

ABSTRACT

Clustering is a discipline devoted to find and describe cohesive or homogeneous chunks in data, the clusters. An example of clustering problem is the automatic revealing of meaningful parts in a digitalized image. The motivation for the focus on data clustering is the fact that data clustering is an important process in pattern recognition and machine learning. Clustering algorithms are used in many applications such as image segmentation, vector and color image quantization, compression, etc. Therefore, finding an efficient clustering algorithm is very important for researchers in many different disciplines.

The primary objective of this thesis is to utilize *Genetic Algorithm* (GA) as a clustering tool for the unsupervised classification of grayscale image data. It presents two variants of GA: the first variant is based on the canonical GA while the second variant is based on *compact* GA, cGA. The characteristics components of each algorithm are presented in term of individual and population representation, fitness function evaluation, evolution (selection, crossover, and update) operators, and stopping condition. These two genetic algorithms are then coupled with one popular local-search cluster algorithm, known as K-means algorithm. By coupling, the objective is to harness the power of each algorithm: GA search exploration power and K-means search exploitation power. Moreover, the canonical mechanism of perturbation operators symbolized by both crossover and mutation is imitated in a modified version of cGA in an attempt to improve its search power.

To show the applicability of the presented clustering algorithms, Human medical MRI and land sat images, are used in the experiments. Also, the experiments considered different number of clusters. Comparison results are reported in qualitative terms (i.e. visually) and in quantitative terms using quantization error, weighted error (sum of cluster compactness, clusters separation, and quantization error), and compactness-separation ratio. Results demonstrate that cross-fertilization between the two algorithms is of being benefit in image data clustering, and it outperforms K-means and genetic-based algorithms when they operated individually. Additionally and more interestingly, the modified cGA outperforms the traditional cGA, which leverage the influence of the added perturbation operators including two-point crossover and binary mutation.

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Supervisor Certification

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DEDICATED TO

My Parents...

My Husband and Son...

My Sisters and Brothers...

My Friends...

Kholood

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List of Denotations

GA	Genetic Algorithm.
cGA	compact Genetic Algorithm.
MRI	Magnetic reasoning image.
AI	Artificial Intelligent.
PSO	Particle Swarm Optimization.
$DCPSO$	Dynamic Clustering Particle Swarm Optimization.
NP	Non-deterministic Polynomial problem.
EA	Evolutionary Algorithm.
Γ	cGA chromosome decoding function, $\Gamma : \{0,1\}^{8 * K} \rightarrow \{0,255\}^K$.
δ	Positive scaling function.
Φ_{cGA}	Fitness function of a cGA chromosome, $\Phi_{cGA} : \{0,255\}^K \rightarrow R$.
Φ_{GA}	Fitness function of a GA chromosome, $\Phi_{GA} : \{0,255\}^{l_{GA}} \rightarrow R$.
a, ab, b	cGA chromosome, $a, ab, b \in \{0,1\}^{l_{cGA}}$.
$\{S_1, \dots, S_k\}$	Partition of image Z in K disjoint clusters $S_k \subset Z, k = 1, \dots, K$.
$chrom$	Canonical chromosome definition.
$chrom_i$	i^{th} chromosome (individual) in the GA population, $chrom_i = \{c_{i,j}\} = (c_{i,1}, c_{i,2}, \dots, c_{i,l})$.
c_k	Centroid of cluster $S_k, k = 1, \dots, K$.
$c_{i,k}$	k^{th} cluster centroid of the i^{th} GA chromosome.
$d(x, y)$	Distance between two pixel points.
$d_{man}()$	Manhattan distance.
$d_{eucl}()$	Euclidean distance.

d_{\max}	Intra-distance (compactness error).
d_{\min}	Inter-distance (separation error).
g	GA or cGA generation number.
g_{epoch}	An epoch of GA generations.
g_{\max}	Maximum number of GA generations.
ι	Termination criterion.
J_e	Quantization error.
K	Number of clusters in an image I .
l	Canonical chromosome length.
l_{cGA}	cGA chromosome length, $l_{cGA} = 8 * K$.
l_{GA}	GA chromosome length, $l_{GA} = K$.
l_x	Length of chromosome segment.
m	Number of chromosome segments.
P_m	Mutation rate.
n	GA and cGA population size.
n_k	Number of pixels in cluster $S_k, k = 1, \dots, K$.
N_p	Number of patterns i.e. pixel in image Z , $N_p = ImageHeight * ImageWidth$.
p	l_{cGA} -dimensional probability vector, $p = [0,1,0]^{l_{cGA}}$.
POP	GA population, $Pop = \{chrom_1, \dots, chrom_n\}$.
P_c	Crossover rate.
$U()$	Uniformly distributed random number.
T	GA population subset
w_1	Priority of quantization error, $0 \leq w_1 \leq 1.0$.
w_2	Priority of compactness error, $0 \leq w_1 \leq 1.0$.

w_3

Priority of separation error, $0 \leq w_1 \leq 1.0$.

Z

Data set of grayscale image pixels $Z = \{z_1, z_2, \dots, z_{Np}\}$.

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Clustering Approach for Unsupervised Image Classification using Genetic Algorithm

A Thesis

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الخلاصة

العنقدة هي نظام خصص لإيجاد ووصف قطع متماسكة ومتجانسة في البيانات، هي العناقيد. مثال عن مسألة العنقدة هو الإظهار أو الكشف الأوتوماتيكي لأجزاء ذات معنى في الصورة الرقمية. الحث على التركيز على عنقدة البيانات بسبب إن عنقدة البيانات هي عملية مهمة في تمييز الأنماط و التعليم الآلي. خوارزميات العنقدة تستخدم في عدة تطبيقات مثل تقطيع الصور، حساب متجه ولون الصورة، ضغط البيانات... الخ. لذلك، إيجاد خوارزمية عنقدة كفوءة هو شيء مهم جدا للباحثين في عدة أنظمة مختلفة.

الهدف الرئيسي لهذه الأطروحة هو استخدام الخوارزمية الجينية كأداة عنقدة للتصنيف غير الموجه للصورة ذات تدرج رمادي. هذه الأطروحة تقدم نوعين مختلفين من الخوارزمية الجينية: النوع الأول يعتمد على خوارزمية جينية بسيطة، بينما النوع الثاني يعتمد على الخوارزمية الجينية المضغوطة. المكونات الخصائصية لكل خوارزمية تعرض بصيغة تمثيل الفرد والمجموعة، حساب دالة الملائمة، عمليات التطور (الانتقاء، التقاطع، والتحديث)، و شرط التوقف. هاتان الخوارزميتان الجينيتان سوف تربطان كل على حدة مع خوارزمية عنقدة بحث محلي تعرف بـ (*K means* algorithm). الهدف من الربط هو تسخير قوة كل خوارزمية: قوة الخوارزمية الجينية و قوة (*K means*). بالإضافة الى ذلك، الآلية القانونية لعمليات التشويش التي يرمز لها بالتقاطع والطفرة المفاجئة تحاكي بنسخة محدثة من الخوارزمية الجينية المضغوطة في محاولة لتحسين قوة بحثها.

لعرض قابلية تطبيق خوارزميات العنقدة، تم استخدام صور أشعة رنين مغناطيسي لدماع الإنسان، صور أقمار صناعية. أيضا تم استخدام أعداد عناقيد مختلفة في الاختبارات العملية. نتائج المقارنة سجلت بصيغة نوعية (مرئية) و صيغة كمية باستخدام (*Quantization Error*) و (*Weighted Sum of cluster compactness, cluster separation, quantization error*) والنسبة بين (*cluster compactness and cluster separation*).

النتائج أظهرت أن (*cross-fertilization*) بين الخوارزميتين يعتبر فائدة في عنقدة الصورة، و يعمل بشكل أفضل من خوارزمية (*K-means*) و الخوارزميات الجينية عندما يعملان بشكل منفرد. بالإضافة إلى ذلك وهو الأكثر أهمية، الخوارزمية الجينية المضغوطة المحدثة تعمل بشكل أفضل من الخوارزمية الجينية المضغوطة العادية، لأنها زادت من قوة تأثير معاملات التشويش المضافة والتي تتضمن التقاطع ذو نقطتين و الطفرة الثنائية.



جمهورية العراق
وزارة التعليم العالي والبحث العلمي
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كلية العلوم

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رسالة
مقدمة إلى كلية العلوم في جامعة النهرين كجزء من متطلبات
نيل درجة الماجستير في علوم الحاسبات

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