GENETIC PROGRAMMING FOR THE BOUNDARY RECONSTRUCTION IN CASE OF THE HEAT EQUATION

A. Marchenko[1]

[1]Ivan Franko National University of Lviv, Lviv, Ukraine

arkadii.marchenko@lnu.edu.ua

Boundary reconstruction problems arise in numerous engineering applications, including non-destructive testing and electrical impedance tomography. Classical iterative methods for such inverse problems typically rely on Fréchet derivatives, a good initial guess, and substantial analytical work. In this work we apply genetic programming [4] as a standalone method to the boundary reconstruction problem governed by the heat equation in two- and three-dimensional domains, circumventing the need for derivative information.

Consider a doubly connected domain $D \subset \mathbb{R}^d$, $d = 2, 3$, with inner boundary Γ_1 and outer boundary Γ_2, where each boundary is a non-intersecting simple closed curve (or surface for $d = 3$) of class C^2. The direct initial-boundary value problem for the heat equation reads

$$\begin{cases} \dfrac{\partial u}{\partial t} = \Delta u & \text{in } D \times [0, T], \\ u = f_\ell & \text{on } \Gamma_\ell \times [0, T], \quad \ell = 1, 2, \\ u(\cdot, 0) = 0 & \text{in } D, \end{cases} \tag{1}$$

where f_ℓ, $\ell = 1, 2$, are given smooth functions satisfying the compatibility condition $f_\ell(\cdot, 0) = 0$, and $T > 0$ is the final time. Problem (1) is well-posed; for a detailed analysis we refer to [3].

With $f_1 = 0$ and $f_2 \neq 0$, the inverse geometric problem consists of reconstructing the interior boundary Γ_1 from supplementary heat flux data on the outer boundary Γ_2,

$$\frac{\partial u}{\partial \boldsymbol{\nu}} = g_2 \quad \text{on } \Gamma_2 \times [0, T], \tag{2}$$

where g_2 is a given smooth function and $\boldsymbol{\nu}$ is the outward unit normal to $\Gamma = \Gamma_1 \cup \Gamma_2$. The inverse problem (1)–(2) belongs to the class of nonlinear ill-posed problems. It is well established that the unknown boundary Γ_1 can be uniquely identified from the Cauchy data on Γ_2, as stated in the following theorem proved in [3].

Theorem 1. *Let D and $\tilde{D}$ be two doubly connected domains with a common exterior boundary Γ_2 and interior boundaries Γ_1 and $\tilde{\Gamma}_1$, respectively. Denote by u and $\tilde{u}$ the classical solutions of (1) in D and $\tilde{D}$, respectively, with $f_1 = 0$ and $f_2 \neq 0$. If*

$$\frac{\partial u}{\partial \boldsymbol{\nu}} = \frac{\partial \tilde{u}}{\partial \boldsymbol{\nu}}$$

on $\Gamma_2 \times [0, T]$, then $\Gamma_1 = \tilde{\Gamma}_1$.

In this work, the technique of multi-gene genetic programming [1] as a standalone solver has been adopted. A population of candidate boundaries Γ_1 is evolved through an iterative selection and recombination procedure.

The interior boundary is assumed to be star-shaped and is parameterized by a radial function

$$\Gamma_1 = \begin{cases} r(s)(\cos s, \sin s),\ s \in [0, 2\pi], & d = 2, \\ r(\theta, \phi)(\sin\theta\cos\phi, \sin\theta\sin\phi, \cos\theta),\ \theta \in [0, \pi],\ \phi \in [0, 2\pi], & d = 3, \end{cases}$$

where $r : \mathbb{R}^{d-1} \to (0, \infty)$ is an unknown periodic function. Each individual $v^{(r)}$ encodes r as a linear combination of K symbolic trees (genes) f_i,

$$v^{(r)} = w_0 + \sum_{i=1}^{K} w_i f_i,\ w_i \in \mathbb{R},\ f_i : \mathbb{R}^{d-1} \to \mathbb{R}. \tag{3}$$

Recombination operators act on individual values defined by (3), followed by refitting the weights w_i via least squares. Crossover performs linear combination and gene blending, while mutation is responsible for gene exploration and fine-tuning.

The fitness of a candidate is given by the regularized functional of the inverse problem (1)–(2),

$$J(v^{(r)}) = \left\| \frac{\partial u^{(r)}}{\partial \boldsymbol{\nu}} - g_2 \right\|^2_{L_2(\Gamma_2)} + \alpha \left\| r \right\|_2^2, \quad \alpha > 0,$$

where $u^{(r)}$ denotes the solution of (1) for the candidate boundary defined by r. The forward problems are solved via the method of fundamental sequences [2], which reduces the parabolic problem (1) to a recursive sequence of modified Helmholtz problems.

The algorithm is formulated for two- and three-dimensional domains. Robustness of the proposed scheme is assessed on several numerical examples with exact and noisy data.

[1] Searson D.P., Leahy D.E., Willis M.J., GPTIPS: An Open Source Genetic Programming Toolbox for Multigene Symbolic Regression, *Lecture Notes in Engineering and Computer Science* **2180** (2010).

[2] Borachok I., Chapko R., A fundamental sequences method for an inverse boundary value problem for the heat equation in double-connected domains, *Inverse Problems and Imaging* **19** (2025), no. 3, 523–538.

[3] Chapko R., Kress R., Yoon J.-R., On the numerical solution of an inverse boundary value problem for the heat equation, *Inverse Problems* **14** (1998), no. 4, 853–867.

[4] Michalewicz Z., Genetic Algorithms + Data Structures = Evolution Programs, 3rd ed., Springer-Verlag, Berlin, 1996, xvi+340 pp.