_4. This situation is possible, as the ranges of the voices overlap, but in this type of composition it is not recommended.

Rule 3: no *parallel octaves*. Parallel octaves happen when two voices, which have between each other an interval of an octave, move by parallel motion to two new notes that still create an interval of an octave. This type of motion must be avoided, as it destroys the independence of the voices, by creating the sense of not two voices, but of one voice doubled at the octave.

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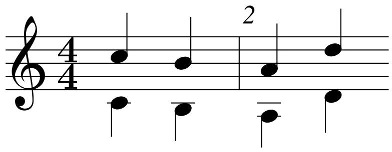

Rule 4: no *parallel perfect fifths*. Parallel fifths work exactly like the previously described parallel octaves, obviously with intervals of a fifth. In the same way they convey the sense of a single voice doubled and should then be always avoided. A parallel fifth movement can be accepted if it goes from a perfect 5th to a diminished 5th if the notes of the diminished 5th resolve. However, as we already explained, **rule 1** prevents the creation of diminished intervals, so we can ignore this exception.

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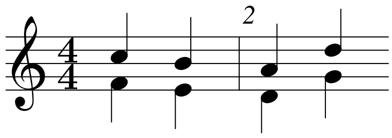
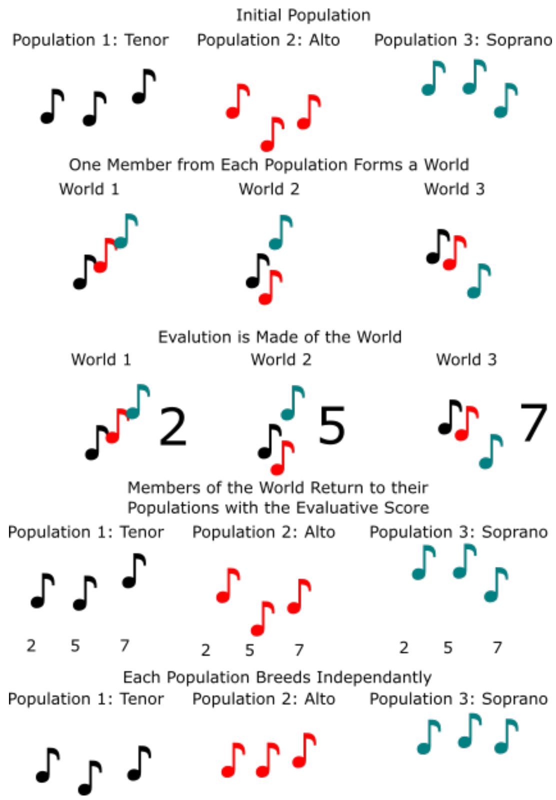


4 MULTIPLE WORLDS MODEL

4.1 Collaborative Fitness Model

In this study there is a change to the fitness evaluation from previous models, while previous models were looking at a competitive this application is collaborative. It implements the collaborative model of fitness proposed in (Brown, 2014), that each member of a world is scored the same as the world score, rather than the individual being given points only if it captures the modeled point better than the other models. This makes the fitness not just dependant upon a single voice, but on how it interacts with other voices in the model.




```
for some number of generations do
    randomize the worlds
    for all worlds do
        for all datapoints do
            (competitive) award the point to the model with the best fitness
            (collaborative) award the same fitness to each model based on their com-
            bined ability to solve the problem
        end for
    end for
    for all populations do
        Select breeding pairs based on fitness
        Apply Crossover/Mutation
    end for
end for
```

Figure 2: Demonstration (collaborative models) and Pseudocode (competitive and collaborative models) of the Multiple Worlds system.

4.2 Genome Representation

The genome representing an individual (or voice line) is composed of an array of n integers, where n is the amount of notes of the given bass line or a user defined number if the bass line is left free to evolve with the other voices. These integers represent the amount of semi-tones from the lower note of the voice's range, for example this means that the *soprano*'s genes can go from 0 (C_4) to 19 (A_5).

We can express each note belonging to the range, allowing us to evolve melodies fitting any key, even if the rules we selected (see Section 3) prevent alterations inside a specific key.

4.3 Fitness Evaluation

The rules discussed in Section 3 are implemented as fitness penalties. The evolution aims to minimize the number of violations of this rule set, each with an associated penalty score. A fitness score of zero is an arrangement with no rules violations. Therefore, it is a 'valid' composition.

$$fitness = \sum_{i=0}^{n}(Double(s_i,a_i,t_i,b_i)+ \\ +10*Mixing(s_i,a_i,t_i,b_i)+30*Stuck(s_i,a_i,t_i,b_i))+ \\ +\sum_{i=0}^{n-1}(10*Fifth(s_i,a_i,t_i,b_i)+Octave(s_i,a_i,t_i,b_i)) \tag{1}$$

As you can see from equation 1 we have all the four rules we discussed before: we check for each set of notes to **form a triad with one voice doubling one of the others** (*Double*), we check for **voice mixing** (*Mixing*), for **parallel fifths** (*Fifth*) and **parallel octaves** (*Octave*). We also had to add an extra part in the fitness function: *Stuck*. This function checks if a **voice is in the situation where, between the voice above and the one below, there is less than 7 semitones**. If this is so, we can have the situation where the two other voices are occupying pitches which are "good" (they satisfy the doubling rule) and the middle voice is stuck in a loop trying to reach one of the two pitches that are already occupied effectively bringing evolution to a dead end(note that most of the problem comes from the voices having limited, different and partly overlapping ranges). With the introduction of this part of the fitness function we can avoid these situations, and as it is a very unwanted situation it has a weight modifier of 30.

The *Double* function creates a proximity matrix of the notes that are being evaluated in respect to the possible pitches that can compose the triad, then it calculates and returns the minimum distance (in semitones) from an acceptable solution. For each couple of adjacent voices *Mixing* checks if they have overlapped, so for example if the alto is playing a note above the soprano or below the tenor. *Octave* and *Fifth* check for each possible couple of voices if they for a parallel octave or fifth between the notes at the i index and the $i+1$. *Mixing*, *Stuck*, *Octave* and *Fifth* are boolean functions, yet they represent violations of very strong rules, which is why they have a fairly high weight modifier.

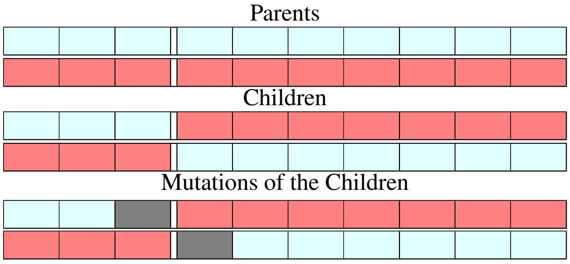


Figure 3: Example of breeding (crossover and mutation) between the representations of notes. Parent one is the first note sequence of size ten in light blue. Parent two is the second note sequence of size ten in the darker red. A one-point crossover then occurs between the two parents at the third loci creating child one and two. The mutations of the children then happen in child one at the third position and the second child at position four, labeled in dark gray.

4.4 Selection

First, an elitist strategy is applied, copying to the new generation the best individual of the current generation, the rest of the population is filled with offspring from individuals selected by a simple tournament selection algorithm (Miller and Goldberg, 1995). Finally, a mutation chance for each individual of the new generation (1%) is applied. This is a low mutation rate of the best individuals that this should help to avoid inbreeding and promote exploration of the problem space.

4.5 Variation Operators of Crossover and Mutation

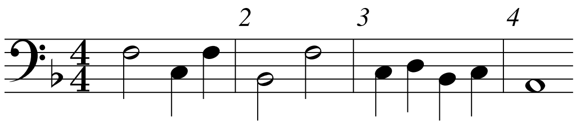
In this section we discuss how we have implemented the production of a new generation; remember that we have three (or four, depending on the setup) populations, the following method is applied to all of these.

We apply a simple one-point crossover: given two parents we select randomly a point in their genomes and create two new individuals containing the data from one parent up to the crossover index and the data from the other parent afterwards (see Figure 3).

When we mutate an individual, we give each gene a chance of $\frac{1}{NumberOfGenes}$ to mutate, effectively obtaining in general only one gene mutation per individual mutation, but allowing for more (or no) mutation. As we discussed in Section 4.2, each gene represent a note; when a gene mutates we take a random point from a Gaussian distribution bound in the interval $[-5,5]$ and transform the note by adding the value obtained in semi-tones. For example, if our gene represents a C_4 and we obtain a -2 from our random selection, we subtract two semitones from C_4 obtaining an $A\sharp_3/B\flat_3$.

5 EXPERIMENTAL SETTINGS

We have conducted two trial run consisting of 100 evolutions of a four-part harmony composition given an already written bass line. This choice was motivated firstly to try to simulate typical pedagogical exercises in composition (where generally one of the voices is already given to the students, which then have to write the remaining three) and secondly because it seemed a more complicated problem for our evolutionary approach. The difference between the two trial was the introduction of a constraint: **forcing the note played by the *bass* to be always the root of the chord**. The introduction of the constraint allows us to explore if we can generate variations within the same harmonic framework. Indeed, we have observed (but will not discuss in this paper) that the evolutionary process has much more success if given freedom to also evolve the bass line. This stands to reason, as giving a static bass line restricts the solution space, effectively giving less freedom to the evolution.



We have obtained 85 solutions from the evolution of compositions without the constraint, while out of the 100 runs with the constraint we have only obtained 8 solutions, those with a fitness score of 0, denoting no rules violations. You can access the midi of solutions/non-solutions for the two experiments at *msci.itu.dk/fourpart*. Often the evolution gets stuck in local optima from which it cannot move out with our current approach.

6 RESULTS AND DISCUSSION

The mean fitness of the populations proceeds to reach a plateau after 120 generations, this seems to indicate that evolution progresses correctly to a optimum. Sadly most of the times in the constrained experiment, instead of finding a solution we get stuck in a local optimum. We should note that the evolution is also not very expensive in time usage criteria: it takes about one to two seconds to reach the plateau. This seems to indicate how the solution space for our constrained problem is composed by many suboptimal points.

We have calculated distance matrixes between the solutions/non-solutions and between non-solutions/non-solutions. These give us information on how the solution space is composed. The distance metric we used is fairly naive, when confronting two different evolved compositions we check how distant (in amount of semitones) each note of each voice is compared to it's counterpart in the other composition. We are aware that there are better distance measures (like the Tonal Pitch Step Distance (De Haas et al., 2008)), but most focus on harmonic distance. In our constrained case this would make little sense between solutions, as we defined a harmonic constraint on the given bass's notes always being the root of the chord.

In this paper we will focus on the data gathered through the constrained experiment, as it gives us some more interesting information on the solution space of variations with the same harmonic structure.

6.1 Constrained Experiment Results

We have conducted an unpaired t test on the distances between the solutions and between the non-solutions. The mean minimum distance between the eight solutions ($\bar{x} = 34.5$, $\sigma = 26.2$) and the minimum distance from one of erred pieces the to one of the solutions ($\bar{x} = 55.3$, $\sigma = 17.7$) was found to be statistically significantly lower ($p = 0.0304$) using a two-tailed t-test between means. Thus, there is in general more similarity between the closest correct pieces to each other than the errors being close to the known solutions. This implies that either the known solutions are valleys in the search landscape which more than one non-conflicted song exists in with a number of local optima to bypass or that there are other unknown good songs which are also moving the population. A possible explanation for this phenomenon might be given by the harmonic constraints we have introduced. We expect that by lifting such a constraint we will have well distributed solutions, that might still cluster depending on the harmonic qualities of the compositions.

In the eight solutions, there are two pairs of arrangements with close features, less than twenty units of the distance measure. Yet, the same arrangement was never found twice, demonstrating the diversity of solution which is present due to the genetic approach. This makes for eight unique songs meeting with the baseline, see Fig. 4 for all the solutions, we highlight two very similar ones and two very different ones. For comparison we also present a human-made solution from the *Genevan Psalter* (Fig. 5). Note that the notes that appear in the solution with a *diesis* (♯) correspond in this key not to a *A*♯ but to a *B*♭, which appears normally in Fig. 5, because the *B*♭ is included in the key notation. They all share some common chords and characteristics. This is due, as already discussed, to the harmonic limitations we have enforced on the compositions. Yet, we obtain some different

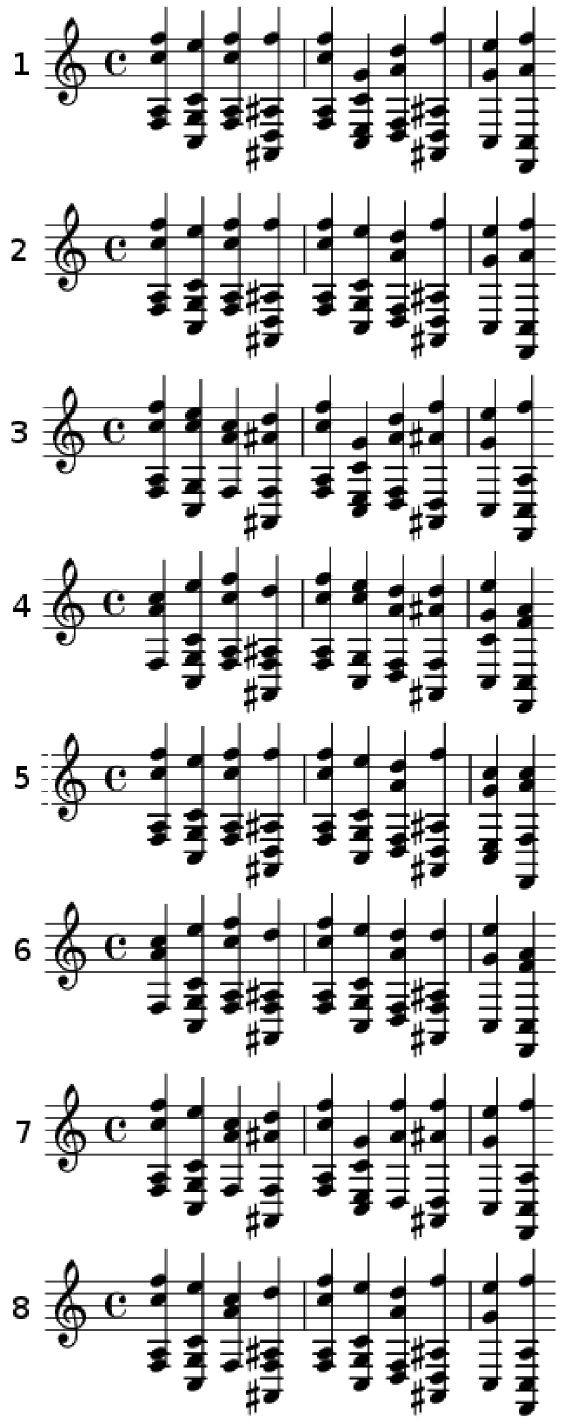


Figure 4: The eight solution obtained by the **constrained** experiment. The distances between solution 7 and solution 6 is 76 (semitones), while the distance between the solution 7 and solution 8 is only 6.

notes dispositions, that show how we can obtain many variations even considering this limitations. We can especially see this between the second and third solu-

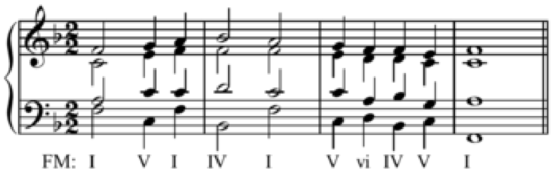


Figure 5: An example of human composed four part harmony using the same bass line and harmonic sequence, from the *Genevan Psalter: Old 124th*.

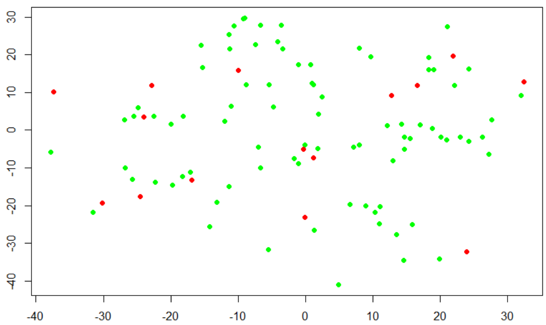


Figure 6: Representation of the distance matrix calculated for all runs in the **unconstrained** experiment calculated using *Multidimensional Scaling*. In green you can see the solutions we found.

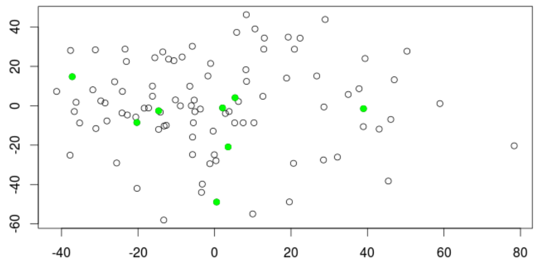


Figure 7: Representation of the distance matrix calculated for all runs in the **constrained** experiment calculated using *Multidimensional Scaling*. In green you can see the solutions we found.

tion which, while being very similar still have managed to present some small variation. The variation in question appears at the 7th crotchet (which, in this case, corresponds with the 7th beat), where we have (from the bass to the soprano) $\{D, F, A, D\}$ for the second score and $\{D, D, A, F\}$ for the third one. Even if the voices are still doubling the root of the chord, the three free voices sing different notes.

6.2 Unconstrained Experiment Results

Out of 100 runs we obtained 85 solutions when we allow the algorithm to choose which voice plays the root of the chord. This means that, as we still are giving a static bass line, the algorithm can choose one of three possible chords to build per each bass note. This is because the bass note can then be interpreted as the root of the chord, as its third or its fifth; so if the bass note is F, the possible chords would be F, *Dminor* and $B\flat$. It should be noted that these compositions might present weird chord sequences, as the choice of which of the three possible chords to choose is stochastic and the algorithm has no information or rules about chords. We have not conducted an study to investigate these aesthetic questions yet, but we believe most compositions sound pleasant (you can find the solutions at *msci.itu.dk/fourpart*).

We found no statistically significant relationship between distances of solutions and non-solutions as in the Constrained experiment. This seems to suggest that these solutions occupy more evenly the solution space and the same seems true for the non-solutions (see Figure 6). We believe these result make sense: we are exploring a wider search space and our algorithm then is able to find more solutions without getting stuck in local optima. This also helps us interpret the results from the Constrained experiment: that experiment had some constraints that limited the acceptable solutions to a specific part of the solution space, which would explain why they seems to be grouped in a valley. That might be an indicator that our fitness function has issues navigating through the solution space when the individual is far away from any possible solutions.

7 CONCLUSION

In this paper we present a novel approach to generating four-parts harmonies by using the Multiple Worlds Model evolutionary approach. We have shown how we can generate multiple compositions correctly, which present variations within and outside a harmonic constraint. This study also allowed us to notice the solution space, for constrained music, appears to be composed by many suboptimal points. Their is a solution valley where some of the most similar found cluster.

At this time we cannot say that we can generate better harmonies than other approaches, in fact our ruleset is restricted.While rule based expert systems, e.g. CHORAL (Ebcioğlu, 1988), or the use of planning (Yi and Goldsmith, 2007) might create just as good compositions or even better compositions. The variety of solutions offered by our approach is very interesting. A user using this system to harmonize a voice line would, instead of having to be happy with the one solution the system returns, be presented with a variety of variations could be selected.

One of the major questions raised by this work is the issue of human competitive performance of the result. This can be first demonstrated by showing that the system given a baseline will produce the same composition as a human composer. The best method of testing the claim to human competitive performance would be for this system along with a group of student musicians to be given the same set of baselines in a larger study. The generated harmonies being played in a random order for an audience in a Turing test or Imitation Game (Turing, 1950), attempting to decide between human and computer generations.

In conclusion we believe that this work, while needing much improvement, has given us a very interesting glance in how the solution space of these composition is made and has shown that we can use collaborative evolution to achieve speciation between the voices.

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