Toward Greater Artistic Control for Interactive Evolution of Images and Animation

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Interactive Evolution of Images

• Sims 1991

- Artificial Evolution
 - Survival of the fittest

Interactive evolution





Interactive Evolution of Images

- Genotype (DNA): functions
- Phenotype (individual): images
- *Expression* (birth): genotype \Rightarrow phenotype



Workflow

Create a "population"

Select a small number of survivors

Mate & mutate to produce next generation

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• This workflow provides only 1 control: selection



- Selection is surprisingly good, but
 - Passive & Indirect
 - Best suited to a novice user

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 "A price paid for this complexity is that the user often loses the ability to maintain sufficient control over the results."

• s/ complexity / simplicity /

→ Control requires balance

- Select / Mask mutation types
- Adjust relative mutation probability
- Adjust node mutation probability (e.g. height bias)



- Create new variable / function
- Simplification, factorization, expansion
- Inject genotype with constants $x \Rightarrow 1^*x + 0$

Dynamic Range

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I really like L/(1+L) [Reinhard 2002]
 +warm / -cool / desaturated colors



New Mutations

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• Warp mutations



Harmonic mutations







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• Motivation: 3D look w/ 2D genes





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• Motivation: Organic & representational vs symmetric & patterned





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• Motivation: Life & sexuality / conceptual recursion













Animation

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Genetic Cross Dissolve



Genetic Cross Dissolve

- Match identical expressions
- Interpolate differing expressions
- ⇒ First Difference Alignment



Genetic Cross Dissolve

- Match identical expressions
- Interpolate differing expressions
- ⇒ First Difference Alignment



First Difference Alignment





Genetic Cross Dissolve

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• Are deep alignments possible, in general?



First Difference Alignment

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• Example: blend (x > -1) with (x >= 1)



- Arrange each tree into a matrix
- Align rows



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- Arrange each tree into a matrix
- Align rows
- Align columns (per row)
 - Random, order-preserving bijections



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- in practice, requires selection or multiple tries

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- optimal solution may not be possible

- + simple
- + fast O(min(N,M)) (linear)
- + randomized & selectable (control)
- + becomes optimal as trees become similar

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 <u>Alignment of Trees - An Alternative to Tree Edit</u> Jiang, Wang, Zhang 1995, Theoretical CS

From computational biology, intended for ordered phylogenetic trees.



- Test every possible combination of alignments
- Measure each one
 (modified metric mu)
- Dynamic programming
- (Non) binary trees
- (Un) ordered trees



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- slow & large O(N*M) (quadratic)
- no control

+ optimal solution (under metric mu)
+ works very well in practice

Video

- Sequential blends
- All genotypes during a 1-year period
- Optimal alignment



Results (340 blends)

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Nodes

Min=4 Max=2090

Median=99 Mean=185.1

Time: 4 minutes total

Min=0.025 sec. Max=3.581 sec.

Median=0.109 sec. Mean=0.69 sec.

Results

Mean = ~185 Nodes



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Results

• Max = 2090 Nodes



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Results: Total Matches

	First- Difference	Random	Optimal
Min	1	3	4
Max	1215	1215	1215
Median	7	69	70
Mean	82.71	135.4	137.0

Results: Total Scores

	First- Difference	Random	Optimal
Min	0	0	0
Max	2817	2470	1388
Median	81	93	33
Mean	211.3	210.6	104.7

	EVO
Results' Root Matches	MUS
Results. Noot matches	ART
	2007

• 200 roots match

• 140 roots differ

Results: MatchesEvo
MUS(w/ Matching Roots)ART
2007

	First- Difference	Random	Optimal
Min	2	9	9
Max	1215	1215	1215
Median	69	87	88
Mean	139.9	170.3	173.12

Results: Matches (w/ Differing Roots)

	First-	Random	Optimal
	Difference		
Min		3	4
Max	1	496	495
Median	1	54	50
Mean		85.5	85.4

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Results: ScoresEvo
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	First- Difference	Random	Optimal
Min	0	0	0
Max	2817	2470	1388
Median	36	57	17
Mean	129.8	164.7	61.0

Results: Scores (w/ Differing Roots)

	First- Difference	Random	Optimal
Min	14	2	2
Max	1602	1512	1172
Median	213	167	97
Mean	327.7	276.2	167.1

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Summary

- New Tree Alignments provide:
 - Superior results (esp. optimal alignment)

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- Ability to visualize evolution
- Greater Artist flexibility

Questions?

Contact & info: dahart.com



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