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GRADUATION DATE: 06C MAJOR DEPT: CPSC

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TITLE: TERRAINOSAURUS: REALISTIC TERRAIN SYNTHESIS USING GENETIC ALGORITHMS

DATE SUBMITTED: 10-20-06
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(5) Title page - • title crosses over the left and right margins – you will need to use 2 lines for the title
• the submittal statement needs to be single spaced.

(6) page ii – title needs to be on 2 lines
– submittal statement needs to be on 3 lines, single spaced, and use the same wording as used on the Title page.
– names of Committee Chair and Committee members needs to be single spaced.

(7) p. iii – leave 2 single spaces between ABSTRACT and title.

(8) p. 1 - delete the superscript ' from line 1 and the journal model sentence.

Registration can be waived only if the student has completed all requirements for the degree (including clearing thesis office corrections) by the last day to add courses in the semester of graduation. All students with fellowships, assistantships, student loans or visa status must check to determine if registration is necessary. In addition, students must check with their departments to make certain that registration is not required.

(9) Table of Contents – see attached – add numbers for subheadings.

(10.) p. 48 and 49. and p. V. Figures IV.7 and IV.8 have the same title. you need to differentiate between them since 2 figures may not have the same title. You need only have 1 word to differentiate, such as (bend) after the first sentence of Figure IV.7 title.

(11.) p. V and p. 54. Figure IV.11 title – need word agreement. ... #6 ... on p. V vs ... σ_6 ... on p. 54

(12.) p. V and VI – use the spacing of the text between the figure titles.

(13) p. 99 – Table title needs to be above the table – like your journal does.

(14) p. Vii – word 'TABLE' and word 'Page' should be on the same line – with a 1½ space before listing the Table title.

(15.) p. V – word 'FIGURE' and word 'Page' should be on the same line with a 1½ space before beginning the figure titles.

p. Vi – add words 'FIGURE' above figure column and 'Page' above page column.

(16.) I did not find text mentions for Figures V.4, V.6, V.7, V.8, V.9, V.11, and Vi.10.

(17.) p. 14. Insufficient text. Each text page must have a minimum of 4½" of text on it unless it is the last page of the Chapter or it also includes

(17. contd) a table or figure. Suggest you move the text from the bottom of p. 13 to p. 14.

(18.) p. 27, 110, 111, 112, 113. Remove hyperlinks (put text in black print and delete underlining).

(19.) p. 12. Equation III.1 and all the other equations — you need to place the equation number to the right of the equation and in parentheses — see the attached photocopied page from your journal and follow this example for all your equations. The equations should not have titles — you need to place this in the text.

(20.) Reference section — you need to provide a journal in the field of Computer Science that follows the style you have used in formatting your references — alphabetized and numbered. If you select a different journal than the one you have indicated at the bottom of page 1, you will need to correct that statement. (see attached). References will be re-checked.

(21.) p. 114 Vita — see attached.

3 spaces needed

ABSTRACT

Terrainosaurus: Realistic Terrain Synthesis Using Genetic Algorithms. (December 2006)
Ryan L. Saunders, B.S., Texas A&M University
Chair of Advisory Committee: Dr. John Keyser

Synthetically generated terrain models are useful across a broad range of applications, including computer generated art & animation, virtual reality and gaming, and architecture. Existing algorithms for terrain generation suffer from a number of problems, especially that of being limited in the types of terrain that they can produce and of being difficult for the user to control. Typical applications of synthetic terrain have several factors in common: first, they require the generation of large regions of believable (though not necessarily physically correct) terrain features; and second, while real-time performance is often needed when *visualizing* the terrain, this is generally not the case when *generating* the terrain.

In this thesis, I present a new, design-by-example method for synthesizing terrain height fields. In this approach, the user designs the layout of the terrain by sketching out simple regions using a CAD-style interface, and specifies the desired terrain characteristics of each region by providing example height fields displaying these characteristics (these height fields will typically come from real-world GIS data sources). A height field matching the user's design is generated at several levels of detail, using a genetic algorithm to blend together chunks of elevation data from the example height fields in a visually plausible manner.

This method has the advantage of producing an unlimited diversity of reasonably realistic results, while requiring relatively little user effort and expertise. The guided randomization inherent in the genetic algorithm allows the algorithm to come up with novel arrangements of features, while still approximating user-specified constraints.

text spacing needed

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Correction #19

Each residue is represented by a vertex in the vertex set V. Each vertex is also associated with the 3D coordinates of its corresponding residue center. Let $D[i]$ denote the set of possible rotamers for residue i. There is an *interaction edge* $(i, j) \in E$ between two residues i and j if and only if there are two rotamers $l \in D[i]$ and $k \in D[j]$ such that at least one atom in rotamer l conflicts with at least one atom in rotamer k. Two atoms conflict with each other if and only if their distance is less than the sum of their radii. Since the distance between any rotamer atom to its associated residue center is bounded above by a constant, there is a constant D_u such that if the distance between two residues is bigger than D_u, then there is no interaction edge between these two residues. In a normal protein, any two residues cannot be arbitrarily close, which is one of the underlying reasons why lattice models can be used to approximate protein folding. We let a constant D_l ($D_l > 0$) denote the minimum distance between any two residues in a protein. According to simple statistics on the PDB database, 99% of inter-residue distances are beyond 3.5Å. These two observations indicate that the residue interaction graph is sparse. In particular, it can be verified that each residue can only interact with at most $\Delta \leq (1+\frac{D_u}{D_l})^3$ residues. This fact enables us to use tree-decomposition technique to cut the residue interaction graph into some very small components so that we can do side-chain assignment to each small component almost independently and quickly.

We say that residues i and j interact with each other if there is one edge between i and j in G. For each rotamer $l \in D[i]$, there is an associated singleton score, denoted by $S_i(l)$. In our energy function, $S_i(l)$ is the interaction energy between rotamer l and the backbone of the protein. $S_i(l)$ also includes the preference of assigning one rotamer to a specific residue. For any two rotamers $l \in D[i]$ and $k \in D[j]$ ($i \neq j$), there is also an associated pairwise score, denoted by $P_{i,j}(l, k)$, if residue i interacts with residue j. $P_{i,j}(l, k)$ is the interaction score between residues i and j when their side-chain conformations are rotamers l and k, respectively.

Let $E(a, b)$ denote the interaction score between two atoms a and b. We use the method in the SCWRL 3.0 article [Canutescu et al. 2003] to calculate $E(a, b)$ as follows.

$$\begin{aligned} E(a,b) &= 0 && r \geq R_{a,b} \\ &= 10 && r \leq 0.8254 R_{a,b} \\ &= 57.273\left(1 - \tfrac{r}{R_{a,b}}\right) && \textit{otherwise} \end{aligned}$$

where r is the distance between atoms a and b and $R_{a,b}$ is the sum of their radii. Let $SC(i)$ and $BB(i)$ denote the set of side-chain atoms and the set of backbone atoms of one residue i, respectively, and $Pr_i(l|\phi, \psi)$ denote the probability of rotamer l given the residue i and two angles ϕ and ψ. Then we calculate $S_i(l)$ and $P_{i,j}(l, k)$ as follows [Canutescu et al. 2003]:

$$S_i(l) = -K \log\left(\frac{Pr_i(l|\phi, \psi)}{\max_{l \in D[i]} Pr_i(l|\phi, \psi)}\right) + \sum_{|i-j|>1} \sum_{s \in SC(i)} \sum_{b \in BB(j)} E(s, b) \quad (1)$$

$$P_{i,j}(l, k) = \sum_{a \in SC(i)} \sum_{b \in SC(j)} E(a, b). \quad (2)$$

example

In Eq. (1), K is optimized to 8 to yield the best prediction accuracy. Please notice that in the above two equations, the position of one side-chain atom depends on its associated rotamer.

Correction #20

REFERENCE PREPARATION AND PROOFING

Select an article from your model journal for reference style. Note the following in the journal's reference list:

Organization of citation: Citations must be organized in one of the following ways, according to the journal reference list:

1) alphabetized by the first author's last name (in this case, citations are referenced by name and date in the text)
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Proofing and checking: Proof the reference list – the Thesis Office will examine it for consistency, accuracy and completeness. Cross check the citations in the text with the reference list.

Correction #21

Your Name needs to be on this page

VITA

Ryan L. Saunders

Contact Information

I may be reached by mail at PO Box 753, Bellevue, WA 98009, or by email at saunders@aggienetwork.com.

Education

I received a Bachelor of Science in Computer Engineering from Texas A&M University in 2002. I continued on to pursue my Master of Science (~~this degree~~) also at Texas A&M, graduating in December of 2006.

Professional Experience

My professional experience includes:

- Hewlett Packard (Richardson, TX) Intern—FORTRAN compiler team
- Dynetics, Inc. (Huntsville, AL), Intern—Industrial automation division
- Self-employed (College Station, TX), Independent Contractor—Dynamic website development
- Microsoft Corporation (Redmond, WA), Software Development Engineer—Microsoft Office (current)

Publications

In the course of my Master's degree studies, I was co-author of a paper, *Terrain Generation Using Genetic Algorithms*, which was accepted to the *Genetic and Evolutionary Computation Conference (GECCO) 2005.*