Tree Model Reconstruction Innovization Using Multi-objective Differential Evolution

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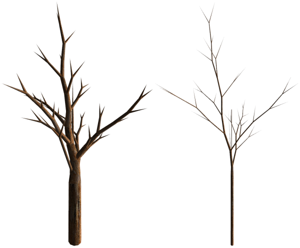
Motivation

- New approach for construction of trees
  - three-dimensional spatial models,
  - in computer graphics and animation,
  - the user had to sketch basic branches.
- Our **tree reconstruction** includes:
  - *evolutionary algorithms* and
  - *procedural modelling* of trees.

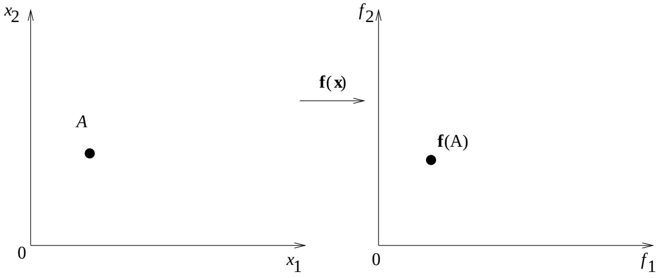
Source:
→ CEC 2009

- An approach (CEC'09): uses procedural models in a 2D plane, we extend it:
  - on 3D procedural models and
  - more complex trees.
- Our approach combines open-sources:
  - ecosystem framework **EcoMod** and
  - algorithm **MOjDE** (DEMOwSA$_{\text{CEC2007}}$ + jDE$_{\text{TEC2006}}$).



Multi-objective optimization

- Numerical function, consisting multiple criteria ($\mathbf{f}(\mathbf{x})$),



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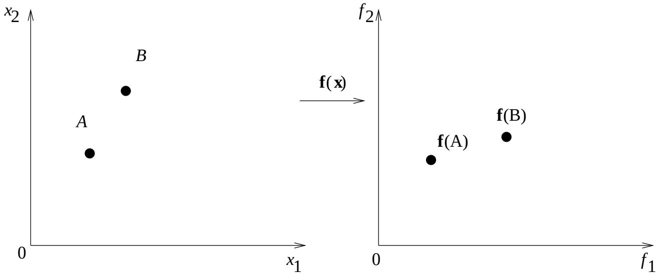

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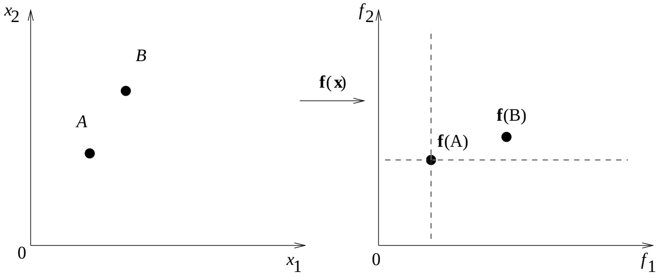

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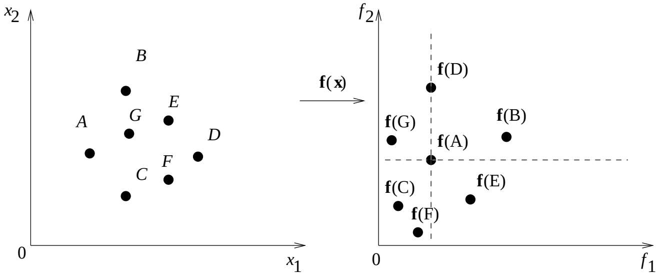
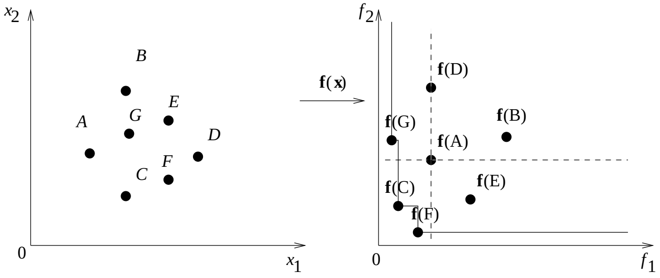


Multi-objective optimization

- Numerical function, consisting multiple criteria ($\mathbf{f}(\mathbf{x})$),
- meta-criterion ($A \preceq B$): make criteria ordered by **dominance**,
- optimization: search for **Pareto optimal approximation set**.

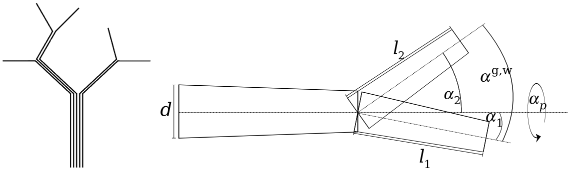


Differential Evolution (DE)

- A floating point encoding EA for global optimization over continuous spaces,
  - trough **generations**,
    the evolution process improves **population of vectors**,
  - iteratively by combining a parent individual and several other individuals of the same population.
- We choose the **strategy** *jDE/rand/1/bin*
  - **mutation**: $\mathbf{v}_{i,G+1} = \mathbf{x}_{r_1,G} + F \times (\mathbf{x}_{r_2,G} - \mathbf{x}_{r_3,G})$,
  - **crossover**:
    $$u_{i,j,G+1} = \begin{cases} v_{i,j,G+1} & \text{if } \mathrm{rand}(0,1) \leq CR \text{ or } j = j_{rand} \\ x_{i,j,G} & \text{otherwise} \end{cases},$$
  - **selection**: $\mathbf{x}_{i,G+1} = \begin{cases} \mathbf{u}_{i,G+1} & \text{if } f(\mathbf{u}_{i,G+1}) < f(\mathbf{x}_{i,G}) \\ \mathbf{x}_{i,G} & \text{otherwise} \end{cases},$
  - includes mechanism of F and CR control parameters self-adaptation.

Problem Domain: Woody Plants Procedural Model

- 3D tree models are compactly represented using a procedural model
  - our EcoMod framework uses a numerically coded procedural model with fixed dimensionality
  - suitable for parameter estimation using DE/MOjDE.
- Parameterized procedural model builds a 3D structure of a tree and all its building parts:
  - by recursively executing a fixed procedure,
  - over a given set of numerically coded input parameters,
    - e.g. branch thickness, relative branch length and branching structure proportions.



Trees Representable by EcoMod Framework

- Foliage or coniferous trees with very different branching structures,
- each branch and each leaf can be animated in real time to show the growth of a tree or its sway in the wind.

procedure branchsegment(g, w, S_0, L_0, l_0, $\mathbf{M}_0$, $\mathbf{M}_{m;0}^{-1}$)

Require: g, w - Gravelius and Weibull index of base branch; S_0 - number of strands in base branch; L_0, l_0 - base branch relative and actual length; $\mathbf{M}_0$ - base branch coordinate system; $\mathbf{M}_{m;0}^{-1}$ - inverse matrix of rotations for gravimorphism in coordinate system for base branch; global (i.e. part of *breeder*) k_d, k_c, l_{type}, $k_s^{g,w}$, $M^{g,w}$, $m^{g,w}$, $k_l^{g,w}$, $\alpha_m^{g,w}$, $\alpha^{g,w}$, t, k_f, w_s, w_g

Ensure: rendered tree image

$d := k_d \sqrt{S_0}$; {thickness calculation from Mandelbrot}

render base branch($\mathbf{M}_0$, l_0, d);

if $S_0 = 1$ **then**

  render leaves(l_{type}); **return**;

end if

$S_1 := \lceil 1 + k_s^{g,w}(S_0 - 2) \rceil$, $S_2 = S_0 - S_1$; {number of strands in subbranches}

$r_1 := \max\left\{\min\left\{\sqrt{\frac{S_1}{S_0}}, M^{g,w}\right\}, m^{g,w}\right\}$; {branch length proportions based on strands}

$r_2 := \max\left\{\min\left\{\sqrt{\frac{S_2}{S_0}}, M^{g,w}\right\}, m^{g,w}\right\}$;

$L_1 := r_1 L_0$, $L_2 := r_2 L_0$; {relative lengths of subbranches}

$l_1 := k_l^{g,w} L_1$, $l_2 := k_l^{g,w} L_2$; {active subbranch lengths}

$\alpha_1 := k_c \sqrt{\frac{S_2}{S_0}} \alpha^{g,w}$, $\alpha_2 := \alpha^{g,w} - \alpha_1$; {branching angles}

$\mathbf{M}_1 := \mathbf{R}_z(\alpha_1)\mathbf{R}_y(\alpha_p)\mathbf{R}_{\mathbf{y}\times\mathbf{y}_m}(\alpha_m^{g,w})\mathbf{T}_y(l_0)\mathbf{M}_0$; {Translation and rotation matrices}

$\mathbf{M}_2 := \mathbf{R}_z(\alpha_2)\mathbf{R}_y(\alpha_p)\mathbf{R}_{\mathbf{y}\times\mathbf{y}_m}(\alpha_m^{g,w})\mathbf{T}_y(l_0)\mathbf{M}_0$;

$\mathbf{M}_{m;1}^{-1} := \mathbf{R}_{\mathbf{y}\times\mathbf{y}_m}(-\alpha_m^{g,w})\mathbf{R}_y(-\alpha_p)\mathbf{R}_x(-\alpha_x(t))\mathbf{R}_z(-\alpha_1 - \alpha_z(t))\mathbf{M}_{m;0}^{-1}$; {refreshing inverse matrix for construction of gravimorphism vector}

$\mathbf{M}_{m;2}^{-1} := \mathbf{R}_{\mathbf{y}\times\mathbf{y}_m}(-\alpha_m^{g,w})\mathbf{R}_y(-\alpha_p)\mathbf{R}_x(-\alpha_x(t))\mathbf{R}_z(-\alpha_2 - \alpha_z(t))\mathbf{M}_{m;0}^{-1}$;

branchsegment($g+1$, $w+1$, S_2, L_2, l_2, $\mathbf{M}_2$, $\mathbf{M}_{m;2}^{-1}$); {minor branch development}

branchsegment(g, $w+1$, S_1, L_1, l_1, $\mathbf{M}_1$, $\mathbf{M}_{m;1}^{-1}$); {major branch development}

return; {from recursive procedure call}

Reconstruction: Image-based Approaches to Tree Modeling

- Image-based approaches have the best potential to produce realistically looking plants
  - they rely on images of real plants.
- Little work has been done to design trees with the use of a general reconstruction from images without user interaction
  - use of sketch based guide techniques or
  - the procedural models reconstructed were two-dimensional.
- We now extended this recognition to the domain of 3D procedural models
  - suitable to model woody plants without user interaction.

Tree Model Reconstruction Innovization Using Multi-objective Differential Evolution

- Based on an optimization procedure with three main parts:
  - Part I: genotype encoding,
  - Part II: genotype-phenotype mapping, and
  - Part III: fitness evaluation:
    - phenotype and reference image comparison.

Genotype Encoding

- An individual genotype vector $\mathbf{x}$ of a DE population represents a set of procedural model parameters,
  - by computing recursive procedure using a set of parameters, EcoMod renders a tree (woody plant),
  - dimensionality of the genotype $\mathbf{x}$ is $D = 4509$,
    - where $g \in \{0, ..G = 15\}$, $w \in \{0, ..W = 50\}$, and
    - each local $G \times W = 750$ real-coded parameter encodes: one matrix of a Gravelius and Weibull ordered parameter for recursive calculations, and
  - all $x_{i,j} \in [0, 1]$, $i \in \{1..NP\}$ and $j \in \{1..D\}$ are linearly normalized.

Bounds and Scaling of Genotype-encoded Parameters $x_{i,j}$

Parameter	Formula	Interval
Number of strands in a tree (tree complexity)	$S = 400x_{i,0} + 10$	$S \in [10, 410]$
Height of base trunk	$l_0^{0,0} = 10x_{i,1}$	$l_0^{0,0} \in [0\ \mathrm{m}, 10\ \mathrm{m}]$
Coefficient of branch thickness	$k_d = 0.05x_{i,2}$	$k_d \in [0,\ 0.05]$
Phyllotaxis angle	$\alpha_p = 360x_{i,3}$	$\alpha_p \in [0^\circ, 360^\circ]$
Branching ratio of subbranch strands distribution	$k_s^{g,w} = 0.5x_{i,j} + 0.5,\ \forall j \in [4, 753]$	$k_s^{g,w} \in [\frac{1}{2},\ 1]$
Branching angle between dividing sub-branches	$\alpha^{g,w} = 180x_{i,j}\ \forall j \in [754, 1503]$	$\alpha^{g,w} \in 0^\circ, 180^\circ$
Maximum relative sub-branch to base branch length	$M^{g,w} = 20x_{i,j}\ \forall j \in [1504, 2253]$	$M^{g,w} \in [0, 20]$
Minimum relative sub-branch to base branch length	$m^{g,w} = 20x_{i,j}\ \forall j \in [2254, 3003]$	$m^{g,w} \in [0, 20]$
Branch length scaling factor	$k_l^{g,w} = 20x_{i,j},\ \forall j \in [3004, 3753]$	$k_l^{g,w} \in [0, 20]$
Gravicentralism impact	$k_c = x_{i,3754}$	$k_c \in [0, 1]$
Gravimorphism impact (i.e. gravitational bending of branches)	$\alpha_m^{g,w} = 360x_{i,j} - 180,\ \forall j \in [3755, 4504]$	$\alpha_m^{g,w} \in [-180^\circ, 180^\circ]$
Enabling leaves display on a tree	$B_l = x_{i,4505} < 0.5?0 : 1$	$B_l \in \{0, 1\}$
Size of leaves	$l_l = 0.3x_{i,4506}$	$l_l \in [0,\ 0.3]$
Density of leaves	$\rho_l = 30x_{i,4507}$	$\rho_l \in [0, 30]$
Leaf distribution type	$l_{type} = 5x_{i,4508}$	*Spiral*, *Stacked*, *Staggered*, *Bunched*, or *Coniferous*1

Genotype-phenotype Mapping

- Reconstruction method is based on reconstruction of two-dimensional images of woody plants $\mathbf{z}^*$ (photo),
- to compare the three-dimensional tree evolved with the use of genotype $\mathbf{x}$ to the reference image $\mathbf{z}^*$, genotype $\mathbf{x}$ must be transformed to its phenotype first,
  - phenotype is a rendered two-dimensional image $\mathbf{z}$,
  - images $\mathbf{z}^*$ and $\mathbf{z}$ are all of dimensionality $X \times Y$ pixels,
    - the reference image is scaled to the given resolution, if necessary.
  - both images are converted to black and white, where white (0) pixels mark *background* and black (1) pixels mark *material*, e.g. wood,
- An evolved procedural model is rendered for comparison twice
  - to favor three-dimensional procedural models generation,
  - projections differ by $\beta = 90^\circ$ camera view angle along the trunk base (i.e. z axis for OpenGL).

Phenotype and Reference Image Comparison

- The recognition success is measured by similarity of
  - the reference original images (2D) and
  - the rendered image (2D) projections of evolved parametrized procedural models.
- Images are compared pixel-wise by **two criteria**:
  1. in the evolved image, for each pixel rendered as material (1):
     - the Manhattan distance to the nearest material pixel in the reference image is computed
     - and vice-versa, for each material (1) pixel of an evolved model image,
  2. count of differing pixels (0/1) among comparing images.

Calculus of the Two Criteria for Image Comparison

- Fitness evaluation of each phenotype are the sums:

$$f_1(\mathbf{x}) = f(\mathbf{g}(\mathbf{x}, \beta_1), \mathbf{g}(\mathbf{x}, \beta_2)) = h_1(\mathbf{z}_1) + h_1(\mathbf{z}_2)$$

$$h_1(\mathbf{z}_i) = \sum_{x,y} m_1(z^i_{x,y}, z^*_{x,y}) + \sum_{x,y} m_1(z^*_{x,y}, z^i_{x,y})$$

$$f_2(\mathbf{x}) = f(\mathbf{g}(\mathbf{x}, \beta_1), \mathbf{g}(\mathbf{x}, \beta_2)) = h_2(\mathbf{z}_1) + h_2(\mathbf{z}_2)$$

$$h_2(\mathbf{z}_i) = \sum_{x,y} w(z^i_{x,y}, z^*_{x,y}) + \sum_{x,y} w(z^*_{x,y}, z^i_{x,y}),$$

  - where $i \in \{1, 2\}$ for the two orthogonal evolved projections,
  - m_1 denotes a function computing Manhattan distance to the nearest material (value 1) pixel in the image $\mathbf{z}^*$, and
  - w denotes a function to count differing pixels in same coordinates.

procedure MO reconstruction($\mathbf{z}^*$)

Require: S_0 - maximum number of strands in base branch; also, other default parameters for MOjDE and EcoMod

Ensure: Pareto set of reconstructed parameterized procedural 3D woody plant models

`uniform randomly generate DE initial population` $\mathbf{x}_{i,0} \in [0,1]$ `for` $i = 1..NP$;

for DE generation loop g (while FEs < 10000) **do**

  for DE iteration loop i (for all individuals $\mathbf{x}_{i,g}$ of a population) **do**

    DE individual $\mathbf{x}_{i,g}$ creation (adaptation, mutation, crossover):

$$F_{i,G+1} = \begin{cases} F_l + rand_1 \times F_u & \text{if } rand_2 < \tau_1, \\ F_{i,G} & \text{otherwise} \end{cases}; \quad CR_{i,G+1} = \begin{cases} rand_3 & \text{if } rand_4 < \tau_2, \\ CR_{i,G} & \text{otherwise} \end{cases};$$

$$\mathbf{v}_{i,G+1} = \mathbf{x}_{r_1,G} + F_{i,G+1}(\mathbf{x}_{r_2,G} - \mathbf{x}_{r_3,G});$$

$$u_{i,j,G+1} = \begin{cases} v_{i,j,G+1} & \text{if } rand(0,1) \leq CR_{i,G+1} \text{ or } j = j_{rand} \\ x_{i,j,G} & \text{otherwise} \end{cases};$$

    DE fitness evaluation (genotype-phenotype mapping, rendering, and comparison):

      $\mathbf{z}_1 = \mathbf{g}(\mathbf{u}_{i,g}, \beta_1)$, $\mathbf{z}_2 = \mathbf{g}(\mathbf{u}_{i,g}, \beta_2)$ {Execute Algorithm `branchsegment` twice}

      $h_1(\mathbf{z}_1) = \sum_{x,y} m_1(z^1_{x,y}, z^*_{x,y}) + \sum_{x,y} m_1(z^*_{x,y}, z^1_{x,y})$; {First difference metric, at 0°}

      $h_1(\mathbf{z}_2) = \sum_{x,y} m_1(z^2_{x,y}, z^*_{x,y}) + \sum_{x,y} m_1(z^*_{x,y}, z^2_{x,y})$; {First difference metric, at 90°}

      $f_1(\mathbf{x}) = f(\mathbf{g}(\mathbf{x}, \beta_1), \mathbf{g}(\mathbf{x}, \beta_2)) = h_1(\mathbf{z}_1) + h_1(\mathbf{z}_2)$; {Fitness evaluation, 1st criterion}

      $h_2(\mathbf{z}_1) = \sum_{x,y} w(z^1_{x,y}, z^*_{x,y}) + \sum_{x,y} w(z^*_{x,y}, z^1_{x,y})$; {Second difference metric, 0°}

      $h_2(\mathbf{z}_2) = \sum_{x,y} w(z^2_{x,y}, z^*_{x,y}) + \sum_{x,y} w(z^*_{x,y}, z^2_{x,y})$; {Second difference metric, 90°}

      $f_2(\mathbf{x}) = f(\mathbf{g}(\mathbf{x}, \beta_1), \mathbf{g}(\mathbf{x}, \beta_2)) = h_2(\mathbf{z}_1) + h_2(\mathbf{z}_2)$; {Fitness evaluation, 2nd criterion}

      $\mathbf{f}(\mathbf{x}) = \{f_1(\mathbf{x}), f_2(\mathbf{x})\}$; {Fitness evaluation, all criteria combined done}

    DE selection:

$$\mathbf{x}_{i,G+1} = \begin{cases} \mathbf{u}_{i,G+1} & \text{if } \mathbf{f}(\mathbf{u}_{i,G+1}) \preceq \mathbf{f}(\mathbf{x}_{i,G}) \\ \mathbf{x}_{i,G} & \text{otherwise} \end{cases}; \text{ \{Multi-objective comparison operator\}}$$

      if not ($\mathbf{u}_{i,G+1} \preceq \mathbf{x}_{i,G}$ or $\mathbf{x}_{i,G} \preceq \mathbf{u}_{i,G+1}$) **then** add $\mathbf{u}_{i,G+1}$ to population archive;

  end for

  Truncate DE population archive to a size of NP using SPEA2 mechanism.

end for

return the best individuals obtained;

Experiment Design

- Sampling rate dimension of the rendered parametrized procedural model set to 250x250,
- the maximal number of strands in the tree $S = 410$,
- size of MOjDE population (approximation set) $NP = 100$,
- maximal number of fitness evaluations (FEs) $FEs = 10{,}000$,
- experiment repeat for $N_{runs} = 30$ independent runs,
- the remaining parameters were kept default as in original algorithms from their literature.

- Reference model to reconstruct:

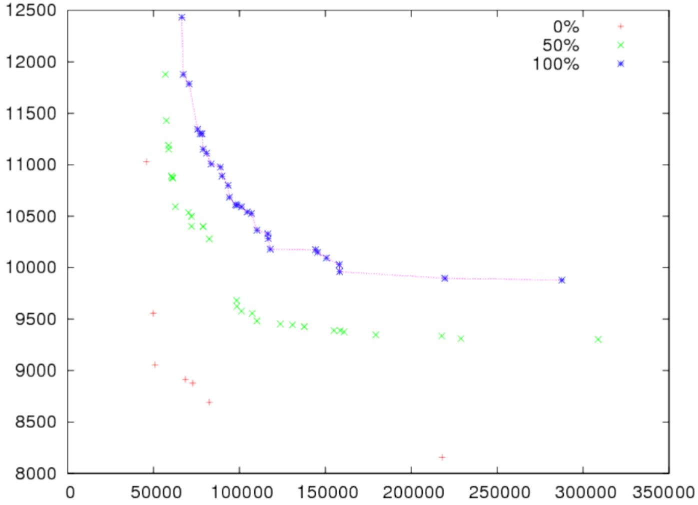
(rendered in EcoMod)

Evolution of a Sample Procedural Model

- Evolved projection image samples for first run ($RN_0 = 1$):
  - Pareto optimal individuals of a current population, through generations.

Rendered evolved models of final approximation set (run 1)

Attainment Surfaces: 0%, 50%, and 100% for NP=100.



Summary Conclusions

- An approach to design woody plant geometrical models,
- parameters of the procedural model are iteratively evolved using multi-objective differential evolution MOjDE algorithm
  - sampled randomly to reconstruct geometrical models,
- procedural models are rendered using EcoMod framework,
- rendered images are compared to the reference source images, for reconstruction, to guide the optimization process.
  - fitness is evaluated by two criteria, which are not pre-weighted,
  - multi-objective optimization finds multiple criteria trade-offs.
- Reconstruction approach results assessment
  - attainment surfaces (trade-offs distribution),
  - renderings of sample evolved models,
  - rendered final approximation set models.

Future Guidelines

- Prepare a combined approach of bi-criteria into single criteria by some sort of tradeoff,
- analyze assigned criteria tradeoff weights,
- segmentation procedures for automatic image alignment and base trunk recognition from natural landscape photography,
- parallell reconstruction of trees (LIDAR scanned forrest),
- use additional metric: volumetric data instead of black and white images,
- implement the application for mobile devices (+AR), and
- add interactive methods for optimization.

Thank you very much for listening!
YOU are welcome to join this research.

Also, greetings from Slovenia by A. Zamuda.

Questions and suggestions?