Creating Music with Evolution and Information Theory

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Information Sources in Music

- Information source: a probability matrix defining the likelihood of each element in an alphabet occurring
- Musical information sources: Pitch, harmony, rhythm, dynamics, form...

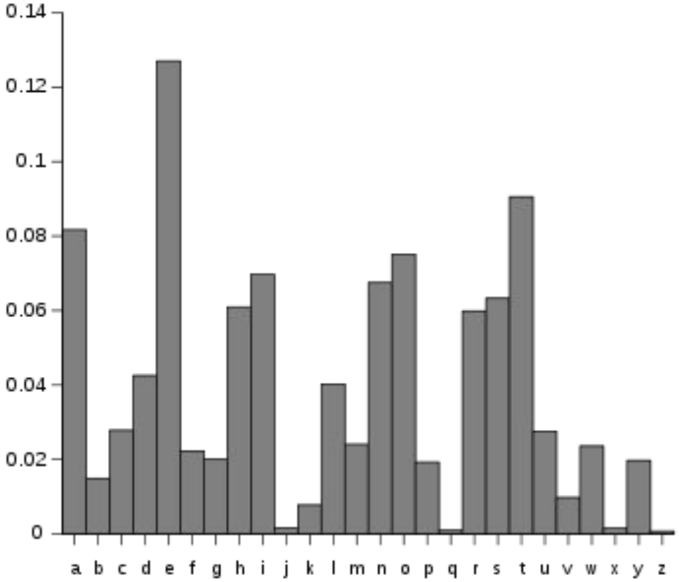
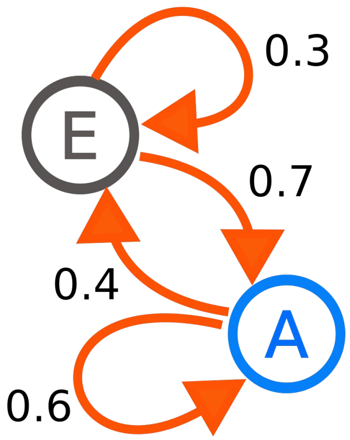


Image credit:
https://en.wikipedia.org/wiki/Letter_frequency

Markov Chains

- When dependencies exist from t to t+1, the matrices are *Markov tables*
    - First order: dependant on last element to occur
    - Second order: last two elements
    - ...



*A and E are variables

Image credit: https://simple.wikipedia.org/wiki/Markov_chain

Information

- *Entropy* describes the amount of uncertainty in an information source
- Defined as:

  H = $-\sum_{i=1}^{n} p(x_i) \log_b p(x_i)$

  - Generally b = 2, so measured in bits
  - CAN use bases other than 2, but consistency helps comparison across instances and domains
  - Max possible entropy for a source (all elements equally likely) is simply log n , where n is the number of letters in the alphabet

Redundancy

- Difficult to compare entropy between sources with different lengths of alphabet or probability matrices
- *Relative entropy* (RH_m), ratio of entropy to max entropy:

$$RH_m = H_m / \log n$$

- *Redundancy* (R), fractional difference between RH & max H:

$$R_m = 1 - H_m/\log n$$

R measures expected “predictability” of source

Redundancy in Studies of Music

- Used to attempt to quantify style via capture of some aesthetic quality
- Exploration vs Exploitation

TABLE 1

REDUNDANCY OF ROMANTIC MUSIC

Composer	% R_1	% $R(i,j)$	% R_2
Schubert	12.5	20.4	35.6
Mendelssohn	14.9	24.0	43.5
Schumann	14.7	22.4	37.3
Cumulative	13.4	20.5	29.2

TABLE 4

INFORMATION-CONTENT AND REDUNDANCY OF ROCK AND ROLL

	Hound Dog	Don't Be Cruel	Combined
Information-content (bits/note)	1.73	2.32	2.61
Redundancy (% R_1)			
7-tone system	38.2	17.2	6.9
12-tone system	51.6	35.2	27.1

[Tables adapted from Cohen, 1962]

Genetic Algorithms

- Populations of data strings “compete” in some fitness landscape
- Simulation progresses in timesteps/generations
- At each step the least fit strings are dropped from the population, while the most fit strings are cloned, replicated, and mutated
    - Cloning: copies of successful strings are made in the next time step
    - Replication: pairs of successful strings “mate”, mixing their data strings to create new strings
    - Mutation: random portions of successful data strings are altered

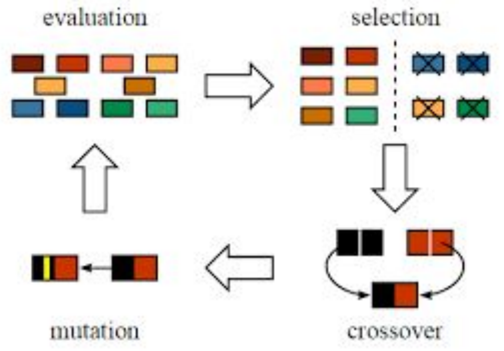


Image credit: analyticsvidhya.com/blog/2017/07/introduction-to-genetic-algorithm/

The Current Study

- Built in NetLogo
- Population of first-order Markov chains
- Evolve via:
  - Single point crossover
  - Mutation
    - preserving normalization
- Fitness is measured in proximity to redundancy target

```
to initialize
  set target-redundancy 0.5
  set population-size 50
  set crossover-rate 0.3
  set mutation-rate 0.05
  set scale "minor pentatonic"

  set update-rate 20
end

to setup
  clear-all
  ;set target-redundancy 0.5
  ;set population-size 50
  ;set crossover-rate 0.3
  ;set mutation-rate 0.05
  ;set scale "minor pentatonic"

  ;set update-rate 20
  setup-scales
  create-notes 16 [
    set shape "circle 2"
    set xcor who
    set color white
  ]

  create-markovs population-size [
    set markov-list (list ) ;;n-values (scale-tones * scale-tones) [random-float 1]
    ifelse order = "first" [
      repeat (scale-tones) [populate-transitions] ] [
      ifelse order = "second" [
       repeat (scale-tones ^ 2) [populate-transitions] ] [
        ifelse order = "third" [
          repeat (scale-tones ^ 3) [populate-transitions] ] [
          repeat (scale-tones ^ 4) [populate-transitions] ]
    ]
    ]
```

[Methodology adapted from Stonedahl & Wilensky, 2008]

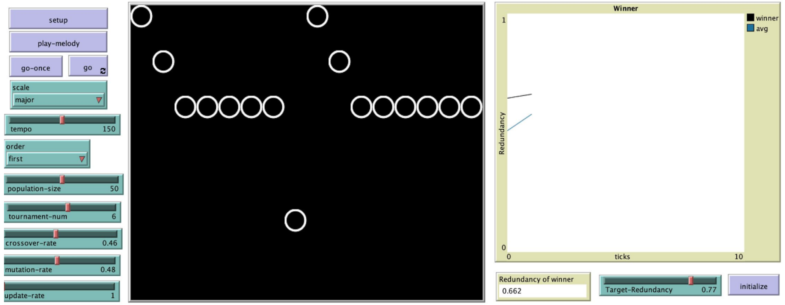
Example Markov table

R_m = 0.247

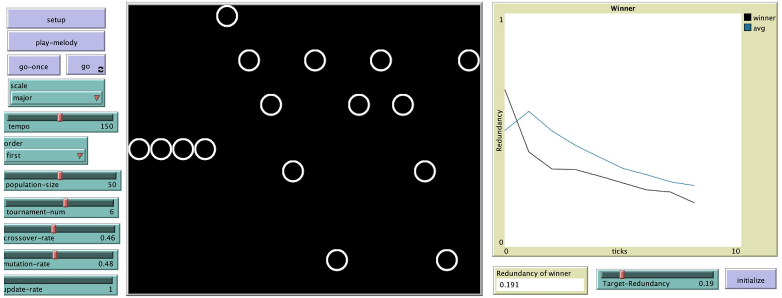
Note name ↓	Scale degree (chromatic) ↓	Note name → / Scale degree (chromatic) → / Scale degree (relative) → ↓	C	Eb	F	G	Bb
			<1>	<4>	<6>	<8>	<12>
			1	2	3	4	5
C	<1>	1	0.65	0.00	0.16	0.16	0.04
Eb	<4>	2	0.15	0.14	0.03	0.51	0.17
F	<6>	3	0.04	0.37	0.02	0.03	0.54
G	<8>	4	0.17	0.18	0.45	0.05	0.14
Bb	<12>	5	0.13	0.33	0.14	0.02	0.38

Examples

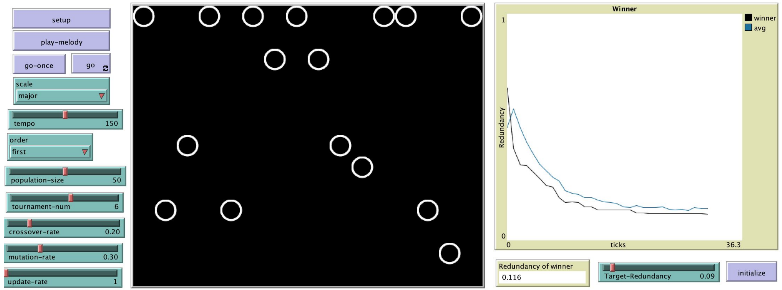
Medium-high R with well ordered, highly musical structure



Low R with some structure



Low R with little structure



References

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Stonedahl, F. and Wilensky, U. (2008). NetLogo Simple Genetic Algorithm model. http://ccl.northwestern.edu/netlogo/models/SimpleGeneticAlgorithm. Center for Connected Learning and Computer-Based Modeling, Northwestern University, Evanston, IL.