Energy Landscape Analysis with Automated Region-of-Interest Selection via Genetic Algorithms

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32 **Abstract**

Understanding brain dynamics is essential for advancing cognitive and clinical
neuroscience. Energy landscape analysis (ELA), based on the pairwise maximum entropy
model, is a powerful framework to characterize brain activity as transitions among discrete
states defined by regional activity patterns. However, traditional ELA relies on the
subjective manual selection of a small subset of regions of interest (ROIs) from whole-brain
parcellations to satisfy mathematical constraints, which limits the scope and reproducibility
of ELA results due to subjective subset selection. To overcome this, we developed
ELA/GAopt, a meta-framework that utilizes a genetic algorithm to automate the selection of
ROI combinations from the entire atlas search space by optimizing a user-defined objective
function. In this study, we implemented a representative objective function balancing model
fitting accuracy with the inter-individual variability of model parameters. We applied
ELA/GAopt to three independent resting-state functional magnetic resonance imaging
datasets. In Scenario 1, using the Creativity dataset (OpenNeuro: ds002330, $n = 61$), the
ROI sets identified by ELA/GAopt achieved significantly higher objective function values
and pattern reproducibility than randomly selected ROI sets ($p < 0.05$). Additional validation
with the large-scale Human Connectome Project Young Adult (HCP-YA) dataset ($n = 270$)
confirmed the robustness of our framework in high-dimensional settings. Stability analysis
using Jaccard and Hamming metrics demonstrated that ELA/GAopt consistently identified
reproducible ROI subsets across independent optimization runs. In Scenarios 2-4, we
analyzed data from the Autism Brain Imaging Data Exchange II dataset using a site-disjoint
validation design to mitigate findings were robust against multi-site artifacts. ELA/GAopt
identified ASD-specific dynamics, where participants tend to visit local minima
characterized by global co-activation of selected ROIs within sensory-motor and visual
networks. These signatures were replicated in an independent cohort consisting of different
scanning sites. Furthermore, ROI sets optimized for one group (ASD or typically developing
controls) did not generalize to the other, highlighting distinct neurodynamic architectures.
These results demonstrate that ELA/GAopt provides a reproducible, data-driven pathway
for characterizing condition-specific brain dynamics, serving as a methodological basis for
future, harmonization-aware and externally validated biomarker studies.

Introduction

Interpreting system behavior from multidimensional observation data is essential in various scientific fields, including neuroscience. Energy landscape analysis (ELA) is one such method that applies the Ising model to multidimensional data, introducing the concept of energy to each pattern and visualizing the stability and transitions of emerging patterns as an energy landscape. The Ising model, also known as the pairwise maximum entropy model (pMEM) (Saberi et al., 2024; Watanabe et al., 2013), was initially introduced in statistical physics to explain the properties of magnetic materials. It is highly versatile and facilitates the interpretation of system dynamics as interactions between paired elements. The energy landscape derived from observed multidimensional data enables a bird's-eye view of the system's dynamics. A notable application in neuroscience was introduced by Watanabe, Hirose, et al. (2014), who applied the ELA to functional MRI (fMRI) data, establishing a data-driven approach to extract brain dynamics from neuroimaging data. Subsequently, Ezaki et al. (2017) investigated fundamental issues of ELA for neuroimaging data and developed the Energy Landscape Analysis Toolbox (ELAT). Their contributions have made ELA applicable to diverse neuroimaging datasets, including various neurological conditions and disorders (Saberi et al., 2024; Xing et al., 2024; Yamashita et al., 2021), and significantly advanced understanding in the neuroscience field (Ezaki et al., 2017, 2018; Hosaka et al., 2025; Jeong et al., 2021; Kang et al., 2019, 2021; Kondo et al., 2022; Saberi et al., 2024; Watanabe, Hirose, et al., 2014; Watanabe, Masuda, et al., 2014; Watanabe & Rees, 2017; Xing et al., 2024).

Despite its success, the current ELA paradigm faces several challenges due to its analytical constraints, including the length of data and the selection of the region of interest (ROI). The ELA requires sufficient data length to ensure the accurate fitting of the pMEM, which necessitates an exponential increase in the required data length with the number of variables, roughly doubling for each additional variable. Masuda et al. (2025) estimated that the practical upper limit for the number of ROIs (i.e., data dimension) that can be included in ELA without compromising accuracy is around 10 to 15, depending on the available data length (Masuda et al., 2025).

In contrast, whole-brain parcellation typically yields hundreds of regions, depending on the atlas used (e.g., 116 for the AAL (Tzourio-Mazoyer et al., 2002), 264 for the Power atlas (Power et al., 2011), and 100 to 1000 for the Schaefer 2018 atlas (Schaefer et al., 2018; Yeo et al., 2011)). This creates a significant gap between the available anatomical resolution (hundreds of regions provided by atlases) and the upper limit imposed by ELA's

mathematical constraints (approximately 10-15 regions mentioned above). Ideally, to find

the system that accurately represents brain dynamics, all possible combinations of regions

should be analyzed; however, selecting 10-15 ROIs from hundreds leads to a combinatorial

explosion, making an exhaustive search impossible. Due to this constraint, traditional

studies have relied on manual subset selection, such as selecting representative regions

involved in relevant cognitive processes based on prior research or choosing

representative regions from known functional networks. While these methods utilize

standard atlases, the choice of the ROI subset often remains subjective and hypothesis-

driven, which can hinder a more systematic, data-driven exploration of ELA outcomes.

To overcome these limitations, we propose ELA/GAopt, a genetic algorithm-based

optimization framework designed to automate ROI selection in ELA while ensuring model

fitting accuracy. Unlike traditional hypothesis-driven selection, our approach treats the

entire brain atlas as a search space to identify an optimal combination of ROIs that satisfies

the mathematical assumptions of pMEM. Genetic algorithms (GAs) are a class of heuristic

optimization techniques inspired by natural selection and evolution. They are widely used to

obtain approximate solutions for nonlinear optimization problems, and particularly suited for

this task due to their ability to navigate complex, non-linear search spaces through

population-based heuristic exploration, allowing for the discovery of interactions that simple

greedy methods such as recursive feature elimination might overlook (Bulut et al., 2025;

Vafaie & Imam, n.d.). In our proposed framework, ROI selection is formulated as a

combinatorial optimization problem where the objective function can be flexibly defined

according to specific research goals. As a representative example in this study, we employ

an objective function that incorporates both pMEM fitting accuracy and the inter-individual

variability of model parameters. This procedure eliminates the subjective bias inherent in

manual ROI selection, enabling a more systematic implementation of ELA—a critical

advancement for automated exploration of condition-specific brain dynamics.

The primary goal of this study is to establish ELA/GAopt as a methodological framework

that resolves ELA's dimensional constraints while preserving anatomical interpretability.

Unlike the conventional methods such as independent component analysis (ICA)-based

parcellations, clustering approaches, and machine learning-driven feature selection, our

focus is on identifying 'analysis-ready' ROI subsets specifically optimized for downstream

energy landscape modeling. To validate the effectiveness and robustness of our approach,

we evaluate it using three open neuroimaging datasets. First, we assess its generalizability

by testing whether the brain state dynamics identified using the proposed method are

reproducible on the dataset of healthy participants using both the Creativity dataset and the

Human Connectome Project Young Adult (HCP-YA) dataset. Then, we investigate its

clinical applicability by analyzing resting-state fMRI data from the Autism Brain Imaging

Data Exchange II (ABIDE II). This analysis enables us to investigate whether the method

can identify condition-specific patterns in brain state transitions between individuals with

autism spectrum disorder (ASD) and typically developing controls (CTL). These

applications demonstrate the potential of ELA/GAopt to enhance the objectivity and

reliability of brain dynamics modeling, thereby contributing to provide analysis-ready ROI

subsets under pMEM constraints.

141   Methods

142   Overview of ELA/GAopt: Energy landscape analysis with automated ROI

143   selection via genetic algorithms

The proposed ELA/GAopt framework aims to automate the selection of ROIs in ELA

through a combinatorial optimization approach. It involves iteratively selecting ROI subsets,

performing ELA, particularly fitting the pMEM, and evaluating the results until specified

conditions are met.

To solve this combinatorial optimization problem, we employ a GA. GAs are heuristic

optimization techniques characterized by multipoint exploration enabling the generation of

multiple candidate solutions (i.e., ROI subsets) in parallel. Each solution is evaluated using

a fitness function that quantifies the goodness of the solution, which is based on the ELA

output in this case. This strategy helps avoid local optima and improves the robustness of

the search process.

A schematic overview of ELA/GAopt in neuroimaging data is presented in Figure 1. The

following sections describe each component of the framework and detailed analysis

procedures.

Figure 1 Schematic overview of ELA/GAopt framework.

Framework of ELA

Binarization of multidimensional time series data

The input to ELA is an *N*-dimensional discrete time series obtained from *N* ROIs:

$$\{\boldsymbol{x}(1), \dots, \boldsymbol{x}(t_{\max})\}$$

where $\boldsymbol{x}(t) \in \mathbb{R}^N$ for $t \in \{1, \dots, t_{\max}\}$ is the ROI signal vector at time t, and $t_{\max}$ is the total number of time points (i.e., the length of the observed time series), Each vector $\boldsymbol{x}(t)$ is defined as:

$$\boldsymbol{x}(t) = \big(x_1(t), \dots, x_N(t)\big)$$

In ELA, multidimensional signals at each time point are converted into binary patterns. Each ROI signal $x_i(t)$ is binarized using a threshold θ_i, where $i \in \{1, \dots, N\}$. The binarized value $\sigma_i(t) \in \{-1, +1\}$ is defined as:

$$\sigma_i(t) = \begin{cases} +1 & \text{if } x_i(t) > \theta_i \\ -1 & \text{otherwise} \end{cases}$$

The full binarized vector at each time point *t* is:

$$\boldsymbol{\sigma}(t) = \big(\sigma_1(t), \dots, \sigma_N(t)\big)$$

Each $\sigma_i(t)$ represents the binary activation state of the *i*-th ROI at time t, where $+1$ indicates "active" and -1 indicates "inactive". Thus, the signal pattern at time t is given by the *N*-dimensional binary vector $\boldsymbol{\sigma}(t)$, also referred to as an activity pattern or active pattern. For notational simplicity, the time index t may be omitted where appropriate. In total, there are 2^N possible activity patterns, representing all binary combinations of ROI states.

Fitting a pMEM

A pMEM is fitted to binarized time series data to estimate the energy associated with each

observed signal pattern. For neuroimaging data, this allows modeling the distribution and

dynamics of brain states based on observed frequencies of binary activation patterns. First,

we compute the empirical distribution $P_{\text{empirical}}(\boldsymbol{\sigma})$ which represents the relative frequency

of each activity pattern observed in the data (Figure 1D). Let $\boldsymbol{\sigma}^{(1)}, \ldots, \boldsymbol{\sigma}^{(2^N)}$ denote all

possible binary activity patterns. Then, $P_{\text{empirical}}(\boldsymbol{\sigma})$ is simply the proportion of time points

where pattern $\boldsymbol{\sigma}$ occurs, calculated by:

187
$$\sum_{k=1}^{2^N} P_{\text{empirical}}\left(\boldsymbol{\sigma}^{(k)}\right) = 1$$

188   That is, the empirical frequency distribution $P_{\text{empirical}}(\boldsymbol{\sigma})$ is calculated by counting how

189   many times each of the 2^N possible binary patterns appear in the binarized time series

190   and dividing by the total number of time points. The empirical mean signal pattern of the i-

191   th ROI is:

192
$$\langle \sigma_i \rangle_{\text{empirical}} = \frac{1}{t_{\max}} \sum_{t=1}^{t_{\max}} \sigma_i(t)$$

193   The empirical pairwise correlation between the i-th and j-th ROIs is:

194
$$\langle \sigma_i \sigma_j \rangle_{\text{empirical}} = \frac{1}{t_{\max}} \sum_{t=1}^{t_{\max}} \sigma_i(t)\sigma_j(t)$$

195   The pMEM estimates a probability distribution $P(\boldsymbol{\sigma})$ that matches these first- and second-

196   order moments while maximizing entropy. The result is the Boltzmann distribution:

197
$$P(\boldsymbol{\sigma}) = \frac{e^{-E(\boldsymbol{\sigma})}}{\sum_{k=1}^{2^N} e^{-E(\boldsymbol{\sigma}^{(k)})}}$$

198   Equivalently, the distribution can be expressed in terms of model parameters $\boldsymbol{h}$ and $\boldsymbol{J}$ as:

199
$$P(\boldsymbol{\sigma}|\boldsymbol{h},\boldsymbol{J}) = \frac{e^{-E(\boldsymbol{\sigma}|\boldsymbol{h},\boldsymbol{J})}}{\sum_{\{\boldsymbol{\sigma'}\}} e^{-E(\boldsymbol{\sigma'}|\boldsymbol{h},\boldsymbol{J})}}$$

200   with the energy function:

201
$$E(\boldsymbol{\sigma}|\boldsymbol{h},\boldsymbol{J}) = -\sum_{i=1}^{N} h_i \sigma_i - \frac{1}{2}\sum_{i=1}^{N}\sum_{i=1,j\neq 1}^{N} J_{ij}\sigma_i\,\sigma_{ij}$$

This formulation models the energy of each pattern based on ROI-wise signal tendencies

(h_i) and pairwise interactions among ROIs (J_{ij}).

In this study, the model parameters $\boldsymbol{h}$ and $\boldsymbol{J}$ were estimated by pseudo-likelihood

maximization, following the implementation described by Ezaki et al. (2017). Full details of

the fitting procedure, including gradient ascent optimization, are available in their original

publication. Specifically, we used a Python implementation of the ELA toolbox developed by

Oku (2023/2025) (https://github.com/okumakito/elapy).

Accuracy metrics for pMEM fitting

To evaluate the quality of the fitted pMEM, we used two metrics that quantify how well the

model approximates the empirical distribution of signal patterns. The first indicator is

defined as:

213
$$\frac{I_2}{I_N} = \frac{S_1 - S_2}{S_1 - S_N}$$

214 where S_k is the Shannon entropy of the MEM considering k-order correlations. It is

215 calculated as:

216
$$S_k = -\sum_{\sigma \in \Sigma} P_k(\boldsymbol{\sigma}) \log P_k(\boldsymbol{\sigma})$$

217 Here, $P_1(\boldsymbol{\sigma})$ corresponds to the independent MEM, $P_2(\boldsymbol{\sigma})$ to the pairwise MEM and $P_N(\boldsymbol{\sigma})$

218 to the empirical distribution observed in the data.

219 The second indicator is based on Kullback-Leibler (KL) divergence and is defined as:

220
$$r = \frac{D_{\mathrm{KL}}(P_1(\boldsymbol{\sigma})||P_N(\boldsymbol{\sigma})) - D_{\mathrm{KL}}(P_2(\boldsymbol{\sigma})||P_N(\boldsymbol{\sigma}))}{D_{\mathrm{KL}}(P_1(\boldsymbol{\sigma})||P_N(\boldsymbol{\sigma}))}$$

221 where the KL divergence is computed as:

222
$$D_{\mathrm{KL}} = \sum_{k=1}^{2^N} P_{\mathrm{empirical}}\left(\boldsymbol{\sigma}^{(k)}\right) \log_2 \frac{P_{\mathrm{empirical}}(\boldsymbol{\sigma}^{(k)})}{P_l(\boldsymbol{\sigma}^{(k)})}$$

Here, D_{KL} quantifies the dissimilarity between the empirical distribution $P_{\mathrm{empirical}}(\boldsymbol{\sigma})$ and

the distribution of signal patterns estimated by the l-th order MEM $P_l(\boldsymbol{\sigma})$ $(l = 1, 2)$.

In this study, the arithmetic mean of above two metrics was used as the quality measure

of a pMEM fitting.

Personalization of pMEM via temperature optimization

In standard ELA, individual data is concatenated into a group-level dataset to estimate a

single set of $\boldsymbol{h}$ and $\boldsymbol{J}$ parameters representing group characteristics. Although it is

theoretically possible to fit pMEM to individual data, this approach is rarely adopted in

practice because it requires a large amount of data to achieve stable estimation. For

example, in typical fMRI datasets, the number of time points per individual is often

insufficient to reliably estimate all parameters of the model. Therefore, pMEM is typically

estimated using concatenated group-level data for robustness and accuracy. However,

when individual variability needs consideration, personalization of the pMEM becomes

essential. Ruffini et al. (2023) proposed a two-step pMEM parameter optimization method

in which the inverse temperature parameter β, which characterizes the Boltzmann

distribution, is optimized for each individual data while keeping the group-derived $\boldsymbol{h}$ and $\boldsymbol{J}$

parameters fixed. This approach allows group-level trends to be captured by $\boldsymbol{h}$ and $\boldsymbol{J}$,

while individual differences are partly parameterized by β within this personalization

scheme. Here, we use β as a practical personalization parameter without asserting it as

the sole source of inter-individual variability.

Here, the distribution for the individual is defined as:

244
$$P(\boldsymbol{\sigma}|\boldsymbol{h},\boldsymbol{J},\beta) = \frac{e^{-\beta E(\sigma|\boldsymbol{h},\boldsymbol{J})}}{\sum_{\{\sigma'\}} e^{-\beta E(\sigma'|\boldsymbol{h},\boldsymbol{J})}}$$

245   The optimization of β is performed by maximizing the approximate log-likelihood using a

246   gradient ascent algorithm. The update rule is:

247
$$\beta^{\text{new}} - \beta^{\text{old}} = -\varepsilon\left(\langle E\rangle_{\text{empirical}} - \langle E\rangle_{\tilde{P}}\right)$$

248   Where ε is the step size of the gradient ascent, $\langle E\rangle_{\text{empirical}}$ is the average energy

249   computed from the data, and $\langle E\rangle_{\tilde{P}}$ is the model-based expected energy. These are derived

250   from the log-likelihood expression:

251
$$\log\mathcal{L}(\boldsymbol{h},\boldsymbol{J}) = \sum_{t=1}^{t_{\max}} \log P(\sigma(t)|\boldsymbol{h},\boldsymbol{J}) = \sum_{t=1}^{t_{\max}} \left(-\beta E(\sigma(t)|\boldsymbol{h},\boldsymbol{J}) - \log Z(\boldsymbol{h},\boldsymbol{J},\sigma_{/i}(t),\beta)\right)$$

252
$$Z(\boldsymbol{h},\boldsymbol{J},\beta,t) = \sum_{\sigma_i'} \exp\left[-\beta E_i(\sigma_i'|\boldsymbol{h},\boldsymbol{J},\sigma_{/i}(t))\right]$$

253
$$\langle E\rangle_{\tilde{P}} = -h_i\langle\sigma_i\rangle_{\tilde{P}} - \sum_{j\neq i\leq N} J_{ij}\langle\sigma_i\sigma_j\rangle_{\tilde{P}}$$

This procedure enables the personalization of the energy landscape while preserving

group-level structure. The implementation in this study closely followed the approach

described by Ruffini et al. (2023) and all equations and optimization steps are reproduced

here for clarity and reproducibility.

Energy landscape and local minimum

By fitting a pMEM to the observed time series, the energy associated with any given

pattern $\boldsymbol{\sigma}$ can be estimated. Since each pattern $\boldsymbol{\sigma}$ lies in a high-dimensional binary space

defined over N ROIs, its neighboring patterns are those that differ from $\boldsymbol{\sigma}$ by exactly one

bit (i.e., Hamming distance = 1). For example, consider $\boldsymbol{\sigma} = (1, 1, -1, 1)$ with $N = 4$. This

pattern has four neighbors obtained by flipping each element. These N neighbors form

vertices of an N-dimensional hypercube surrounding $\boldsymbol{\sigma}$. This structure allows us to
interpret the temporal dynamics as transitions among vertices within this energy-defined
space (that is, energy landscape).

Under the Boltzmann distribution, states with lower energy tend to appear more frequently,
making local minima in the energy landscape particularly important. In ELA, such local
minima are interpreted as representative signal patterns (states). The dynamics between
these stable patterns, that is, how the system transitions from one to another, provide
insights into the system structure. Moreover, the characteristics of the constructed energy
landscape can be visualized using a contour plot, which highlights the energy barriers
between local minima, as shown in Figure 1E.

Automated ROI selection using a genetic algorithm
We introduce a mechanism to automatically determine the optimal subset of ROIs within
the aforementioned ELA framework. In this study, we formulate ROI selection as a
combinatorial optimization problem. To provide a representative example of how this
optimization can be implemented, the goal is set to select a subset of ROIs that maximizes
the quality of the pMEM fitting while capturing individual variability.

A critical aspect of combinatorial optimization is defining the objective function, which
quantifies how well a candidate solution satisfies the desired properties. In this work, we
define the objective function as the sum of:
● The fitting accuracy of the pMEM is represented by the similarity between the model
and empirical distributions.
● The variance of the personalized inverse temperature parameter (β) across all
participants, derived from the individualized Boltzmann distribution.

Here, the first term ensures the sufficient accuracy of pMEM fitting with the chosen ROIs,
and the second is incorporated as a heuristic to maintain sensitivity to inter-individual
variation in the energy landscape, preventing the selection of ROIs that merely maximize
the fit to the population mean at the expense of inter-individual diversity. By using β as a
parameter to account for these differences, we aim to identify ROI subsets that may better
capture the individual dynamical characteristics of each participant's brain state.

Let $\boldsymbol{x} \in \{0,1\}^d$ be a binary vector encoding the selection of d ROIs available, where
$x_k = 1$ if the k-th ROI is selected and zero otherwise, and $N \leq d$ is the total number of
ROIs to select. Then, the optimization problem is formulated as:

296
$$\text{Maximize } f(\boldsymbol{x}) = r(\boldsymbol{x}) + \frac{1}{m} \sum_{k=1}^{m} (\beta_k(\boldsymbol{x}) - \bar{\beta})^2$$

297
$$\text{subject to } \sum_{k=1}^{d} x_k = N$$

Here, $r(\boldsymbol{x})$ denotes a pMEM fitting accuracy when ROIs specified by $\boldsymbol{x}$ are used, and

$\beta_k(\boldsymbol{x})$ is the optimized inverse temperature for the k-th participant using the selected ROI

subset $\boldsymbol{x}$. The mean value of $\beta_k(\boldsymbol{x})$ for m participants is denoted by $\bar{\beta}$. The constraint

ensures that exactly N ROIs are selected from the d available candidates.

This objective function can be flexibly determined based on the analysis goals. For

example, if the analyst expects the pMEM model parameters to correlate with data

features, such correlations can be included as an additional term in the objective function.

The objective function defined above serves as a representative instance to demonstrate

the framework's utility; however, the framework itself is independent to the specific choice

of metrics, allowing users to incorporate various criteria depending on their research

questions. By optimizing this function with a GA, the proposed framework enables data-

driven selection of ROI subsets.

Regarding the search scope, the optimization process in ELA/GAopt performs a global

search to identify a single, optimal ROI subset that is common across all participants within

a study group. In this study, the optimization does not involve subject-level ROI selection;

instead, it evaluates the fitness of candidate ROI sets based on the pMEM fitting accuracy

and inter-individual variability, both of which are derived from the same cohort of

participants. At each evaluation step of the GA's objective function, the inverse temperature

parameter β is individually optimized for every participant using the gradient ascent

algorithm detailed in the previous section ("Personalization of pMEM via temperature

optimization"). These optimized β parameters, derived for all participants, are then used to

calculate the inter-individual variability term in the objective function.

For the implementation of a GA, we used a standard evolutionary framework based on

Holland's original design (Baeck et al., 2018), using the Deap library (F.-A. Fortin et al.,

2012). We employed tournament selection, two-point crossover, and bit-flip mutation. To

ensure the feasibility of the solutions, we incorporated a repair strategy called Lamarckian

repair (Ishibuchi et al., 2005), which iteratively modifies infeasible solutions until they satisfy

the specified constraints. Specifically, if the number of selected ROIs exceeds the

prescribed limit, a subset of ROIs with a value of 1 (i.e., indicating selection) is randomly

chosen and flipped to 0. The GA iteratively explored the optimal combinations of the ROIs

for ELA. The full implementation details and parameter settings are provided in Algorithm 1

and Table 1, respectively.

Algorithm 1. Procedure of a genetic algorithm.

331	1:	Initialize $k \leftarrow 0$
332	2:	Initialize population $P(k)$ with binary vectors
333		(each gene = 1 if the corresponding ROI is selected)
334	3:	Evaluate fitness of all individuals in $P(k)$
335	4:	**while not** converged **do**
336	5:	Select individuals from $P(k)$ via tournament selection
337	6:	Apply two-point crossover to selected individuals to generate offspring $Q(k)$
338	7:	Apply bit-flip mutation to $Q(k)$
339	8:	Apply Lamarckian repair to $Q(k)$ to enforce constraint feasibility
340	9:	Evaluate fitness of all individuals in $Q(k)$
341	10:	Replace population $P(k)$ with $Q(k)$ (full replacement)
342	11:	Increment $k \leftarrow k + 1$
343	12:	**end while**

344 **Table 1 Parameters of GA.**

GA Parameter	Value
Population size	100
Gene length	160 for Scenario 1(Creativity dataset),
	264 for Scenario 1 (HCP-YA dataset) and Scenarios 2-4
Number of generations	1000
Crossover method	Two-point crossover
Crossover rate	1.0
Mutation rate	1/ Gene length
Selection method	Tournament selection (tournament size: 3)
Trial	100

The source code for our proposed ELA/GAopt, along with example data and step-by-step

usage instructions, is publicly available on GitHub at https://github.com/MIS-Lab-

Doshisha/ela-gaopt. The repository includes a README file that details the installation

process, data formatting, and execution of the pipeline. This facilitates easy adoption by

new users.

Datasets

To evaluate the performance and generalizability of the proposed ELA/GAopt framework,

we applied it to three independent resting-state fMRI datasets. In the following sections, we

overview the datasets used, including their preprocessing methods, as well as the analysis

scenarios that utilize these datasets.

Creativity Dataset

We employed a publicly available dataset related to creativity, hosted on OpenNeuro

(dataset ID: ds002330) (Sunavsky & Poppenk, 2020). A total of 66 healthy adults

completed a neuroimaging session and four creativity assessments: the Abbreviated

Torrance Test for Adults (ATTA) in verbal and visual formats, the Creative Behavior

Inventory (CBI), and the Creative Achievement Questionnaire (CAQ). One participant did

not complete the ATTA due to logistical reasons. The sample consisted of 29 males, 36

females, and one non-binary individual, with a mean age of 26.6 years (SD = 4.3).

MRI data included T1- and T2-weighted structural images, resting-state fMR images, and

diffusion-weighted images (DWIs). After excluding participants with missing ATTA scores or

insufficient data quality, the final analytic sample included 61 participants. These were

stratified into a discovery set ($n = 31$) and a test set ($n = 30$) based on their ATTA verbal

scores. The descriptive characteristics of two subsets are provided in Table 2.

Table 2 Basic descriptive characteristics of discovery and test sets.

	Data validation	
	Discovery	Test
N	31	30
CBI score	0.904 ± 0.509	0.941 ± 0.541
ATTA verbal score	16.300 ± 6.415	14.516 ± 6.597
ATTA visual score	29.017 ± 12.058	29.403 ± 10.139
CAQ score	4.172 ± 1.411	3.873 ± 1.769

ABIDE II Dataset

We used data from the Autism Brain Imaging Data Exchange II (ABIDE II), which provides

a large multi-site resting-state fMRI and anatomical dataset for investigating ASD. Data

from 17 sites were included after excluding two sites due to preprocessing incompatibility.

The original dataset included 1,114 participants (ASD: 521, CTL: 593); 81 participants were

removed due to preprocessing issues, resulting in a final sample of 1,033 participants.

Each remaining participant provided at least one resting-state fMRI scan and a high-

resolution T1-weighted structural image. Basic demographic and cognitive data (e.g., age,

sex, IQ) were available for all individuals. Detailed acquisition protocols and site-specific

procedures are described in the related publications (Di Martino et al., 2014, 2017).

To balance site-specific variance, we grouped the dataset into three cohorts of

approximately 300 participants each (A, C, and D) and an additional cohort (B) of around

100 participants used for independent validation. The distribution of participants across

sites and cohorts is provided in Table 3.

Table 3 Distribution of creativity indicators in each cohort of ABIDE II Dataset.

Cohort	Sites	Total N	N: ASD	N: Control
A	NYU1, ONRC, SDSU, TCD, UCD, UCLA	293	157	136
B	OHSU, USM	126	54	72
C	IU, KKI, KUL, NYU2	306	131	175
D	BNI, EMC, ETH, GU, IP	308	140	168

HCP-YA Dataset

We also utilized the Human Connectome Project Young Adult (HCP-YA) 2025 release

dataset as a large-scale benchmark for healthy participants (Feinberg et al., 2010; Moeller

et al., 2010; Setsompop et al., 2012; Van Essen et al., 2013; Xu et al., n.d.). The HCP-YA

dataset provides a comprehensive investigation of brain function and structure in 1,113

healthy young adults aged 22–35 years. After excluding participants with missing data or

insufficient image quality, a final analytic sample of 1,009 individuals was retained. From

this sample, we extracted two independent subsets with balanced age distributions: a

discovery set ($n = 180$) and a test set ($n = 90$). The discovery set had a mean age of 27.17

years (SD = 3.30), while the test set had a mean age of 27.54 years (SD = 3.77). A Welch's

t-test confirmed that there were no statistically significant age differences between these

two subsets ($p = 0.42$).

Data preprocessing

Three independent datasets, the Creativity dataset, the ABIDE II dataset and HCP-YA

dataset, were preprocessed in the following steps. It should be noted that the ABIDE II and

HCP-YA data were originally provided in non-BIDS format and were converted to BIDS

format using the procedure outlined by Ran et al.

(https://github.com/thebrisklab/ABIDE_Preprocessing) (Brain Research in Imaging

Statistics Kit, 2022/2024) and Suyash et al (https://github.com/suyashdb/hcp2bids)

(Suyash, 2016/2025). For the ABIDE II dataset, the first five volumes were excluded to

remove non-equilibrium effects of magnetization. This exclusion step was not applied to the

Creativity dataset due to its limited number of subjects and time points. For the HCP-YA

dataset, no slice timing correction was performed following to the prior study (S. M. Smith

et al., 2013). Functional MR images from both datasets were then preprocessed using

fMRIPrep version 23.1.4, a robust and standardized preprocessing pipeline built on Nipype.

First, a reference volume was generated from each run to use as a reference for head

motion correction. The head motion parameters (transformation matrix and six parameters

corresponding to translations and rotations) for this reference image were then estimated

before spatiotemporal filtering was performed. Slice timing correction was further performed

to correct the temporal misalignment of each slice. The EPI image was then aligned with

the T1w image in six degrees of freedom using boundary-based registration.

Several confounding time series were subsequently estimated from the preprocessed

BOLD data, including framewise displacements (FD), DVARS, and global signals from the

cerebrospinal fluid (CSF), white matter (WM), and whole-brain mask.

Further preprocessing was carried out using the Nilearn package in Python (*Nilearn*, n.d.).

This included spatial smoothing with a Gaussian kernel (FWHM = 6 mm), high-pass filtering

at 0.01 Hz, low-pass filtering at 0.1 Hz, and regressing out of confounding variables ("high-

pass", "motion", "wmcsf", "scrub"). The denoising strategy followed established procedures

in prior studies (H.-T. Wang et al., 2023).

Additionally, we used different atlases for each dataset: the Dosenbach atlas for Creativity

Dataset ($d = 160$) (Dosenbach et al., 2006, 2007, 2010; Fair et al., 2009; Fox et al., 2005),

and the Power 264 atlas for HCP-YA and ABIDE II Dataset ($d = 264$) (Power et al., 2011),

respectively. The BOLD time courses were extracted from the spherical mask with a 4 mm

radius centered at each ROI coordinate, then averaged within the ROI. The average time

courses were considered representative of brain activity in each ROI. Finally, the ROI-

averaged activity data was then binarized using the threshold of the time-averaged value of

each activity for the ELA input.

Statistical analysis

Statistical analyses were conducted independently for each scenario, as they addressed

distinct research questions using different datasets. False Discovery Rate (FDR) correction

using the Benjamini-Hochberg procedure was applied to all multiple comparisons, with the

significance level set at adjusted $p < 0.05$. Specifically, FDR correction was applied to: (1)

the comparison of optimized vs. randomly selected ROI sets in Scenario 1 (permutation

tests for objective function values and Hamming distances), (2) the binomial tests for ROI

selection frequency across all scenarios, and (3) the tests for occurrence probabilities of

local minimum patterns in Scenario 2 (corrected for the number of identified patterns).

Scenario 1: Validation of generalizability of ELA/GAopt using the Creativity

dataset and HCP-YA dataset

The objective of Scenario 1 was to evaluate whether the proposed automated ROI

selection method avoids overfitting and selection bias. To ensure a rigorous evaluation, the

partition between the discovery and test datasets was maintained at the subject level and

remained fixed throughout across all 100 optimization runs. The GA-based optimization

was conducted exclusively on the discovery dataset; the test dataset was completely

excluded from the optimization process and reserved solely for independent validation. We

applied ELA/GAopt to the discovery dataset in 100 independent runs, each with a different

initial GA population and a different random seed, resulting in 100 optimized ROI sets.

Following Ezaki et al. (2017), who demonstrated that the accuracy of pMEM fitting scales

with $l/2^N$ (i.e., the average number of visits per activity pattern), the number of ROIs in

Scenario 1(Creativity dataset) was fixed at 10 ($N = 10$). They reported that each activity

pattern should be visited approximately 5 and 16 times on average to achieve accuracies of

0.8 and 0.9, respectively. For the $l = 9170$ data points in this scenario, choosing $N = 10$

($2^{10} = 1024$) yields $l/2^N \approx 9.0$ visits per pattern, which lies between 5 and 16; thus, we

expect an accuracy between 0.8 and 0.9. Moreover, to ensure the generalizability of the

results, we performed the same analysis on the HCP-YA dataset ($n = 270$). This larger

sample size allowed us to further validate our method by testing a higher-dimensional

model with 15 ROIs ($N = 15$), while still maintaining sufficient data volume per pattern to

ensure robust pMEM fitting.

With the resulting ROIs chosen by ELA/GAopt for 100 trials, a one-tailed binomial test was

performed to assess whether each brain region was selected more frequently than

expected by chance. False discovery rate (FDR) correction was performed for multiple

comparisons. To quantify the effect size for these binomial comparisons, Cohen's h was

calculated. This process ensured the detection of consistently selected ROIs for multiple

GA optimization runs.

Furthermore, to quantify the stability of ROI selection across the 100 independent GA

runs, we conducted a pairwise similarity analysis. Each optimized ROI set was represented

as a binary vector $\mathbf{v} \in \{0, 1\}^d$, where d denotes the total number of candidate regions in

the atlas; elements were set to 1 for selected ROIs and 0 otherwise. We then calculated

471 pairwise overlaps across all possible combinations of the 100 optimized ROI sets ($\binom{100}{2} =$

472 $4,950$) using two metrics: the Hamming distance, which counts the number of differing bits

473 between two vectors, and the Jaccard index, defined as the size of the intersection divided

474 by the size of the union of the selected ROI sets. For comparison, these metrics were also

475 computed for 100 randomly selected ROI sets. The distributions of these metrics were

476 compared between the optimized and random groups using the Mann-Whitney U test, with

477 statistical significance assessed at $p < 0.05$. Additionally, Cohen's d was calculated to

478 quantify the effect size of the observed differences in stability between the optimized and

479 random ROI sets.

480 Next, each of the 100 optimized ROI sets was applied to the test dataset using standard

481 ELA. In parallel, we generated 100 randomly selected ROI sets, each also consisting of 10

482 ROIs for Creativity data and 15 ROIs for HCP-YA data. Then we applied them to both the

483 discovery and test datasets using the same ELA procedure. In total, this yielded two groups

484 of ROI sets, optimized, and randomly selected, for comparative analysis.

485 We tested two hypotheses: 1) the optimized ROI sets provide better objective function

486 values (i.e., the sum of pMEM fitting accuracy and inter-individual variance of the inverse

487 temperature) than random sets, and this advantage generalizes to the test data, and 2) the

488 local minimum patterns identified in the discovery dataset are reproducible in the test

489 dataset.

490 For Hypothesis 1, we compared the objective function values of the optimized and random

491 ROI sets on the test dataset using permutation testing. Specifically, the objective values

492 from both sets were pooled and the group labels (optimized vs. random) were shuffled

493 10,000 times to generate a null distribution. For each permutation, the mean objective

494 value for each group was computed. A p-value was then derived by comparing the actual

495 difference in mean objective values between the optimized and random groups to this null

496 distribution. Statistical significance was assessed at $p < 0.05$. In addition, effect size

497 (Cohen's d) was calculated to quantify the observed differences between optimized and

498 random ROI sets.

499 For Hypothesis 2, we quantified the similarity of local minimum patterns between the

500 discovery and test datasets. Each pattern among the 2^N possible signal patterns (for N

501 ROIs) were assigned a unique ID. For each ELA run, we generated an ID vector indicating

502 the presence (1) or absence (0) of each pattern as a local minimum in the estimated energy

503 landscape. We then calculated the Hamming distance between ID vectors from the

504 discovery and test datasets for each ROI set. A smaller Hamming distance indicates

greater reproducibility of the local minimum patterns. The Hamming distances of the

optimized and random ROI sets were compared using a permutation test (with 10,000

permutations), with significance assessed at $p < 0.05$. In addition, Cohen's d was

computed to quantify the effect size of the difference in the Hamming distance. All

permutation tests were one-tailed.

Scenario 2: Group-level comparison of brain dynamics on the ABIDE II Dataset

Scenario 2 investigated whether the different brain dynamics of two separate groups were

observed on the single energy landscape constructed using ELA/GAopt on the

concatenated dataset. Specifically, we aimed to observe group-specific brain dynamics on

the energy landscape estimated on the mixed dataset of ASD and CTL groups, in a fully

data-driven manner using ELA/GAopt. To confirm this, we extract the local minimum

patterns more frequently visited in each group.

To ensure a rigorous evaluation and avoid selection bias, the partition between the

discovery and test datasets was maintained at the subject level and remained fixed across

all optimization runs. The GA optimization was conducted exclusively on the discovery

dataset (Cohort A: $n = 293$; 157 ASD and 136 CTL); the test dataset (Cohort B: $n = 126$;

54 ASD and 72 CTL) was completely excluded from the optimization process and reserved

solely for independent validation. The number of selected ROIs for the ABIDE II dataset in

Scenarios 2 was fixed at 13, following the same procedure as in Scenario 1. Regarding the

search scope, ELA/GAopt performed 100 independent optimization runs on the entire

discovery cohort to identify single, optimal ROI subsets common across all participants in

the cohort. Then, we evaluated how frequently each ROI was selected across trials. To

determine whether specific ROIs were selected more frequently than expected by chance,

a binomial test was performed for each ROI. The test assessed whether the observed

selection frequency exceeded the expected frequency under a null hypothesis of random

selection. The resulting p-values were corrected for multiple comparisons using FDR

correction, and statistically significant ROIs (FDR-adjusted $p < 0.05$, one-tailed) were

identified. To quantify the magnitude of deviation from chance-level selection, Cohen's h

was calculated as the effect size. Furthermore, to quantify the algorithmic stability, we

evaluated the consistency of the optimized ROI sets using the pairwise Jaccard index and

Hamming distance, following the same procedure described in Scenario 1. ROI sets

identified as significant in the binomial tests were considered consistently important and

served as the basis for further group comparisons.

538  To perform group-level comparisons of local minimum patterns, we selected

539  representative ELA/GAopt trials in which all selected ROIs were among those identified as

540  statistically significant in the above binomial tests. These representative trials then

541  estimated energy landscapes, and the probability of visiting each local minimum was

542  computed for all individuals.

543  To compare these probabilities between the ASD and CTL groups, we applied the Mann-

544  Whitney U test for each identified local minimum (FDR-adjusted $p < 0.05$, two-tailed). To

545  quantify group difference magnitude, we also calculated the effect size (r) based on the Z-

546  statistic from the Mann-Whitney U test. To evaluate the robustness of observed group-

547  level differences, the same analysis was repeated on an independent validation dataset

548  (Cohort B), following the same ROI configuration and statistical testing procedures.

549  **Scenarios 3 and 4: Estimation of ASD- or CTL-optimized energy landscapes on**

550  **the ABIDE II Dataset**

551  In Scenario 3, we investigated whether a set of ROIs optimized for the ASD group could

552  yield distinctive brain state characteristics. The GA-based optimization was performed

553  exclusively on the ASD group (Cohort C, $n = 131$); to prevent overfitting and selection bias,

554  the CTL group (Cohort C, $n = 175$) from the same cohort was maintained as an

555  independent test set and was completely excluded from the optimization process. The

556  number of selected ROIs was fixed at 12, following the same procedure as in Scenario 1.

557  As in Scenario 2, we assessed the selection frequency of each ROI across trials and

558  identified consistently selected ROIs using a binomial test (FDR-adjusted $p < 0.05$, one-

559  tailed). For these binomial tests, Cohen's h was calculated as the effect size.

560  The resulting ASD-optimized ROI set was then applied to an independent CTL dataset

561  (175 participants from Cohort C) to evaluate whether the same ROI configuration would

562  produce distinct energy landscape characteristics. Specifically, the number of local minima

563  identified in the CTL group was compared to that in the ASD group using the Mann-Whitney

564  U test. To quantify the magnitude of group differences, we also calculated the effect size

565  (r) based on the Z-statistic from the Mann-Whitney U test (two-tailed). We hypothesized

566  that if the ASD-optimized ROIs reflect ASD-specific brain state dynamics, applying them to

567  CTL data would result in significantly different energy landscape structures—particularly in

568  the number or configuration of local minima—between the two groups.

569  Scenario 4 mirrored this procedure for the CTL group. The GA optimization was conducted

570  exclusively on the CTL participants (Cohort D, $n = 168$), while the ASD group (Cohort D,

571  $n = 140$) served as an independent test set. The optimization involved 100 global runs on

the CTL discovery cohort to identify single, optimal ROI subsets. ROI selection analysis and

statistical testing were conducted in the same manner as in Scenario 3. We hypothesized

that if the CTL-optimized ROIs captured control-specific dynamics, applying them to ASD

data would similarly yield distinct energy landscape structures. Finally, to quantify the

algorithmic stability of ROI selection, we calculated the pairwise Jaccard index and

Hamming distance across the 100 runs for both groups, following the same procedure

described in Scenario 1.

Computational environment

We used a computing workstation equipped with an Intel Core (TM) i9-14900K CPU, a 7.7

GHz 24-core processor, and an NVIDIA GeForce RTX 4080 16GB GPU for ELA/GAopt

execution.

Result

Scenario 1

First, we summarize the results of Creativity dataset. Supplementary Figure 1 shows the

convergence of the objective function with ELA/GAopt over 1000 generations for 100 runs

with different starting populations. As the optimization problem was formulated as a

maximization task, the objective function value increased with each generation. All runs

converged to a range between 1.00 and 1.10.

Based on the 100 ELA/GAopt runs, a binomial test was conducted to assess whether

each ROI was selected more frequently than expected by chance. Eighteen ROIs were

statistically significant after FDR correction ($p < 0.05$), as listed in Figure 2 and

Supplementary Table 1, which also includes the anatomical coordinates and associated

functional networks for each ROI. Additionally, the distribution of selected ROIs across the

100 runs is presented in Supplementary Figure 2, which shows the total number of times

each ROI was selected. Furthermore, evaluation of the stability of the entire ROI set across

repeated runs are shown in Figure 3. The pairwise Hamming distances between optimized

ROI sets (ROI selection vectors) were significantly smaller than those between random

sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's d: 3.57, Figure 3A).

Additionally, the pairwise Jaccard index between optimized ROI sets was significantly

higher than that of randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-

corrected, Cohen's d: 2.83, Figure 3B). These results demonstrated that ELA/GAopt

exhibited high reproducibility in ROI selection.

Figure 2 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenario 1,

on Creativity Data).

Figure 3 Stability evaluation of ROI selection using ELA/GAopt compared to random

selection (Scenario 1, on Creativity data).

To test the reproducibility of the local minimum patterns across datasets, we calculated the

Hamming distance between ID vectors of the discovery and test datasets. Figure 4A and D

show that the Hamming distances were significantly smaller for the optimized ROIs

compared to the randomly selected ROIs (permutation test, 10,000 permutations, $p =$

0.0025, FDR-corrected, Cohen's d: 0.408), indicating greater pattern stability with the

optimized ROIs.

Finally, Figure 4B, C, E, and F summarize the comparison of the objective function values

in both the discovery and test sets. Permutation testing revealed that the values for the

optimized ROI sets were significantly higher than those of the randomly selected sets in the

discovery set ($p < 0.001$, FDR-corrected, Cohen's d: 5.63). Crucially, this significant

advantage also generalized to the independent test set ($p < 0.001$, FDR-corrected,

Cohen's d:2.51), confirming the generalizability and effectiveness of the proposed ROI

selection framework.

Figure 4 Reproducibility of local minimum patterns across discovery and test

datasets (on Creativity data).

Next, results using the HCP-YA dataset are described. Supplementary Figure 4 shows the

convergence of the objective function over 1000 generations using ELA/GAopt across 100

runs with different initial populations. All runs converged within the range of 0.96 to 0.98

objective function value.

With the 100 ELA/GAopt runs, binomial tests were performed to evaluate whether each

ROI was selected more frequently than expected by chance. After FDR correction ($p <$

0.05), 20 ROIs were statistically significant as shown in Figure 5. Supplementary Table 2

lists the anatomical coordinates and associated functional networks for each ROI.

Furthermore, the distribution of selected ROIs across 100 runs is shown in Supplementary

Figure 5, where the total number of selections for each ROI can be confirmed.

The stability of the optimized ROI set across iterative runs were also evaluated using

HCP-YA dataset. As shown in Figure 6, the pairwise Hamming distances between ROI

selection vectors were significantly smaller than those between random sets (Mann-

Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's d: 5.81, Figure 6A). Additionally, the

pairwise Jaccard index between optimized ROI sets was significantly higher than that of

randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's d:

4.71, Figure 6B). These results confirmed that ELA/GAopt exhibited high reproducibility in

ROI selection, also in HCP-YA dataset.

Figure 5 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenario 1,

on HCP-YA Data).

$\ast\ast\ast\ast$: p < 0.0001

649 **Figure 6 Stability evaluation of ROI selection using ELA/GAopt compared to random**

650 **selection (Scenario 1, on HCP-YA data).**

$\ast$: p < 0.05

Figure 7 Reproducibility of local minimum patterns across discovery and test

datasets (on HCP-YA data).

Regarding objective function values, the optimized set showed significantly higher values

than the random set in both the discovery dataset ($p < 0.01$, FDR-corrected, Cohen's d:

6.22, Figure 7B, E) and the independent test dataset ($p < 0.01$, FDR-corrected, Cohen's

d: 6.95, Figure 7C, F). In contrast, for pattern reproducibility quantified by the Hamming

distance between local-minima states, we observed a trend opposite to that in the

Creativity dataset. A one-tailed permutation test in the hypothesized direction (ELA/GAopt <

Random) did not support a reduction in Hamming distance for the optimized ROI sets

relative to the random ROI sets ($p = 0.99$, Figure 7A, D), indicating an effect opposite to

the expected direction. We discuss possible reasons for this discrepancy from the

Creativity dataset in the Discussion. As a post-hoc analysis, the optimized ROI sets

contained a significantly larger number of identified local-minima states than the random

ROI sets (discovery data: $p = 0.0085$, Cohen's $d = 0.34$; test data: $p = 0.0001$, Cohen's

$d = 0.54$). After controlling for this difference in state count using a normalized comparison,

we still observed no evidence that optimization reduced Hamming distance (permutation

test, $p = 0.99$). Furthermore, the number of consistent local-minimum states did not differ

between optimized and random ROI sets (permutation test, $p = 0.43$).

Scenario 2

Supplementary Figure 6 illustrates the convergence of the objective function over 1000

generations during ELA/GAopt, conducted in 100 independent runs with different initial

populations. As with Scenario 1, the optimization process consistently improved the

objective function value, with most runs converging by the end of the generation window.

Based on the ROI selection results from the 100 runs, we performed a statistical analysis

using a binomial test to determine whether each brain region was selected more frequently

than expected by chance. The resulting p-values were adjusted using the FDR correction

to account for multiple comparisons. Brain regions identified as significant are presented in

Figure 8 and Supplementary Table 3. Furthermore, stability analysis confirmed the

robustness of ROI selection in Scenario 2 (Figure 9). The optimized ROI set exhibited

significantly lower Hamming distance between ROI selection vector compared to random

selection (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's d: 4.90, Figure 9A)

and a higher Jaccard index（Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's

d: 4.32, Figure 9B).

Additionally, the overall distribution of ROI selections across the 100 trials is presented in

Supplementary Figure 7. The selection frequency indicates how often ROIs from each

functional network were selected during the automated ROI selection process in

ELA/GAopt.

Figure 8 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenario

2).

Figure 9 Stability evaluation of ROI selection using ELA/GAopt compared to random

selection (Scenario 2).

To compare the probability of visiting each local minimum between the ASD and CTL

groups, a representative trial was selected from the 100 ELA/GAopt runs. Since the

objective function values were sufficiently high across all trials, they were not suitable as

selection criteria. Instead, we focused on two trials where all selected ROIs were identified

as being significantly more frequently selected than expected by chance, based on the

binomial test with FDR correction ($p < 0.05$).

In the first representative trial, 13 ROIs were selected (Figure 10A), and 12 distinct local

minimum states were identified in Cohort A (Figure 10A, left panel). To assess group

differences in the probability of visiting each of the four most prominent local minima (as

listed in Table 4), Mann-Whitney U tests were conducted, followed by FDR correction.

Significant between-group differences were observed (FDR-corrected $p < 0.05$).

To validate the robustness of these findings, the same analysis was repeated on the

independent validation dataset (Cohort B). In this cohort, six distinct local minimum states

were observed Figure 10A, right panel), and notably, the local minimum state common to

both cohorts (shared the same state number). These validation results supported the

conclusion that the ASD group exhibited a higher probability of visiting a local minimum

characterized by the simultaneous activation of all selected ROIs.

A second representative trial was similarly identified based on ROI selection consistency

(Figure 10B). In this trial, 13 ROIs were selected, and 10 unique local minimum states were

observed in Cohort A (Figure 10B, left panel). Mann-Whitney U tests revealed significant

differences in the occurrence probability for seven states between groups ($p < 0.05$, FDR

corrected; see Table 5). Again, several states were more frequently visited by the ASD

group, while others were predominant in the CTL group.

Validation on Cohort B confirmed the presence of seven local minima (Figure 10B, right

panel), with overlapping state numbers across cohorts. Group differences in visiting specific

states (notably States 2) were replicated, further supporting the generalizability of the

observed ASD-specific dynamics.

Figure 10 Observed local minimum states for representative trials: (A) trial 1 and (B) trial 2.

Table 4 Frequency of local minimum occurrence in representative trial 1 (Significant results in bold; FDR-corrected p-value).

State number	Cohort	probability of appearance		p-value (FDR corrected)	Effect size r
		ASD	CTL		
1	A	0.367	0.361	0.436	0.0531

State number	Cohort	ASD	CTL	p-value (FDR corrected)	Effect size r
1	B	0.464	0.466	**0.00386**	-0.276
2	A	0.349	0.344	**0.00897**	0.179
2	B	0.463	0.461	**0.00386**	0.285
3	A	0.106	0.111	0.0536	-0.129
4	A	0.104	0.107	0.0888	-0.114
5	A	0.0175	0.0176	0.432	-0.0577
5	B	0.0156	0.0152	0.767	-0.0266
6	A	0.0168	0.0174	0.498	-0.0435
6	B	0.00662	0.00734	**2.41E-10**	-0.588
7	A	0.00784	0.00846	**0.00941**	-0.173
7	B	0.0297	0.0293	0.742	-0.0446
8	A	0.00797	0.00820	0.0526	-0.134
8	B	0.0210	0.0207	0.143	0.149
9	A	0.00665	0.00741	**0.00897**	-0.194
10	A	0.00751	0.00801	**0.00897**	-0.179
11	A	0.00562	0.00552	0.290	0.0760
12	A	0.00444	0.00460	0.699	-0.0226

727 **Table 5 Frequency of local minimum occurrence in representative trial 2 (Significant**
728 **results in bold; FDR-corrected p-values)**

State number	Cohort	probability of appearance		p-value (FDR corrected)	Effect size r
		ASD	CTL		
1	A	0.369	0.365	0.540	0.0359
1	B	0.472	0.475	**3.09E-05**	-0.396
2	A	0.355	0.351	**0.00740**	0.174
2	B	0.461	0.456	**2.08E-08**	0.529
3	A	0.0948	0.0984	**0.0380**	-0.130
4	A	0.0950	0.0981	0.162	-0.0851
5	A	0.0193	0.0202	**0.0319**	-0.137
6	A	0.0197	0.0215	**0.000559**	-0.235
7	A	0.0105	0.0109	**0.007399**	-0.174
7	B	0.00863	0.00894	**0.0167**	-0.240
8	A	0.0127	0.0127	0.0584	0.116
8	B	0.00828	0.00828	0.815	-0.0386
9	A	0.0121	0.0109	**0.00937**	0.165
9	B	0.0137	0.0136	0.815	0.0347

10	A	0.0125	0.0117	**0.00684**	0.187
11	B	0.0203	0.0209	0.894	-0.0121
12	B	0.0166	0.0174	0.815	-0.0641

Scenarios 3 and 4

Supplementary Figures 8 and 10 show the convergence of the objective function across
1000 generations during 100 independents ELA/GAopt runs for the ASD and CTL groups,
respectively. To evaluate the consistency of selected ROIs, binomial tests were performed
on the selection results from each group's 100 runs. Statistically significant ROIs after FDR
correction are presented in Figure 11 and Supplementary Tables 4 (ASD) and 5 (CTL). The
selection frequency distribution across all ROI candidates is shown in Supplementary
Figures 9 (ASD) and 11 (CTL), reflecting how often each ROI was selected over 100
optimization trials. Similar to previous scenarios, ROI selection in Scenarios 3 and 4
showed high stability as shown in Figure 12 and Figure 13, respectively. In both the ASD
and CTL groups, the pairwise Hamming distance between the 100 optimized sets (ROI
selection vector) was significantly lower compared to the random set (Scenario 3: Mann-
Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d = 6.08$, Figure 12A; Scenario 4:
Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d = 5.44$, Figure 13A). The
pairwise Jaccard index was significantly higher compared to the random set (Scenario 3:
Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d = 5.04$, Figure 12B;
Scenario 4: Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d = 4.84$, Figure
13B).

Using the ASD-optimized ROIs from Cohort C, we estimated energy landscapes for both
ASD and CTL groups. The number of local minima obtained for each group was computed,
and a group comparison was performed using the Mann-Whitney U test. The test revealed
that the ASD group exhibited a significantly lower number of local minima than the CTL
group ($U_{200} = 4238.5$, $p = 0.043$, effect size r: 0.13), suggesting that the ASD-optimized
ROI configuration captures group-specific features of brain state dynamics.

Conversely, using the CTL-optimized ROIs from Cohort D, the CTL group exhibited
significantly fewer local minima than the ASD group ($U_{200} = 5924.5$, $p = 0.019$, effect size
r: 0.16), again suggesting that the CTL-optimized ROIs capture group-specific differences
in brain state dynamics.

758
759 **Figure 11 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenarios**
760 **3 and 4).**

Figure 12 Stability evaluation of ROI selection using ELA/GAopt compared to random selection (Scenario 3).

Figure 13 Stability evaluation of ROI selection using ELA/GAopt compared to random selection (Scenario 4).

Discussion

Overview and advantages of the proposed method

The ELA/GAopt framework proposed in this study is designed as a versatile meta-

framework that integrates energy landscape analysis with genetic algorithm-based feature

selection. Its core architecture allows for the objective, data-driven identification of ROIs by

optimizing a user-defined objective function tailored to specific research goals. In this study,

we implemented a representative instance of this framework where the objective function

was defined based on pMEM fitting accuracy and inter-individual variability of the

personalized inverse temperature parameter. This specific configuration was chosen to

enhance reproducibility and objectivity in brain dynamics modeling by ensuring model

validity while capturing individual differences. However, it is important to emphasize that the

ELA/GAopt framework itself is independent of these specific metrics; it can be flexibly

extended to incorporate other criteria, such as correlations with clinical phenotypes or task

performance, depending on the analysis requirements.

Traditional ROI selection approaches in neuroimaging studies often depend on

established anatomical or functional priorities derived from previous research. While such

hypothesis-driven selection improves consistency across studies, it may also introduce

confirmation bias, limiting the analysis framework to existing knowledge and potentially

missing emergent patterns not captured by prior findings.

In contrast, ELA/GAopt mitigates this bias by enabling fully data-driven ROI selection. This

allows the model to explore brain region combinations not considered a priori, thereby

expanding the search space for novel insights into brain dynamics. Such exploratory

capacity is particularly crucial for advancing our understanding of complex and

heterogeneous conditions, such as ASD. Hereafter, we discuss the results obtained in

multiple scenarios to demonstrate the effectiveness and clinical applicability of our

proposed ELA/GAopt.

In this context, it is important to clarify that the local minima identified by this framework

correspond to metastable functional configurations, or attractor states, within the brain

dynamics. These states represent specific patterns of recurrent co-activation among the

selected ROIs that the system tends to revisit and maintain over time. Transitions between

local minima reflect dynamic shifts in the functional organization of brain networks.

Furthermore, it should be recognized that brain states derived from ELA are inherently

constrained by the binarized pMEM framework. Thus, while local minima provide a

powerful mathematical abstraction for characterizing macroscopic network dynamics,

caution is warranted against over-interpreting these discrete states in strictly biological

terms. Guided by this interpretive framework, we now assess the findings across multiple

scenarios to clarify how ELA/GAopt supports the identification of both generalizable and

condition-specific brain dynamics.

Evaluation of reproducibility (Scenario 1)

Scenario 1 evaluated the generalizability of ELA/GAopt using the publicly available

Creativity dataset (OpenNeuro: ds002330), which includes resting-state fMRI data.

ELA/GAopt was applied to the discovery set, and the optimized ROI sets were

subsequently applied to the test set. These ROI sets achieved similarly high objective

function values in both datasets (Figure 4B, C, E, and F; $p < 0.05$, FDR-corrected),

demonstrating that ELA/GAopt avoids overfitting and yields generalizable ROI selection.

Regarding the stochastic nature of GAs, we empirically validated the convergence stability

through 100 independent runs using random initialization with different random seeds. The

results demonstrated consistent convergence to high-fitness solutions with minimal

variance across different seeds, supporting the robustness of the optimization process.

Nevertheless, a more formal theoretical analysis of seed dependency remains a subject for

future research to further characterize the algorithmic properties of ELA/GAopt.

It is also noteworthy that the effect sizes observed in the discovery set were remarkably

large (Cohen's $d > 5$). Unlike clinical effect sizes that measure biological differences

between groups, the metric in this context quantifies the degree of separation achieved by

optimization against a random baseline. Since the GA explicitly maximizes the objective

function, it can produce objective values that are far from the distribution of random ROI

selections, resulting in a large Cohen's d. This should be interpreted as the magnitude of

optimization gain relative to the random baseline, rather than a neurobiological effect.

Moreover, the similarity of local minimum states between the discovery and test sets was

significantly higher (Hamming distance difference was smaller) for ROI sets selected by

ELA/GAopt than for randomly selected ROIs (Figure 4A and D; $p < 0.05$, FDR-corrected).

Because local minimum represents stable brain states, this result suggests ELA/GAopt

effectively identifies ROI sets capturing stable, reproducible patterns.

Reproducibility is a critical issue in neuroimaging research, especially for clinical

translation. Traditional ROI-based analyses may underestimate reproducibility because

fMRI signals are inherently non-stationary and exhibit considerable inter-individual and

temporal variability (Song et al., 2014, 2016). In contrast, ELA/GAopt potentially enhances

repeatability by excluding noisy or irrelevant features during ROI selection. Importantly, the

objective function of ELA/GAopt explicitly considers inter-individual variance (i.e., inverse

temperature parameter of pMEM), which may further promote reproducibility in group-level

energy landscape analyses. These improvements enhance the robustness of the findings

and increase the potential for future clinical applications, including and personalized

modeling of brain dynamics.

Our analysis using the high-dimensional HCP-YA dataset ($N = 15$, i.e., 2^{15} state space)

revealed a significant trade-off between model fitting and stability of pattern reproducibility.

ELA/GAopt achieved remarkably high reproducibility in objective function values with

Cohen's $d > 6$ in both discovery and test sets, confirming the algorithm's robustness in

maximizing pMEM fit and variance of the personalized inverse temperature parameter.

However, the structural reproducibility of local minima states, specifically the Hamming

distance between local minima, did not exhibit a significant advantage over random

selection.

Detailed post-hoc validation indicated that optimized ROI sets consistently identified a

significantly higher number of local minima compared to random sets. This suggests that

ELA/GAopt captures more complex energy landscapes reflecting subtle dynamic

transitions, whereas random selection tends to yield flatter, simpler landscapes with fewer

states. In high-dimensional spaces, this increased complexity inherently makes the exact

replication of specific local minimum patterns more challenging (i.e., the "curse of

dimensionality"). Consequently, while ELA/GAopt ensures highly optimized model fitting,

researchers should recognize that the precise configuration of local minima may exhibit

greater cross-dataset variability in high-dimensional settings ($N \geq 15$) compared to lower-

dimensional configurations ($N = 10$). This highlights a fundamental trade-off between

maximizing model accuracy and maintaining the structural stability of the energy

landscape.

Furthermore, the ROIs selected by ELA/GAopt were primarily centered in the occipital and

somatomotor networks, as well as core components of the default mode network (DMN)

such as the angular gyrus, precuneus, and inferior temporal lobe. We acknowledge that the

selection of these primary sensory-motor and visual regions is, to some extent, an

expected consequence of the mathematical characteristics of pMEM. Since participants in

resting-state fMRI often engage in subtle visual processing or motor activity (e.g., small

hand movements), these regions naturally exhibit high neural variability (Koba et al., 2021;

Mao et al., 2015), which can contribute to higher model fitting accuracy. Therefore, the

consistent identification of these areas serves as a basic validation that ELA/GAopt

effectively captures the major sources of variance within the data. This is consistent with

recent evidence suggesting that motor-related regions exhibit significant coordinated

activity even during the resting state (Seitzman et al., 2019; J. A. Smith et al., 2023).

It is important to emphasize that the objective function employed in this study serves as a

representative implementation to demonstrate the framework's fundamental utility. As

ELA/GAopt is designed as a versatile meta-framework independent of specific metrics, it

can be flexibly extended to incorporate diverse optimization criteria, depending on the

research objective. Crucially, however, even within the current implementation, ELA/GAopt

is not a mere 'variance maximizer.' If maximizing fitting accuracy alone were the goal, the

algorithm might converge toward selecting trivial high-amplitude regions or noise artifacts.

To prevent such a result, our objective function specifically incorporates a term representing

the inter-individual variability of the personalized inverse temperature parameter (β). This

design ensures that the identified ROI sets, including the DMN regions associated with self-

referential thought and memory integration, are selected not only for their fitting accuracy to

the group-level model but also for their ability to capture individual differences in brain

dynamics. By balancing model fidelity with individual variability, ELA/GAopt enables the

data-driven discovery of ROI combinations that reflect complex collective dynamics rather

than simple recording-condition manifestations.

Detection of ASD-specific dynamics (Scenarios 2–4)

Scenarios 2, 3, and 4 employed the ABIDE II dataset to investigate whether ELA/GAopt

could detect ASD-specific features in brain state dynamics.

In Scenario 2, ROIs selected by ELA/GAopt were mainly located within the sensory

somatomotor hand network (Figure 8). Significant group differences in specific local minima

probability were observed between the ASD and typically developing (CTL) groups (Table

4, Table 5 and Figure 10; $p < 0.05$, FDR-corrected). Notably, ASD participants more

frequently visited local minimum characterized by the co-activation of all selected ROIs.

This dynamic signature was replicated in an independent validation cohort (Cohort B),

providing support for its robustness.

These findings are consistent with prior reports that identified local overconnectivity and

long-range underconnectivity as characteristic features of brain organization in individuals

with ASD (Fu et al., 2025). The predominance of globally 'active' local minimum (e.g., State

2 identified in Scenario 2, where all selected ROIs are in the active state $+1$) suggests

excessive synchronization of neural activity in ASD, potentially reducing the flexibility of

brain state transitions. This observation aligns with previous ELA studies showing

overstability of neural dynamics (Watanabe & Rees, 2017), and increased functional

connectivity among visual and sensorimotor networks in infants with ASD, which correlated

with symptom severity (Chen et al., 2021). Moreover, manifold learning studies identified

connectivity patterns in sensorimotor networks as discriminative features for distinguishing

ASD from schizophrenia (Hao et al., 2024).

Taken together, these results suggest that ASD is associated with a distinct neurodynamic

profile characterized by reduced state variability and increased co-activation within specific

functional networks. The ELA/GAopt demonstrated its effectiveness in uncovering such

network-specific dynamic biomarkers in a fully data-driven manner.

Scenario 3 further evaluated this hypothesis by applying the ROI set optimized for the

ASD group to the CTL group. The ROI sets optimized for the ASD group primarily consisted

of visual network regions, as indicated in Figure 11. The application of the ASD-optimized

ROIs to the ELA on the CTL group led to a significant increase in the number of observed

local minima in CTL participants ($p < 0.05$), indicating that ASD-optimized ROIs poorly

capture the neurodynamic patterns of typically developing individuals. This supports

previous work suggesting that ASD is characterized by atypical over-coupling of visual

networks, which may limit brain state transitions (Sadeghian et al., 2021; Yamasaki et al.,

2017).

Scenario 4 provided a complementary test by applying CTL-optimized ROIs to the ASD

group. Similarly, the number of local minima observed in ASD participants was significantly

increased ($p < 0.05$). Considering the results in Scenario 3, they suggest that the two

groups exhibit fundamentally different brain state dynamics and network configurations.

This further strengthens previous findings that ASD and CTL groups possess distinct

neurodynamic architectures (Chen et al., 2021; Fu et al., 2025; Hao et al., 2024;

Kozhemiako et al., 2020; Watanabe & Rees, 2017; Yamasaki et al., 2017).

These inter-application results suggest that ELA/GAopt can identify ROI sets that are not

only discriminative but also specific to particular neurodevelopmental conditions. This

highlights its potential utility for characterizing condition-specific brain state dynamics,

serving as a steppingstone for future biomarker research. While these findings warrant

further validation across diverse and larger independent clinical cohorts to ensure clinical

utility, our proposed ELA/GAopt demonstrates strong potential as a data-driven framework

for identifying meaningful brain dynamics and holds promise for future applications in both

basic and translational neuroscience research.

Comparison with other ROI selection strategies

It is essential to distinguish ELA/GAopt from other data-driven dimensionality reduction

methods commonly employed in neuroimaging, such as ICA-based parcellation, PCA

(Calhoun et al., 2009; Guo & Pagnoni, 2008; Seewoo et al., 2021; Varoquaux et al., 2010)

and clustering-based approaches (Craddock et al., 2011; Thirion et al., 2014). Although

these techniques effectively reduce data complexity, they typically generate spatial maps or

components that do not align with established anatomical boundaries, complicating the

biological interpretation of the resulting energy landscape nodes. In contrast, ELA/GAopt

performs subset selection within predefined anatomical atlas spaces, such as the

Dosenbach or Power atlases used in the current study. This approach ensures that the

selected nodes retain their original anatomical labels (e.g., "posterior cingulate cortex"),

thereby maintaining high interpretability and facilitating direct comparisons with existing

literature. While this study demonstrates the utility of the framework, rigorous comparative

work evaluating energy landscapes derived from GA-selected subsets versus ICA- or

clustering-based components remains an important next step for validation.

Furthermore, ELA should be distinguished from other dynamic modeling approaches, such

as dynamic functional connectivity (dFC) or dynamic graph theory. Whereas dFC often

relies on sliding-window correlations to track continuous fluctuations in coupling strength

(Hindriks et al., 2016), ELA models brain dynamics as transitions between discrete, energy-

defined metastable states within a global landscape. ELA/GAopt contributes to this

paradigm by providing a data-driven method to identify the specific ROI combinations that

are well-suited to this energy-based representation under a user-defined objective.

Moreover, the inherent flexibility of our meta-framework allows future studies to integrate

graph-theoretic metrics, such as global efficiency or modularity, directly into the objective

function. This could help bridge the gap between energy-based and connectivity-based

perspectives on macroscopic brain dynamics.

Finally, unlike standard feature selection techniques such as recursive feature elimination

(RFE), which primarily aim to maximize predictive accuracy for external labels (Bulut et al.,

2025; Vafaie & Imam, n.d.), ELA/GAopt is a model-dependent selection framework. Its

primary objective is to satisfy the specific mathematical constraints of the pairwise

maximum entropy model (pMEM), notably the limitation of 10-15 ROIs, while maximizing

(or minimizing) the objective function specified by researchers based on their research

objective. Given the non-linear nature of pMEM fitting, in which complex interactions

between nodes determine system energy, heuristic global optimization via genetic

algorithms is theoretically superior to greedy methods that may overlook critical

interactions. Although direct performance comparisons with other reduction strategies are

left for future work, this study establishes the fundamental utility of GA-based optimization

for biologically interpretable energy landscape analysis.

Methodological limitations and future directions

While this study introduced ELA/GAopt as a novel data-driven method for ROI selection

and demonstrated its utility across multiple neuroimaging datasets, several methodological

limitations should be acknowledged.

First, although genetic algorithms (GAs) are well suited for nonlinear and high-

dimensional optimization problems, they are computationally more expensive than

commonly used gradient-based algorithms. While GAs has the advantage of conducting

global search through multipoint exploration, they require numerous objective function

evaluations—in this case, involving repeated pMEM fitting steps. For example, 10,000,000

function evaluations were required across 100 trials of ELA/GAopt in Scenario 1, resulting

in a total computation time of 100,000 seconds. Because the necessary computational

effort depends on the problem's complexity, analysts must determine suitable termination

criteria (e.g., the number of generations) empirically, which can be burdensome. In this

study, we adopted conservative parameter setting (1,000 generations across 100

independent runs) to rigorously validate the convergence and stability of the algorithm.

However, for practical applications, such extensive iterations may be reduced once solution

stability has been empirically established. Furthermore, genetic algorithms are inherently

parallelizable: because the evaluation of each individual within a population (i.e., pMEM

fitting for a candidate ROI set) is computationally independent, computation scales

approximately linearly with the number of available CPU or GPU cores. Future

implementations that leverage high-performance computing clusters could substantially

reduce execution time, thereby facilitating the application of ELA/GAopt to even larger

datasets.

Second, the objective function used in this study was defined as the weighted sum of two

components: pMEM fitting accuracy and the inter-individual variance of the inverse

temperature parameter. While this single-objective formulation, with a weighted sum of

multiobjective components, provides a practical means to combine multiple objectives, it

requires the analyst to determine the relative importance of each component a priori.

Moreover, controlling the importance is often not easy. A more flexible approach would be

to adopt a multiobjective optimization framework that simultaneously optimizes each

objective without requiring predefined weights. This strategy would explicitly characterize

the trade-offs between competing goals and generate a Pareto front of optimal solutions,

from which the most appropriate configuration could be selected based on study-specific

needs. Incorporating multiobjective optimization into ELA/GAopt in future work may

improve the robustness and diversity of the automated ROI selection.

Third, for the multi-site ABIDE II dataset, explicit data harmonization techniques such as

ComBat (J.-P. Fortin et al., 2018) were not applied directly to the BOLD time-series data.

Site-related variability is a well-recognized confounder in multisite neuroimaging studies.

However, standard harmonization methods are typically optimized for summary statistics,

such as functional connectivity matrices or cortical thickness, rather than raw time-series

data (J.-P. Fortin et al., 2017; Y.-W. Wang et al., 2023). Directly applying such corrections to

BOLD signals carries the risk of distorting temporal autocorrelation structures and nonlinear

dynamics that are essential for ELA (Sahoo & Davatzikos, 2021; Saponaro et al., 2022).

Instead, we mitigated the risk of site-specific overfitting through a rigorous site-disjoint

validation design. As shown in Table 3, the discovery set (Cohort A) and validation set

(Cohort B) consisted of completely non-overlapping sites (e.g., NYU and UCLA in Cohort A;

OHSU and USM in Cohort B). The replication of the identified ROI sets and brain dynamics

in Cohort B suggests that our results are less likely to be driven solely by site-specific

artifacts; nevertheless, residual site effects cannot be ruled out without explicit

harmonization. Although standard denoising was performed, future work should investigate

advanced harmonization frameworks specifically designed for dynamic time-series analysis

to further reduce inter-site variability.

Furthermore, this study accounted for inter-individual variation by incorporating the

variance of the inverse temperature parameter (β) into the objective function. We

acknowledge that attributing inter-individual differences solely to β is a strong assumption.

As suggested by recent literature, individual variability is also likely driven by structural

differences in the energy landscape itself, such as the number and configuration of local

minima. In the current framework, the β-variance term was employed primarily as a

computational heuristic to prevent the algorithm from converging toward trivial solutions

that maximize fitting accuracy while ignoring subject-level diversity. Future research should

explore alternative objective functions that directly quantify topological differences in energy

landscapes across individuals.

Finally, while the ASD-related findings in Scenarios 2-4 are promising, they should be
interpreted with caution. The identification of group-specific dynamics in the ABIDE II
dataset serves primarily as a representative application of the ELA/GAopt framework,
rather than as evidence for definitive clinical biomarkers suitable for immediate diagnostic
use. The primary value of our method lies in its ability to objectively identify candidate ROI
subsets and landscape-derived features (e.g., state transition probabilities) that
characterize condition-specific dynamics, thereby providing a reproducible pathway for
feature selection in future diagnostic modeling. Although our findings were validated using
an independent cohort within the same dataset, further replication in completely
independent, larger-scale cohorts is necessary to ensure generalizability to the broader
ASD population. Future studies should also investigate how these dynamic signatures
relate to specific clinical symptoms or behavioral measures.

Despite these methodological limitations, our results demonstrate that ELA/GAopt offers a
powerful and generalizable approach for exploring brain dynamics in a fully data-driven
manner, with potential for broader applications in neuroscience research.
1051

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1307

Figure legends

Figure 1 Schematic overview of ELA/GAopt framework.

The proposed framework ELA/GAopt combines energy landscape analysis (ELA) with a

genetic algorithm (GA)-based optimization for automatic region of interest (ROI) selection.

(**A**) Candidate ROI sets are generated as binary vectors by the GA, where each gene

indicates whether a specific ROI is selected (1) or not (0). (**B**) Brain activity data are

extracted from the selected ROIs. (**C**) The brain activity data are binarized (active: $+1$ or

inactive: -1) to form discrete activation patterns over time. (**D**) The frequency of

occurrence of each available activation pattern is analyzed. (**E**) A pairwise maximum

entropy model (pMEM) is fitted to the binarized time series data to estimate the energy

associated with each observed signal pattern. The resulting energy landscape visualizes

the probability and energy of each activation pattern, characterizing brain dynamics. (**F**) A

two-step pMEM parameter optimization method, in which the inverse temperature

parameter—which defines the Boltzmann distribution—is optimized for each individual

dataset while keeping the group-derived pMEM parameters fixed. (**G**) The ELA-derived

parameters (e.g., model accuracy and personalized parameters) are fed back into the GA

as a fitness score to evaluate each candidate ROI set. The GA then iteratively updates the

ROI sets through selection, crossover, mutation, and repair operations.

1326

Figure 2 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenario 1,

on Creativity Data).

The bar graph illustrates the frequency with which each ROI was selected across 100

independent optimization runs. A binomial test was used to determine if the frequency of

each ROI was higher than chance, and 18 ROIs were found to be statistically significant

($p < 0.05$, FDR-corrected) and indicated in the figure. The ROIs are arranged in order from

most to least frequently selected. Their anatomical locations are also displayed on the

glass brain plot. The circle size in the brain plot represents the frequency at which each

ROI was chosen, with larger circles indicating higher frequencies.

1336

Figure 3 Stability evaluation of ROI selection using ELA/GAopt compared to random

selection (Scenario 1, on Creativity data).

(**A**) The pairwise Hamming distances between ROI sets (ROI selection vectors). The

pairwise Hamming distances between optimized ROI sets were significantly smaller than

those between random sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's

$d = 3.57$). (**B**) The Jaccard index between ROI sets (ROI selection vectors). The pairwise

1343 Jaccard index between optimized ROI sets was significantly higher than that between

1344 randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d =$

1345 2.83).

1346

1347 **Figure 4 Reproducibility of local minimum patterns across discovery and test**

1348 **datasets (on Creativity Data).**

1349 (**A** - **C**) Null distributions (10,000 permutations) of the difference in mean values between

1350 optimized and randomly selected ROI sets: (**A**) Hamming distance, (**B**) objective function

1351 value in the discovery set, and (**C**) objective function value in the test set. (**D**) The

1352 Hamming distances between local-minima state ID vectors of the discovery ($n = 31$) and

1353 test ($n = 30$) datasets. The Hamming distances were significantly smaller for the optimized

1354 ROI sets compared to the randomly selected ROIs (permutation test, $p = 0.0025$, FDR-

1355 corrected, Cohen's $d = 0.408$). (**E**) The objective function values in the discovery data for

1356 the optimized ROI sets were significantly higher than those of the randomly selected ROI

1357 sets (permutation test, $p < 0.001$, FDR-corrected, Cohen's $d = 5.63$). (**F**) The significant

1358 advantage of optimized ROI sets also generalized to the test set when compared to

1359 randomly selected ROI sets (permutation test, $p < 0.001$, FDR-corrected, Cohen's $d =$

1360 2.51). We generated 100 optimized ROI sets and 100 randomly selected ROI sets.

1361

1362 **Figure 5 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenario 1,**

1363 **on HCP-YA Data).**

1364 The bar graph illustrates the frequency with which each ROI was selected in 100

1365 independent optimization runs. A binomial test was used to determine if the selection

1366 frequency of each ROI was higher than chance, and 20 ROIs were found to be statistically

1367 significant ($p < 0.05$, FDR-corrected), as shown in the figure. The ROIs are arranged in

1368 order from most to least frequently selected. Their anatomical locations are also displayed

1369 on the glass brain plot. The circle size in the brain plot represents the frequency of each

1370 ROI's selection, with larger circles indicating higher frequencies.

1371

1372 **Figure 6 Stability evaluation of ROI selection using ELA/GAopt compared to random**

1373 **selection (Scenario 1, on HCP-YA data).**

1374 (**A**) The pairwise Hamming distances between ROI sets (ROI selection vectors). The

1375 pairwise Hamming distances between optimized ROI sets were significantly smaller than

1376 those between random sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's

1377 $d = 5.81$). (**B**) The Jaccard index between ROI sets (ROI selection vectors). The pairwise

1378 Jaccard index between optimized ROI sets was significantly higher than that between

1379 randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d =$

1380 4.71).

1381

Figure 7 Reproducibility of local minimum patterns across discovery and test

datasets (on HCP-YA Data).

(**A** - **C**) Null distributions (10,000 permutations) of the difference in mean values between

optimized and randomly selected ROI sets: (**A**) Hamming distance, (**B**) objective function

value in the discovery set, and (**C**) objective function value in the test set. The vertical

dashed line indicates the observed mean difference. (**D**) The Hamming distances between

local-minima state ID vectors of the discovery ($n = 180$) and test ($n = 90$) datasets. The

optimized ROI sets did not yield a significantly smaller Hamming distance compared to the

randomly selected ROI sets (one-tailed permutation test, hypothesized direction:

ELA/GAopt < Random, $p = 0.99$). (**E**) The objective function values in the discovery data

for the optimized ROI sets were significantly higher than those of the randomly selected

ROI sets (permutation test, $p < 0.001$, FDR-corrected, Cohen's $d = 6.22$). (**F**) The

significant advantage of optimized ROI sets also generalized to the test set when compared

to randomly selected ROI sets (permutation test, $p < 0.001$, FDR-corrected, Cohen's $d =$

6.95). We generated 100 optimized ROI sets and 100 randomly selected ROI sets.

1397

Figure 8 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenario

2).

The bar graph illustrates the frequency with which each ROI was selected in 100

independent optimization runs. A binomial test was used to determine if the selection

frequency of each ROI was higher than chance, and 14 ROIs were found to be statistically

significant ($p < 0.05$, FDR-corrected), as shown in the figure. The ROIs are arranged in

order from most to least frequently selected. Their anatomical locations are also displayed

on the glass brain plot. The circle size in the brain plot represents the frequency of each

ROI's selection, with larger circles indicating higher frequencies.

1407

Figure 9 Stability evaluation of ROI selection using ELA/GAopt compared to random

selection (Scenario 2).

(**A**) The pairwise Hamming distances between ROI sets (ROI selection vectors). The

pairwise Hamming distances between optimized ROI sets were significantly smaller than

those between random sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's

$d = 4.90$). (**B**) The Jaccard index between ROI sets (ROI selection vectors). The pairwise

Jaccard index between optimized ROI sets was significantly higher than that between

randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d =$
4.32).

1417

1418   **Figure 10 Observed local minimum states for representative trials: (A) trial 1 and (B)**
1419   **trial 2. .** State numbers denote unique binary patterns; matching numbers indicate the
1420   same pattern across cohorts (if applicable).

1421

Figure 11 Selection frequency of each ROI across 100 runs of ELA/GAopt (Scenarios
3 and 4).
The bar graph illustrates the frequency with which each ROI was selected across 100
independent optimization runs. A binomial test was performed to determine whether the
frequency of each ROI exceeded chance levels. As a result, 16 ROIs were identified as
statistically significant in Scenario 3 and 22 ROIs in Scenario 4 ($p < 0.05$, FDR-corrected).
The ROIs are sorted in descending order of selection frequency. Their anatomical locations
are also displayed on the glass brain plot. The circle size in the brain plot represents the
frequency of each ROI's selection, with larger circles indicating higher frequencies.

1431

Figure 12 Stability evaluation of ROI selection using ELA/GAopt compared to
random selection (Scenario 3).
(**A**) The pairwise Hamming distances between ROI sets (ROI selection vectors). The
pairwise Hamming distances between optimized ROI sets were significantly smaller than
those between random sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's
$d = 6.08$). (**B**) The Jaccard index between ROI sets (ROI selection vectors). The pairwise
Jaccard index between optimized ROI sets was significantly higher than that between
randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d =$
5.04).

1441

Figure 13 Stability evaluation of ROI selection using ELA/GAopt compared to
random selection (Scenario 4).
(**A**) The pairwise Hamming distances between ROI sets (ROI selection vectors). The
pairwise Hamming distances between optimized ROI sets were significantly smaller than
those between random sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's
$d = 5.44$). (**B**) The Jaccard index between ROI sets (ROI selection vectors). The pairwise
Jaccard index between optimized ROI sets was significantly higher than that between
randomly selected sets (Mann-Whitney U test, $p < 0.0001$, FDR-corrected, Cohen's $d =$
4.84).

G Candidate ROI sets generation by GA

ROI sets: #1 #2 #3

	#1	#2	#3
x_1	1	0	1
x_2	0	0	0
x_3	1	1	0
x_4	1	1	0
x_5	0	0	1
$\vdots$			
x_n	1	0	1

$f(x)$ 0.85 0.91 **0.95**

Objective function (fitness) values

Give a candidate ROI set

Return the ELA parameters to GA for evaluating the candidate ROI set.
e.g.,
• Accuracy of pMEM fitting
• Personalized pMEM parameters

Energy Landscape Analysis

A Regions of Interest (ROI) selection based on the candidate ROI set

● Selected ROI
● Unselected ROI

B Time

Extraction of brain activity data from selected ROIs

C Time
1
-1

Binarization of brain activity data

D

Pattern	1	2	3	...	2^N
σ_1	-1	1	1	...	-1
σ_2	-1	-1	1	...	1
σ_3	-1	-1	-1	...	1
$\vdots$	$\vdots$	$\vdots$	$\vdots$		$\vdots$
σ_N	-1	-1	-1	...	1
$P(\sigma)$	0.08	0.10	0.12		0.05

Frequency analysis of each activation pattern

E Energy barrier in the state transition

Energy
E_1 E_2

● Active (1) ● Inactive (-1)

Energy landscape construction using pMEM fitting

F

Participants

Personalization of pMEM via inverse temperature optimization

**** : p < 0.0001

**** : p < 0.0001

**** : p < 0.0001

A

	Discovery	Test

Uncertain 2
Sensory Somatomotor Hand 18
Sensory Somatomotor Hand 19
Sensory Somatomotor Hand 21
Sensory Somatomotor Hand 23
Sensory Somatomotor Hand 24
Sensory Somatomotor Hand 27
Sensory Somatomotor Hand 36
Sensory Somatomotor Hand 37
Uncertain 142
Sensory Somatomotor Hand 28
Sensory Somatomotor Hand 34
Sensory Somatomotor Hand 35

1 2 3 4 5 6 7 8 9 10 11 12   2 1 7 8 5 6

Local minimum states (in representative trial 1)

B

	Discovery	Test

Uncertain 2
Sensory Somatomotor Hand 18
Sensory Somatomotor Hand 19
Sensory Somatomotor Hand 23
Sensory Somatomotor Hand 24
Sensory Somatomotor Hand 27
Sensory Somatomotor Hand 31
Sensory Somatomotor Hand 36
Sensory Somatomotor Hand 37
Uncertain 142
Sensory Somatomotor Hand 28
Sensory Somatomotor Hand 34
Sensory Somatomotor Hand 35

1 2 3 4 5 6 7 8 9 10   1 2 11 12 9 7 8

Local minimum states (in representative trial 2)

Active (+1)   Inactive (-1)

**** : p < 0.0001

**** : p < 0.0001