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Feature Extraction of Center of Pressure Signals for the Diagnosis of Fall Risk in Older Adults

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ABSTRACT

Purpose: This study aimed to develop feature extraction strategies for center of pressure (CoP) signals using adaptive genetic programming to characterize fall risk in older adults. Methods: The individual performance of CoP indices reported in the state of the art was optimized through adaptive genetic programming across mathematical domains, such as entropy, time-based (distance, area, hybrid measures), and frequency-based. The validity of the new CoP indices was tested using mean difference tests for groups with and without fall risk, measuring the correlation with existing measures, as well as through the performance of univariate and multiple logistic regressions, which were reported in terms of the macro-average F1-score, recall, accuracy, specificity, sensitivity, and Area Under the Curve (AUC). Results: The newly generated genetic CoP indices outperformed state-of-the-art indices in fall risk identification. The genetic-frequency CoP index achieved the best performance in univariate logistic regression, with an AUC of 0.763 using five-fold cross-validation. Moreover, all genetic indices showed statistically significant differences between older adults with and without fall risk. Conclusion: These results suggest that the proposed methodology provides some simple calculation formulas that facilitate its future adoption in clinical settings and increase fall risk classification performance by up to 27.0%.

KEYWORDS Adaptive Genetic Programming, fall risk assessment, center of pressure (CoP), older adults, feature extraction, signal processing

Introduction

As people age, various physical and functional changes progressively deteriorate their balance ability, leading to increased fall risk. Multiple consequences result when an older adult experiences a fall, including muscle injuries, dislocations, contusions, and bone fractures [39]. At the same time, there may be psychological consequences, such as loss of confidence, restriction of activities, and reduced physical functions and social interactions. Taken together, all these consequences result in financial costs [39], reduced quality of life, and may even lead to death [32].

Annually, an estimated 2.4 million injuries serious enough to require medical attention are recorded, along with approximately 1.6 million fall-related deaths in older adults [16]. This phenomenon is recognized as a serious public health problem [39][16]. Furthermore, with the inversion of the population pyramid, it is expected that the number of fall events will continue to increase in the coming years [39].

A correct assessment of balance and fall risk enables health professionals to implement timely interventions, improving the performance of balance capacity and preventing falls as much as possible [22]. In this sense, different approaches have been developed to assess balance, among which force platforms have been considered the gold standard [14].

A force platform allows the characterization of balance from two time series that evaluate the displacement of the Center of Pressure (CoP) in the Anterior-Posterior (AP) and in the Medio-Lateral direction (ML). According to Quijoux et al. [30] the greater the displacement of the CoP the lower the balance capacity, other studies [15][35] suggest the claim that the variability of the CoP is positively correlated with the ability to respond to external stimuli to avoid a fall. Different CoP indices have been proposed to improve the explainability of the CoP time series, which are mathematical formulas capable of characterizing balance [28][29].

These CoP indices have been used to characterize balance and indirectly assess fall risk. However, their adoption by healthcare professionals has been limited, as their interpretation often requires the simultaneous use of more than 20 different indices [18][25][31]. This not only complicates the assessment and prioritization of relevant features but also requires a certain level of technical expertise.

For the above reasons, in the field of artificial intelligence, CoP indices have traditionally been used as input features in classifiers to automatically identify older adults at risk of falls or balance disturbances, supporting healthcare professionals in making quantitative data-driven decisions [31]. However, the CoP indices that best describe fall risk show poor reliability [5][9]; furthermore, some of them do not show individual statistical significance to identify classes [31].

In addition, studies suggest that current approaches to fall risk prediction may be biased toward overclassifying individuals as at risk [6][31], rather than providing balanced, generalizable predictions. This trend was echoed by Pennone et al. [25], who, after testing six classifiers on 53 CoP indices and anthropometric data, found none could reliably distinguish at risk individuals, likely due to limitations in static CoP data. These findings suggest that the limited specificity and interpretability of current CoP indices may hinder effective classification and clinical utility.

In this context, although it has been reported that CoP indices are capable of describing balance [31], uncertainty arises as to whether they can truly describe fall risk and if it is possible to enhance the performance of current methods. As mentioned above, attempting to characterize

an event as sudden as a fall can be a challenging task. In addition, there is a limited amount of stabilometic data [33], which complicates maximizing the potential of deep learning algorithms [1][11][18]. A paradigm shift is needed in the way CoP information is extracted for fall risk identification [18]. For this reason, it is proposed to extract features from the stabilometric signals of the CoP that directly characterize the risk of falling using Genetic Programming (GP).

GP is an evolutionary computation method that evolves potential solutions to generate optimal outcomes for complex problems, drawing inspiration from biological processes. While derived from Genetic Algorithms (GA), GP distinguishes itself by representing candidate solutions as binary tree structures, enabling the optimization and evolution of both programming code and mathematical expressions [2][36].

In this sense, it is possible to generate optimal solutions using binary trees that represent mathematical expressions [21]. GP has been reported to be especially useful for feature extraction in situations where the relationships between the problem variables are unknown, or when the underlying mathematical model is not well-defined or difficult to specify. Due to its ability to explore and adapt to the problem structure, GP can find acceptable and even optimal solutions in contexts where other optimization approaches may be less effective [7].

In addition, to improve the convergence process, Adaptive Genetic Programming (AGP) dynamically adjusts mutation and crossover probabilities during algorithm execution. This adaptation is based on the optimization progress and the characteristics of the problem, allowing for more efficient exploration of the solution space [27]. Although GA are more widely used in the biomedical field [12][19][20], GP has proven to be useful in biomedical applications such as tuberculosis screening from raw X-ray images [4], predicting established cervical spine disease [38], and detection of confounding drug names [37].

This study aimed to develop feature extraction strategies of CoP signals using APG to characterize older adult fall risk, intending to optimize the performance of the classification algorithms previously used and create formulas by mathematical domain to facilitate the interpretation of results without reducing performance in the identification of individuals with and without fall risk.

Materials and Methods

In this study, the AGP algorithm was employed to enhance the effectiveness CoP indices in identifying fall risk among older adults. Its process focuses on generating a new genetic CoP

index by combining the optimal components from existing CoP indices within each mathematical domain. Figure 1 illustrates the primary workflow of the current proposed methodology. In subsection "Stabilogram signals", the dataset used and the data balancing process are described. Then, in section "Original CoP indices", the coding of the CoP indices is explained. Finally, in section "Genetic Programming", the parameters of the adaptive genetic algorithm are detailed, and its logistic regression fall risk detection.

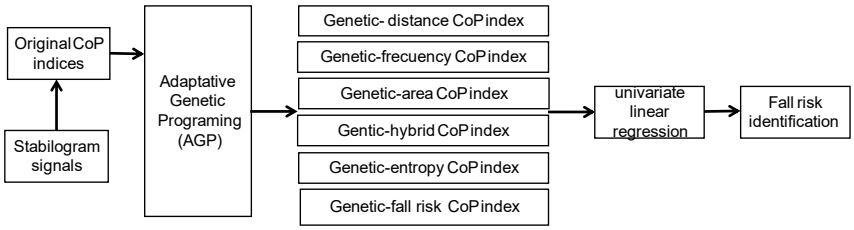

Figure 1. Block diagram of the proposed approach

Stabilogram signals

This study utilized the 'A Public Data Set of Human Balance Evaluations' [34], which comprises both qualitative and quantitative balance assessments from 163 participants, including 116 females and 47 males. The dataset includes information such as fall history, Short Falls Efficacy Scale International (Short FES-I) scores, and time series data of stabilograms in both anteroposterior (CoP_y) and medio lateral (CoP_x) directions, for equilibrium assessment repeated on 3 occasions using a laboratory-grade force platform (OPT400600-1000; AMTI, Watertown, MA, USA).

Exclusively, the time series data of the CoP for older adults (aged 60 years or older) were utilized under the eyes-open condition and on a firm surface. This decision was made to safeguard the physical well-being of older adults, avoiding potentially challenging maneuvers such as closing their eyes or standing on unstable surfaces, which could compromise their safety during the study [18].

The fall risk variable was defined as participants aged 60 or older who had experienced at least one fall in the past 12 months or scored above 14 on the Short FES-I clinical scale [18][24][31]. Those not classified as fall risk were assigned to the non-fall risk class. Only the first and second sets of repeated tests were selected for the fall risk class, while the non-fall risk class registry was selected for all 3 repeated tests to balance the dataset concerning the number of registers per class [18].

Original CoP indices

The existing mathematical expressions of the CoP indices [28][29] were encoded using binary trees. Operators include arithmetic, relational, statistical aggregates, and NumPy functions, while operands such as signals and numbers are described in Table A1 in the APPENDIX A1. In addition, chromosomes were cataloged into distance, area, hybrid, frequency, and entropy-based types (see Table A2 in APPENDIX A1). Figure 2 shows the coding for the Mean distance-AP index, given by the following expression:

$$\mathrm{MDISTAP} = \frac{\mathrm{AP[n]}}{N} = \frac{\sum_{n=0}^{N}\left(\mathrm{CoP}_y[n] - \mathrm{mean}\left(\mathrm{CoP}_y\right)\right)}{N}$$

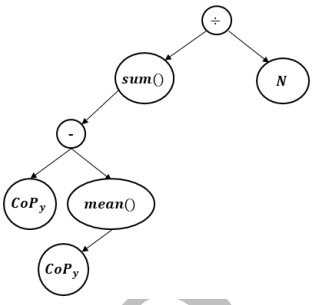

Figure 2. Coding of the MDISTAP index

Genetic Programming

Six strategies were developed to generate the initial population. The first five focused on optimizing the CoP indices for each mathematical domain listed in Table A1 in APPENDIX A1. In the first five experiments to reduce the search space, and take advantage of existing features, the initial population consisted of 100 chromosomes: n chromosomes represented the CoP indices known in the state of the art for each respective mathematical domain, while the remaining $100 - n$ individuals were randomly generated. Similarly, in the sixth experiment, all 45 CoP indices and 55 random indicators were included as part of the initial population. For all experiments, 1,000 generations were used as the stopping criterion. The fitness function focuses on maximizing the macro-average F1-score. We proposed to evaluate the macro-average F1-score of a logistic regression model to identify fall risk, validating the performance by a 5-fold cross-validation method to avoid over-fitting.

The genetic operators of elitism (20%), selection by size 2 tournament, and adaptive crossover and single-point mutation were used. The cataclysm operator was used to avoid premature convergence, which consisted of eliminating the entire current population at generation 750 except for the best chromosome, and then adding randomly without replacement individuals

corresponding to the existing CoP indices according to the mathematical domain to be optimized.

The probability of adaptive crossover $(p(c))$ for each chromosome is determined based on the fitness values of the current population average (f_{avg}) and the second parent $(f_{\text{selcross2}})$, following these rules [27]:

$$p(c) = \begin{cases} k_{1_{\text{cross}}}\left(\frac{f_{\text{selcross}_2} - f_{\text{avg}}}{f_{\max} - f_{\text{avg}}}\right) + k_{1_{\text{crossbias}}}, & f_{\text{selcross}_2} \geq f_{\text{avg}} \\ k_{2_{\text{cross}}}\left(\frac{f_{\text{selcross}} - f_{\min}}{f_{\text{avg}} - f_{\min}}\right) + k_{2_{\text{crossbias}}}, & otherwise \end{cases}$$

where $k_{1_{\text{cross}}} = 0.5$, $k_{2_{\text{cross}}} = 0.2$, and $k_{2_{\text{crossbias}}} = 0.3$.

Similarly, the adaptive probability of mutation $(p(m))$ for each chromosome will be given by the fitness value of the chromosome currently selected (f_{selmu}) and (f_{avg}), following these rules [27]:

$$p(m) = \begin{cases} k_{1_{\text{mu}}}\left(\frac{f_{\max} - f_{\text{selmu}}}{f_{\max} - f_{\text{avg}}}\right) + k_{1_{\text{mubias}}}, & f_{\text{selmu}} \geq f_{\text{avg}} \\ k_{2_{\text{mu}}}\left(\frac{f_{\text{avg}} - f_{\text{selmu}}}{f_{\text{avg}} - f_{\min}}\right) + k_{2_{\text{mubias}}}, & otherwise \end{cases}$$

where $k_{1_{\text{mu}}} = 0.01$, $k_{2_{\text{mu}}} = 0.09$, $k_{1_{\text{mubias}}} = 0.005$, and $k_{2_{\text{mubias}}} = 0.01$.

A descriptive analysis of the new CoP indices was conducted, reporting means and standard deviations for the entire sample, as well as for the fall risk and non-fall risk groups. The normality of the new genetic CoP indices was assessed using the Kolmogorov-Smirnov (KS) tests with Lilliefors correction. Fall risk condition group Mean Difference (MD) comparisons were made using a T-test for parametric variables, and a Mann-Whitney U test for nonparametric variables. All statistical tests were performed with a significance level of $\alpha = 0.05$ using IBM SPSS Statistics (version 26.0, Armonk, NY, USA).

The predictive validity of new genetic CoP indices for fall risk detection was assessed by a logistic regression model was individually fitted for each of the genetic CoP indices. Additionally, a multivariate logistic regression model will be trained using all genetic CoP indices as input features. Both modeling approaches will be evaluated using 5-fold cross-validation, and their performance will be reported in terms of macro-average F1-score, recall, accuracy, specificity, sensitivity, and AUC, using Python (version 3.11). Finally, the evaluation coefficient between the genetic indices with respect to those described in the state of the art and

the evaluations obtained in the Short FES-I and Balance Assessment Systems Test (BEST) instruments were measured.

Results

The study included data from 76 older adults, with an age mean of 71.31 ± 6.47 years. The majority of participants were female (78.94%). In addition, 38.15% of the individuals were reported to be at fall risk condition. The repeated assessments of the subjects represented 181 stabilometric evaluations, distributed in 94 records corresponding to the non-fall risk category and 87 to the fall-risk condition.

Manual encoding of 45 CoP indices (see Table A1 in APENDIX A1) was implemented using binary tree structures. These indices were distributed across the time domain: 15 distance, 3 area, and 6 hybrid indices in the temporal domain, 18 indices in the frequency domain, and 3 entropy-based indices were included.

In AGP experiment 1, CoP indices were optimized in the distance temporal domain, leading to the construction of the $genetic - distance$ index using the following formula:

$$\sum_{n=1}^{N}\left\{\left\{\left[\left(\left(\left(\left(\left(\left(\left(\left(cumsum\left(\mathrm{CoP_y}[n]\%\alpha\right)^2\%\,86.10\right)\%-\beta\right)\%\,\alpha\right)+\gamma\right)\%\,\alpha\right)\%\,\delta\right)\%-\beta\right)\%\,\gamma-\alpha\right)\%\,\delta\right]^2\right\}^2\right\}$$

Where $\alpha = 12.27$, $\beta = 91.84$, $\gamma = 89.13$, and $\delta = 4.62$.

At the deepest node of the $genetic - distance$ index, a nonlinear transformation is applied, where the CoP_y modulus is calculated with a decimal divisor of 12.27. This operation selectively amplifies negative values, corresponding to body displacements in the posterior direction. Additionally, this transformation is accumulated over time by $cumsum$, squared, and weighted through a series of additional operators including multiple modulus with different constants, additions and subtractions, before final aggregation is performed.

In AGP experiment 2, the $genetic - area$ index was generated, resulting in the following formula:

$$\sum_{n=1}^{N}\left(47.39*\left(18.84*\left(-45.68\%\left(18.84*\left(18.84\%\left(18.84*\left(CoP_{rd}[n]-\sum_{n=1}^{N}\frac{CoP_y[n]}{N}\right)\right)\right)\right)\right)\right)$$

The $genetic - area$ index begins by shifting the CoP_{rd} signal by subtracting the mean value of CoP_y, then amplifying this difference by a factor of 18.84, approximately 6π. Subsequently, the operation 18.84 modulus is applied to the previous result, generating a signal whose values are constrained within the range $(-\infty, 18.84)$. These values are again amplified and then the modulus with respect to -45.68 is calculated on the previous transformation.

This series of operations allows highlighting cyclic patterns in the signal, and components with extreme values are attenuated, delimiting their values within the range $(-45.68, 309.617)$. Finally, the transformed signal is weighted by additional multiplications, and the total sum of the resulting vector is performed. Although the exact details of the saturation thresholds are not yet fully understood, the $genetic - area$ index is a nonlinear measure capable of capturing relevant features in the CoP_{rd} signal that relate to the fall risk.

In experiment 3, the $genetic - hybrid$ index experienced a growth in node size compared to previous experiments. This is a common occurrence when working with GP, and can make it more difficult to understand the structure of the index fully. However, it remains simple to compute.

In experiment 4, the frequency-based CoP indices were optimized. During the first attempt (experiment 4.1), the AGP algorithm was trapped in a local optimum, as the optimized index contained nested repetitive elements exclusively from the 50% and 95% frequency power indices. This nested behavior led to a considerable increase in the number of nodes, making the final formula incomprehensible. Therefore, experiment 4 was executed again (experiment 4.2), excluding the indicators POWER50RD, POWER95RD, POWER50AP, POWER95AP, POWER50ML, and POWER95ML. As a result, a new $genetic - frequency$ CoP index was obtained through a mathematical formula with fewer terms.

In Experiment 5, mathematical domain optimization was performed using entropy as a foundation. As a result, the $genetic - entropy$ index was formulated based on three equations that incorporate trigonometric and logarithmic components

Although, the $genetic\ hybrid$, $entropy$ and $frequency$ formulas are extensive and difficult to understand, because it was decided to design a custom program to automatically calculate the indices, so the python function, and the full details of the formula can be found in the Github Repository.

Finally, in Experiment 6, all state-of-the-art CoP indices were included as part of the initial population. After optimization, the $genetic - fall\ risk$ CoP index was obtained, which is expressed as follows:

$$\sum_{i=0.15}^{5} \{ freq[i] : \cos\big((54.84 * m + 67.49) * psRD[i]\big) \leq -77.82 * Cov(psML[i]), i \in N \}$$

Where Cov refers to the covariance matrix, $freq$ is the vector of frequencies contained from 0.15 to 5 Hz of the $psRD$ spectrum, and m is a vector containing the indices of $freq$.

Initially, the $psRD$ signal is amplified by the linear operation (54.84 + 67.49), which varies with frequency. Subsequently, the application of the cosine function introduces a nonlinear oscillatory modulation on the amplified signal, which decreases in amplitude as the frequency increases. This modulated signal is then compared to a negative threshold defined by the spectral covariance in the mediolateral direction, scaled by -77.82.

A high covariance in $psML$ indicates a better ability of compensatory movements to achieve balance [15][35], which could justify why adults at risk of falling have a lower mean genetic-fall risk value than those without risk of falling. Since the covariance is in units of mm^2, the amplification factor -77.82 is applied to adjust the threshold scale, making it more sensitive to negative signal values $\cos\big((54.84 \cdot m + 67.49) \cdot \mathrm{psRD}[i]\big)$. The indices that meet the above condition are selected within the frequency vector and their corresponding $freq[i]$ values are summed, producing a single scalar value named $genetic - fall\ risk$. A simplified functional explanation of the genetic CoP indices, as well as their correlation with traditional CoP indices reported in the state of the art, and with the FES-I and BEST clinical scores, is presented in Table 1.

Table 1. Functional explanation of genetic CoP indices

CoP index	Functional description	Maximum correlation with the state of the art
genetic-distance	A nonlinear measure of the cumulative variance of posterior body displacements. It captures the intensity and recurrence of these posterior displacements, weighting the zero-crossings and the persistence of trajectories in the negative CoPy signal.	Fall risk: 0.32 MDIST: -0.22 AREACE: 0.18
genetic-area	A nonlinear measure capable of capturing relevant features in the CoP_{rd} signal that relates to the fall risk.	Fall risk: 0.16 MDIST: -0.15 AREACC: 0.12
genetic-hybrid	A nonlinear index combining temporal asymmetries and variability in the anterior-posterior displacement, spatial interaction between the anterior-posterior and medial-lateral directions, and lateral spectral information. It correlates negatively with the risk of falling.	Fall risk: -0.26 MDIST: -0.20 FREQRD: -0.15

genetic-frequency	A highly nonlinear spectral index that weights energy at high frequencies of the RD spectrum of the CoP. Its negative correlation with the risk of falling suggests that lower values are associated with better postural control.	Fall risk: -0.37 MDIST: 0.26 FREQDRD: -0.24
genetic-entropy	A nonlinear spectral based on the weighted average of the $psRD$ that quantifies the variability of the frequency spectrum in the anteroposterior and medial lateral directions.	Fall risk: 0.31 FREQDRD: 0.19 FES-I score: 0.19
genetic-fall risk	A nonlinear index that could reflect relevant information about the high frequency spectral distribution of postural sway in the anteroposterior and mediolateral directions associated with a lower fall risk. It is moderately correlated with the FES-I score.	MDIST: -0.46 FES-I score: 0.41 TPOWERML: 0.16

The optimization of each mathematical domain of the CoP indices over the 1,000 generations for each of the experiments 1 to 6 are shown in Figure 3. In all experiments, a rapid exploration phase was observed before 150 generations. In experiment 1, the macro-average F1-score remained constant for many generations, and after the cataclysm event showed a considerable increase. In contrast, in experiment 2, the cataclysm did not change the constant value of the maximum macro-average F1-score.

In experiments 3, 4, 5, and 6, the mean fitness value remained oscillating and relatively far from the maximum value, which could indicate the need for a higher number of generations in the exploitation phase. Simultaneously, this suggests that adaptive functions allow slower convergence and make it possible to extend the exploration phase to improve the maximum fitness value in each generation. A common behavior in all experiments was that the lower the macro-average F1-score reported by the state-of-the-art, the higher the optimized performance rate obtained over the known performance. This might suggest that starting from an initial population with worse performance improves the ability of the AGP to find new solutions in the search space.

The descriptive statistical results of the genetic CoP indices are presented in Table 2. The analysis reveals that the fall risk group exhibits lower values for most genetic indices, except for $genetic - fall\ risk$, and $genetic - frequency$. Regarding the data distribution, most indices, except $genetic - entropy$, and $genetic - distance$ followed a normal distribution. In addition, statistically significant differences were found between the groups with and without fall risk for all the genetic indices evaluated.

The results of the logistic regression analysis for each genetic CoP index and for the combined indices are presented in

Table 3. The findings reveal that $genetic - frequency$ is the most sensitive genetic CoP index for identifying individuals at fall risk. This genetic CoP index maintains the most robust relation in discriminating between individuals with and without fall risk, reaching an average AUC of 0.763 in the 5-fold cross-validations performed. As for identifying individuals without risk, the $genetic - area$ CoP index showed the highest specificity, with a value of 0.798. However, it is important to note that this last CoP genetic index has a relatively low sensitivity. Additionally, the performance of the multivariate logistic regression model that combined all genetic CoP indices was lower than that of the univariate model using only the genetic-frequency index. This result may be explained by information redundancy, as suggested by the high correlations observed among the genetic indices, presented in Figure A1 in the APENDIX A1.

Table 2 Statistical analysis of the genetic CoP indices by groups

CoP index	Total	Fall Risk	Non Fall Risk	KS	MD
	n=181	n=87	n=94	p-value	
genetic-distance	$1.784 \times 10^5 \pm 2.957 \times 10^3$	$1.794 \times 10^5 \pm 2.973 \times 10^3$	$1.775 \times 10^5 \pm 2.657 \times 10^3$	0.200	0.000*
genetic-area	$3.977 \times 10^8 \pm 4.715 \times 10^8$	$4.773 \times 10^8 \pm 5.186 \times 10^8$	$3.241 \times 10^8 \pm 4.125 \times 10^8$	0.000*	0.030*
genetic-hybrid	$3.961 \times 10^{14} \pm 1.647 \times 10^{14}$	$3.522 \times 10^{14} \pm 1.720 \times 10^{14}$	$4.367 \times 10^{14} \pm 1.472 \times 10^{14}$	0.001*	0.000*
genetic-frequency	$1.588 \times 10^{33} \pm 1.885 \times 10^{33}$	$8.701 \times 10^{32} \pm 1.143 \times 10^{33}$	$2.253 \times 10^{33} \pm 2.177 \times 10^{33}$	0.000*	0.000*
genetic-entropy	-0.59 ± 0.08	-0.57 ± 0.07	-0.62 ± 0.07	0.200	0.000*
genetic-fall risk	$1.605 \times 10^2 \pm 98.00$	$1.264 \times 10^2 \pm 89.55$	$1.921 \times 10^2 \pm 95.28$	0.012*	0.000*

* Statistical significance

Table 3. Performance of the logistic regression analysis for genetic CoP indices

CoP index	Macro-average						
	F1-score	Prec	Rec	Acc	Spe	Sen	AUC
genetic-distance	0.710	0.716	0.710	0.713	0.787	0.632	0.686
genetic-area	0.581	0.614	0.594	0.602	0.798	0.391	0.568
genetic-hybrid	0.694	0.697	0.694	0.696	0.745	0.644	0.692
genetic-frequency	0.746	0.746	0.746	0.746	0.734	0.759	0.763
genetic-entropy	0.686	0.694	0.687	0.691	0.777	0.598	0.676

genetic-fall risk	0.705	0.708	0.705	0.707	0.755	0.655	0.692
all genetic CoP indices combined	0.710	0.710	0.710	0.710	0.710	0.710	0.763

Prec=Precision, Rec=Recall, Acc=Accuracy, Spe=Specificity, Sen=Sensitivity, AUC=Area Under the Curve

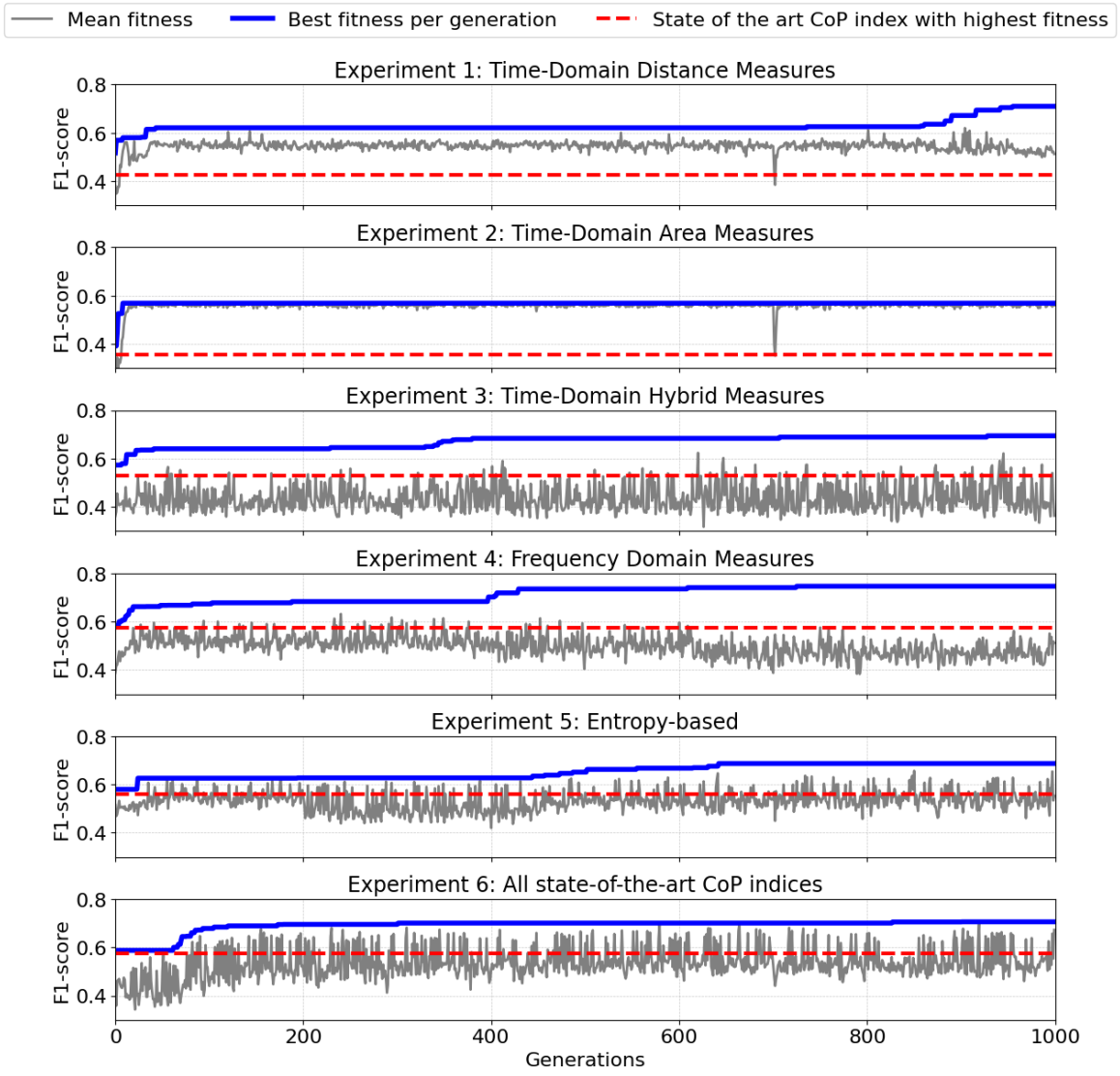

Figure 3. Optimization of the performance of CoP genetic indices by adaptive genetic programming through generations.

Discussion

Fall risk assessments could be described in three main approaches: comprehensive medical, nursing fall risk, and functional mobility assessments. Comprehensive medical assessments look at intrinsic factors such as previous falls, balance, strength, chronic illness, and medication, usually as part of a general or specific geriatric assessment following a fall. Although detailed, they require considerable time, and resources such as multidisciplinary teams. In addition, they do not generate a clear risk index, limiting their standardization [26].

On the other hand, nursing fall risk assessments performed in hospitals and nursing homes, use screening tools such as the STRATIFY to identify risks based on intrinsic patient characteristics, such as history of falls and mobility. These quick and easy-to-apply assessments are frequently updated, but their lack of depth and accuracy may affect their effectiveness depending on the setting and staffing [26].

Finally, functional mobility assessments, used by outpatient physical therapists, employ tests such as the Time Up and Go Test [3] to measure gait and balance limitations. Although they provide standardized measures of functional disability, they do not consider other intrinsic factors and their implementation can be demanding for patients and professionals [18]. These limitations in all three approaches underscore the need for more comprehensive and standardized tools to assess fall risk accurately and efficiently [26].

Our AGP approach aims to be a complementary hybrid alternative to existing methods, highlighting its quantitative characteristics derived from using a force platform. This methodology requires only that the patient remains standing on the platform for 60 seconds, and some anthropometric data. It offers ease of calculation, high sensitivity and specificity to accurately identify older adults with and without fall risk. In addition, a program available on Github Repository, it has been developed that automatically calculates genetic indices from the CoP signal to simplify the analysis process, taking into account parameters such as sampling frequency.

AGP was implemented to optimize the individual performance of CoP indices in the most commonly used mathematical domains according to the state-of-the-art [28][29]. The increase in performance ranged from 14.6% to 27.0%. Table 4 compares the genetic CoP indices improved by AGP and the maximum values previously reported in the literature.

Table 4. Increased performance of genetic indices compared to the state-of-the-art

Mathematical domain	Adaptative Genetic Programming		State-of-the-art		Increment
	CoP index	F1-score	CoP index	F1-score	[%]
Distance measures	genetic-distance	0.710	MVEL	0.433	27.0
Area measures	genetic-area	0.581	AREACC	0.356	22.4
Hybrid measures	genetic-hybrid	0.694	MFREQAP	0.531	16.3
Frequency measures	genetic-frequency	0.746	MFREQML	0.559	18.7
Entropy-based	genetic-entropy	0.686	SEPRD	0.559	12.7

All the domains	genetic-fall risk	0.705	CFREQML	0.559	14.6

Notably, we succeeded in reducing the original 45 state-of-the-art CoP indices across 5 mathematical domains to just 6 genetic CoP indices, 5 characterizing specific mathematical domains, and 1 providing global characterization. Furthermore, both Pennone et al. [25] and Liao et al. [24] point out that CoP indices rarely manage to effectively distinguish between conditions with and without risk of falling. In this context, the observation of statistically significant class differences across all genetic indices demonstrates the robustness of the proposed method.

Contrary to the findings of Pennone et al. [25], who suggest that the low specificity of activities of daily living, about static stabilometric tests, limits the ability to accurately identify the class of fall risk, the present study demonstrated that static stabilometric signals do possess attributes capable of identifying such risk. Furthermore, we suggest that Pennone's results and those reported in the state of the art could be due to the limited capacity of typical CoP indices to adequately characterize fall risk, this limitation is likely due to the overlap between the distributions of individuals with and without fall risk.

Empirically, in our previous studies about the CoP indices [9] [10] [18] [20], we have observed considerable overlap in the distributions of groups with and without fall risk in all the indices analyzed. This overlap makes it difficult to separate the classes of interest in means of a decision frontier, either linear or even nonlinear, using machine learning or deep learning algorithms [8].

This overlap issue is illustrated, for example, in the study by Reilly et al. [31], who reported a recall of 0.82 for the fall risk class, but a much lower recall of 0.64 for the non-risk class. Similarly, Cuaya et al. [6] achieved a sensitivity of 0.81, accompanied by a notably low specificity of 0.19. Considering that high recall values indicate the model's ability to correctly identify the most positive cases, and that specificity reflects the capacity to recognize individuals without the condition of interest [13], this behavior suggests a scenario of overlapping class distributions [8] [23]. In such situations, the class of interest tends to dominate the learning process due to its greater representation, leading to a bias in the prediction. As a result, the decision boundary shifts toward the minority class, causing misclassification of samples of no interest that are close to the overlap region [23].

To illustrate the CoP indices overlapping distributions problem, in Figure 4 a plot of distributions including the CFREQML, TOTEX, and FREQDRD CoP indices is presented,

these represent the best performance in the present study, the best reported in a previous study that only considered the most popular indices in static stabilometry [40], and the worst performance observed in this study, respectively. Also, to compare the above results with the genetic CoP indices, we present the distributions of the $genetic - frequency$, $genetic - fall\ risk$, and $genetic - area$ indices, which correspond to the two best and the worst performance according to their AUC in this analysis.

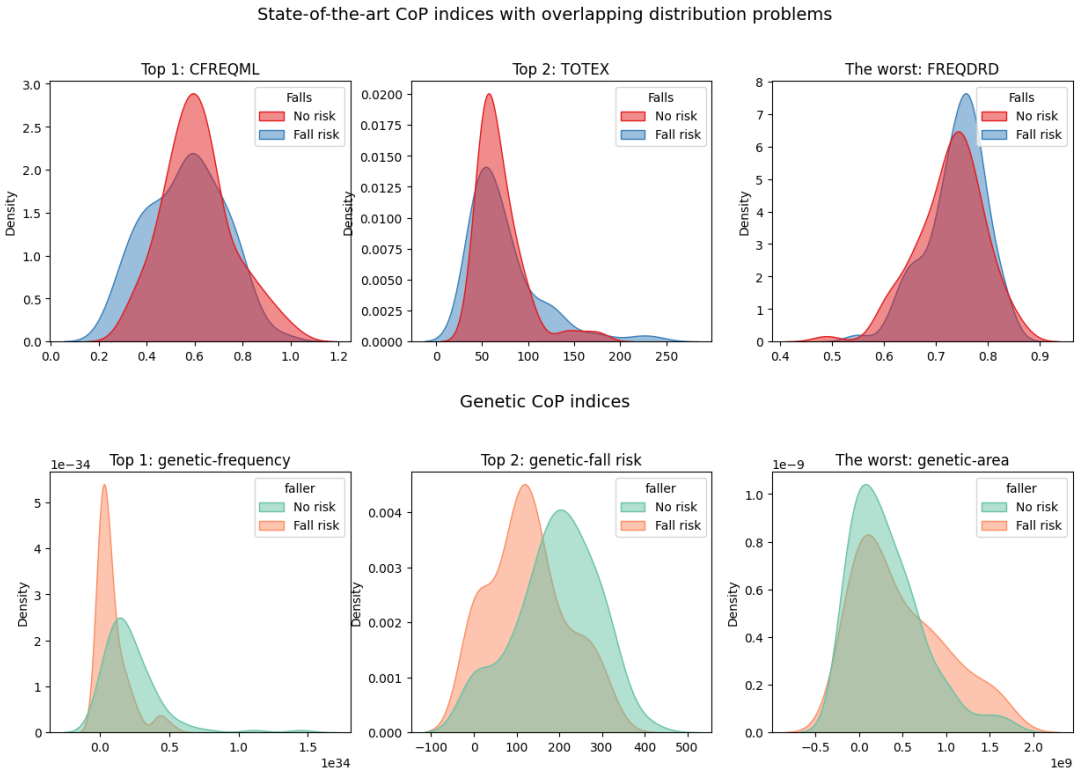

Figure 4. Comparison of the state-of-the-art and genetic CoP indices distribution in the identification of fall risk in older adults

In this context, we suggest that future efforts should not focus exclusively on applying CoP indices with distribution problems to increasingly robust classifiers. Instead, it would be more valuable to directly analyze stabilometric time series or to develop new CoP indices that overcome the problem of overlapping distributions. It is also essential to devote efforts to the creation of heterogeneous, open-access data sets that are free of inter-class imbalance problems.

One of the limitations of this study was the use of CoP signals obtained exclusively from stabilometric tests performed under firm surface conditions and with the eyes open. However, this approach was chosen because the test is simpler and faster to perform, which facilitates its applicability to people of different ages and with diverse cognitive and physical abilities. Another limitation of the study lies in the small size of the sample analyzed, which also presents

a bias due to the predominance of women since only 21.06% of the data corresponds to men. This sex imbalance may introduce bias in the modeling process, potentially limiting the generalizability of the proposed genetic indices to broader or more diverse populations.

The success of these genetic CoP indices suggests a promising direction for fall risk assessment tools. However, before genetic indices can be widely adopted in clinical practice, further research is necessary to establish specific cut-off points, evaluate correlations with validated clinical scales, and explore other relevant aspects to ensure effective clinical implementation. Validation of these indices across diverse populations and clinical contexts will be crucial to consolidate their utility as a reliable tool for fall risk assessment in clinical practice.

Conclusions

The results of this study demonstrate that fall risk identification in older adults can be enhanced through the generation of novel CoP indices using AGP, which are called genetic CoP indices. While previous approaches relied on typical CoP indices that only described balance and partially characterized fall risk, our methodology's use of a targeted fitness function focused on fall risk identification enabled the development of a more effective fall risk index. The proposed approach provides some simple calculation formulas that facilitate future adoption in clinical settings, at the same time these indices could provide input features to classification algorithms to improve the accuracy of current tools.

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APENDIX A1 Dictionary of terms for coding center of the pressure indices, operators and variables

Table A1 Binary tree nodes by type

Type	Operator or variable	Meaning
Statistical aggregates and NumPy operator	max	Maximum value in an array
	min	Minimum value in an array
	mean	Arithmetic mean of elements in an array
	median	Median value in an array
	std	Standard deviation of elements in an array
	mode	Most frequently occurring value
	sum	Sum of all elements in an array
	cumsum	Cumulative sum of elements
	where	Element selection based on condition
	ptp	Range of values in an array (max-min)
	cov	Covariance matrix, $cov(X,Y)$
	sqrt	Square root of each element, $\sqrt{x}$
	log, log2, log10	Logarithms (natural, de base-2 o de base-10)
	arccos, arcsin, arctanh	Inverse trigonometric functions
	rfft	Real-input discrete Fourier Transform
	hfft	FFT of a signal that has Hermitian symmetry
	sin, cos, tan	Trigonometric functions
	radians	Degree-to-radian conversion, $x \cdot \frac{\pi}{180}$
	unwrap	Phase unwrapping for angles
	diff	Discrete difference between elements
	gradient	Rate of change in an array, $\nabla f(x)$
	exp	Exponential function, e^x
	expm1	$expm1: e^x - 1$, for small x
	argmin	Index of the first minimum value
	argmax	Index of the first maximum value
Signals	CoP_y	Difference between AP CoP time-series and its mean
	CoP_x	Difference between ML CoP time-series and its mean
	$CoP_y[t+1]$	CoPy values from sample time 2 to 3,000
	$CoP_y[t-1]$	CoPy values from sample time 1 to 2,999
	$CoP_x[t+1]$	CoPx values from sample time 2 to 3,000
	$CoP_x[t-1]$	CoPx values from sample time 1 to 2,999
	CoP_{rd}	Resultant distance time series according to (Prieto et al., 1996)
	$psRD$	CoP_{rd} power spectrum
	$psAP$	CoP_y power spectrum
	$psML$	CoP_x power spectrum

	Matrix-Distance$_{rd}$	Matrix distance between CoP_x and CoP_y points
	$freq$	Hz frequencies vector from 0.15 to 5 from $psRD$
	m	is a vector containing the indices of $freq$
Arithmetic operators	+	Addition
	-	Subtraction
	*	Multiplication
	/	Division
	**	Exponentiation
	//	Integer division
	%	Modulus
Relational operators	==	Equal to
	¡=	Not equal to
	>	Greater than
	<	Less than
	<=	Less than or equal to
	>=	Greater than or equal to
Constants	N	Length of the CoP signals = 6,000

Table A2 Binary tree nodes by type

Domain	CoP indices [unit]	Abbreviation	Formula
Time Domain "Distance" Measures	Mean distance [mm]	MDIST	$\frac{1}{N}\sum RD[n]$
	Mean distance-ML [mm]	MDISTML	$\frac{1}{N}\sum ML[n]$
	Mean distance-AP [mm]	MDISTAP	$\frac{1}{N}\sum AP[n]$
	RMS distance [mm]	RDIST	$\left[\frac{1}{N}\sum RD[n]^2\right]^{1/2}$
	RMS distance-ML [mm]	RDISTML	$\left[\frac{1}{N}\sum ML[n]^2\right]^{1/2}$
	RMS distance-AP [mm]	RDISTAP	$\left[\frac{1}{N}\sum AP[n]^2\right]^{1/2}$
	Total Length [mm]	TOTEX	$\sum[(AP[n+1]-AP[n])^2+(ML[n+1]-ML[n])^2]^{\frac{1}{2}}$
	Total length ML [mm]	TOTEXML	$\sum[\lvert ML[n+1]-ML[n]\rvert]$
	Total length AP [mm]	TOTEXAP	$\sum[\lvert AP[n+1]-AP[n]\rvert]$
	´ Mean velocity [mm/s]	MVEL	$\frac{TOTEX}{T}$
	Mean velocity-ML [mm/s]	MVELML	$\frac{TOTEXML}{T}$
	Mean velocity-AP [mm/s]	MVELAP	$\frac{TOTEXAP}{T}$
	Range [mm]	RANGE	$\max(p_1,p_2)$
	Range ML [mm]	RANGEML	$\max(CoPx)$
	Range AP [mm]	RANGEAP	$\max(CoPy)$
Time Domain "Area" Measures	95% conf. Circle area [mm^2]	AREACC	$\pi[MDIST+1.645sRD]^2$
	Covariance APML [mm^2]	sAPML	$\frac{1}{N}\sum ML[n]AP[n]$
	95% conf. Ellipse area [mm^2]	AREACE	$6\pi[RDISTAP^2RDISTML^2-sAPML^2]^{1/2}$
Time Domain "Hybrid" Measures	Sway area [mm^2/s]	AREASW	$\frac{1}{2T}\sum_{n=1}^{N-1}\left[AP[n+1]ML[n]-ML[n+1]AP[n]\right]$
	Mean frequency [Hz]	MFREQ	$\frac{MVEL}{2\,\pi MDIST}$
	Mean frequency ML [Hz]	MFREQML	$\frac{MVELOML}{4\sqrt{2}MDISTML}$
	Mean frequency AP [Hz]	MFREQAP	$\frac{MVELOAP}{4\sqrt{2}MDISTAP}$
	Fractal dimension CC [-]	FDCC	$\frac{\log(N)}{\log(2N(MDIST+1.645sRD)/TOTEX)}$
	Fractal dimension CE [-]	FDCE	$\frac{\log(N)}{\log\left(\frac{N\cdot\sqrt{24\cdot(RDISTAP^2\cdot RDISTML^2-SAPML^2)}}{\sqrt{TOTEX}}\right)}$
Frequency Domain Measures	Total power-RD [mm^2/Hz]	TPOWERRD	$\mu_0=\sum_{m=3}^{100}G_{RD}(m)$
	50% power frequency RD [Hz]	POWER50RD	$\sum_{m=3}^{u}G_{RD}(m)\geq 0.5\mu_0$
	95% power frequency RD [Hz]	POWER95RD	$\sum_{m=3}^{u}G_{RD}(m)\geq 0.95\mu_0$
	Total power-ML [mm^2/Hz]	TPOWERML	$\mu_{0ML}=\sum_{m=3}^{100}G_{ML}(m)$

	50% power frequency ML [Hz]	POWER50ML	$\sum_{m=3}^{u} G_{ML}(m) \geq 0.5\mu_0$
	95% power frequency ML [Hz]	POWER95ML	$\sum_{m=3}^{u} G_{ML}(m) \geq 0.95\mu_0$
	Total power-AP [mm^2/Hz]	TPOWERAP	$\mu_{0AP} = \sum_{m=3}^{100} G_{AP}(m)$
	50% power frequency AP [Hz]	POWER50AP	$\sum_{m=3}^{u} G_{AP}(m) \geq 0.5\mu_0$
	95% power frequency AP [Hz]	POWER95AP	$\sum_{m=3}^{u} G_{AP}(m) \geq 0.95\mu_0$
	Centroidal frequency RD [Hz]	CFREQRD	$\left(\frac{\sum_{m=3}^{100}(m\Delta f)^2 G_{rd}(m)}{\mu_{0rd}}\right)^{1/2}$
	Frequency dispersion RD [-]	FREQDRD	$\frac{1-(\sum_{m=3}^{100}(m\Delta f)G_{RD}(m))^2}{\mu_0\sqrt{\sum_{m=3}^{100}(m\Delta f)^2 G_{RD}(m)}}$
	Centroidal frequency ML [Hz]	CFREQML	$\left(\frac{\sum_{m=3}^{100}(m\Delta f)^2 G_{ML}(m)}{\mu_{0ML}}\right)^{1/2}$
	Frequency dispersion ML [-]	FREQDML	$\frac{1-(\sum_{m=3}^{100}(m\Delta f)G_{ML}(m))^2}{\mu_{0ML}\sqrt{\sum_{m=3}^{100}(m\Delta f)^2 G_{ML}(m)}}$
	Centroidal frequency AP [Hz]	CFREQAP	$\left(\frac{\sum_{m=3}^{100}(m\Delta f)^2 G_{AP}(m)}{\mu_{0AP}}\right)^{1/2}$
	Frequency dispersion AP [-]	FREQDAP	$\frac{1-(\sum_{m=3}^{100}(m\Delta f)G_{AP}(m))^2}{\mu_{0AP}\sqrt{\sum_{m=3}^{100}(m\Delta f)^2 G_{AP}(m)}}]$
	Spectral energy [mm^2/Hz]	SERD	$\sum_{i=1}^{n} F_{RD}(n)^2$
	Spectral energy-ML [mm^2/Hz]	SEML	$\sum_{i=1}^{n} F_{ML}(n)^2$
	Spectral energy-AP [mm^2/Hz]	SEAP	$\sum_{i=1}^{n} F_{AP}(n)^2$
Entropy based	Entropy based dimension RD[-]	ENTROPYRD	$-\sum_{i=1}^{n}\left(\frac{psRD[n]}{\sum_{i=1}^{n} psRD}\right) * \log\left(\frac{psRD[n]}{\sum_{i=1}^{n} psRD}\right)$
	Entropy based dimension ML[-]	ENTROPYML	$-\sum_{i=1}^{n}\left(\frac{psML[n]}{\sum_{i=1}^{n} psML}\right) * \log\left(\frac{psML[n]}{\sum_{i=1}^{n} psML}\right)$
	Entropy based dimension AP[-]	ENTROPYAP	$-\sum_{i=1}^{n}\left(\frac{psAP[n]}{\sum_{i=1}^{n} psAP}\right) * \log\left(\frac{psAP[n]}{\sum_{i=1}^{n} psAP}\right)$

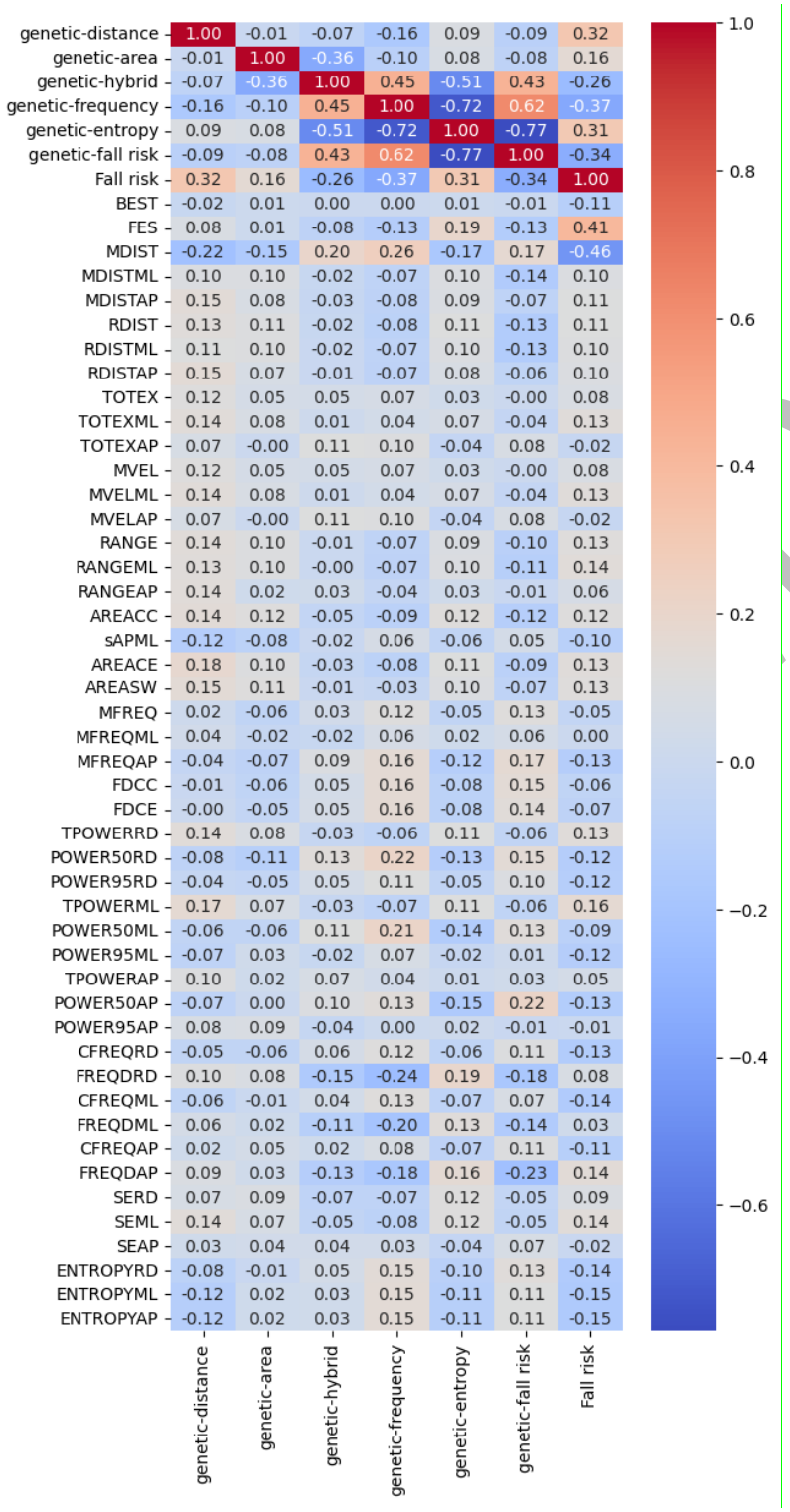

Figure A1 Correlation matrix of CoP genetic indices with respect to state-of-the-art CoP indices and scores on the Falls Efficacy Scale (FES) International and Balance Evaluation Systems Test (BEST)