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Ranked Soft Algebra for Genetic Systems: Toward Intelligent Trait Prediction

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Abstract

In modern genetics, trait prediction and disease susceptibility modeling require tools capable of handling uncertainty, variability, and differential influence of biological and environmental factors. This paper introduces a novel framework based on **Ranked Soft Algebraic Structures**, specifically **Ranked Soft Groups (RSGs)**, to model and analyze complex genetic systems. Genes are modeled as group elements, while biological parameters such as environmental conditions, epigenetic factors, and lifestyle influences are treated as soft set parameters. A ranking function is employed to capture the relative importance or expression level of each parameter, enabling the system to represent weighted gene-environment interactions. The proposed structure allows for flexible classification, hierarchical trait modeling, and context-sensitive inference, providing a mathematically grounded approach for intelligent trait prediction. Applications in gene expression analysis, personalized medicine, and risk assessment are discussed, demonstrating the potential of ranked soft algebra in advancing genetic data interpretation. This work bridges algebraic modeling with biological complexity and offers a new direction in the intersection of soft computing and genomic.

Keywords: ranked soft group; normal sub-RSG; RSG homomorphism; soft algebraic structure; Genetic Trait Modeling; Application in Cow Breeding; Trait-Based Herd Selection; Trait Ranking; Substructure Preservation; AI in Agriculture; Multi-Trait Optimization; Dutch Dairy Cattle; soft set theory; real-world decision systems

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1. Introduction

Classical mathematical methods are not always effective in solving intricate issues in the domains of engineering and economics, environmental sciences, medicine, and social sciences because these problems often involve a number of uncertainties. Consequently, a large number of alternative studies and applications of some specialized techniques, including probability theory, in the literature. Fuzzy and rough sets theories [1–4], vague and interval set s theories [5,6], while the interval set theory is also known asand interval mathematics. As Molodtsov noted, each of these theories has significant challenges even though they are all helpful methods for describing uncertainty [7]. To overcome most of the problems in the above theories Molodtsov [7] suggested a brand-new method for simulating ambiguity and uncertainty known as soft set ($\dot{S}\dot{S}$) theory.

The theory of $\dot{S}\dot{S}$s research is currently advancing quickly. Maji et al. [8] examined how to apply $\dot{S}\dot{S}$ theory to a problem involving decision-making. Garcia [9] defined ranked $\dot{S}\dot{S}$s and developed their core theory. $\dot{S}\dot{S}$s are powerfully improved by this novel, non-numerical paradigm of uncertain information. Aktas and Cagman [10] contrasted $\dot{S}\dot{S}$s with soft groups, soft homomorphisms and soft subgroups.

The study of Aktas and Cagman in [10] is extended by Nisar Ahmad and fatima Afroz [11] toward ranked soft groups (RSGs). The expanded idea of soft groups to RSGs was actually an integrating of a ranking function. This advancement from soft groups to RSGs enables a more precise classification of group elements according to their significance or priority. While soft groups offer a flexible structural framework, RSGs enhance this flexibility by introducing a hierarchical organization among the soft elements. The next paragraph is the biological touch of the current article.

Genetics is the study of how traits and characteristics are inherited and expressed in living organisms through the transmission of genetic material from one generation to the next. Genes, which are specific segments of DNA, serve as instructions for the synthesis of proteins that regulate biological functions and influence observable traits such as eye color, blood type, and susceptibility to certain diseases. However, the relationship between genes and traits is rarely one-to-one; most traits result from the interaction of multiple genes and are further shaped by environmental and epigenetic factors. This complexity has led to the increasing need for predictive models that can account for both genetic variability and contextual influences. Traditional statistical and deterministic models often fall short when dealing with uncertain, overlapping, or context-sensitive genetic behaviors. Therefore, more adaptable and intelligent mathematical frameworks are required to capture the nuanced dynamics of gene expression, inheritance patterns, and trait prediction. In this context, algebraic models that incorporate uncertainty and parameter ranking—such as ranked soft algebraic structures—offer promising tools for representing and reasoning about genetic systems in a more realistic and data-sensitive manner.

Traditional algebraic structures and statistical models have played a foundational role in analyzing genetic data. Classical group theory, for example, assumes strict structure, closure, and deterministic behavior, which may not align with the probabilistic and context-dependent nature of biological systems. Likewise, conventional statistical methods often rely on linear assumptions, fixed parameter significance, or large-sample accuracy, which may oversimplify the true complexity of gene–environment relationships. In reality, the expression of a gene—and thus the trait it influences—can vary significantly depending on external conditions such as nutrition, stress, or exposure to toxins. These environmental factors do not affect all genes equally and may even modify gene behavior across individuals or time. Standard models struggle to integrate such variability, particularly when the influence of parameters is unequal or uncertain. This necessitates the use of more flexible frameworks capable of handling imprecision, parameter prioritization, and contextual variation. Ranked soft algebraic structures, especially Ranked Soft Groups (RSGs), offer a promising alternative by incorporating a ranking function into the group structure, allowing for the modeling of partial influence, parameter weighting, and soft boundaries—key features for accurately representing gene–environment interactions.

Given the inherent uncertainty and complexity of genetic systems, there is a growing demand for mathematical models that can accommodate vagueness, overlapping influences, and hierarchical relationships among parameters. Soft algebra, which generalizes classical algebraic structures using soft set theory, provides the necessary flexibility to model systems with imprecise or context-dependent elements. In soft algebraic structures, parameters can vary across conditions, allowing for the representation of uncertainty without the rigidity of classical algebra. However, in many real-world applications—especially in genetics—not all parameters influence a system equally. For example, a gene's expression may be more heavily influenced by environmental stress than by age, or a particular mutation may contribute more strongly to disease risk than others. To model such asymmetries in influence, *Ranked Soft Groups* (RSGs) are introduced, which extend soft groups by assigning a ranking value in the unit interval $[0, 1]$ to each parameter. This ranking reflects the relative importance or influence of each parameter in a given biological or environmental context. By integrating ranking into soft group theory, RSGs provide a powerful framework to model uneven gene–environment interactions, prioritized genetic traits, and differential gene expression, making them well-suited for intelligent trait prediction and personalized genetic analysis.

2. Preliminaries

The necessary definitions and foundational concepts, including those related to soft sets and RSGs, are presented in the preliminaries section to support the formal development of current article.

2.1. Soft Set

The basic idea presented in this section is soft sets ($\dot{S}\dot{S}$), which was first proposed by D. Molodtsov in 1999 which is a more general mathematical framework for handling ambiguity. Conventional mathematical instruments such as fuzzy sets, rough sets, and probability theory often face limitations when applied to problems that involve vague, incomplete, or parameter-dependent information. $\dot{S}\dot{S}$ theory provides a flexible alternative by allowing uncertainty to be modeled through a parameterized subset family over a given universe.

An $\dot{S}\dot{S}$ is essentially a mapping between the power set and a collection of parameters of a universe. Each parameter is associated with a subset of elements, capturing the idea that the truth or membership of elements can vary with respect to different criteria or viewpoints. This parameterized structure allows $\dot{S}\dot{S}$s to be applied effectively in different domains, such as decision-making, data analysis, pattern recognition, and optimization.

In this section, we formally define $\dot{S}\dot{S}$s, present basic operations, and discuss some illustrative examples. These foundational concepts pave the way for advanced structures such as soft groups, fuzzy $\dot{S}\dot{S}$s, and the RSG framework discussed in later sections.

Definition 2.1. *A couple $(\tilde{F}, C)$ is known as $\dot{S}\dot{S}$ over M (here M is called universal set), where $\tilde{F}$ is a function given by $\tilde{F} : C \to \tilde{P}(M)$. As $\tilde{P}(M)$ is a power set of M.*

Stated differently, a $\dot{S}\dot{S}$ over M is a parameterised collection of subsets of the universal set M. For $\varepsilon \in C, \tilde{F}(\varepsilon)$ could be seen as the collection of ε-elements of the $\dot{S}\dot{S}$ $(\tilde{F}, C)$, or as the collection of ε approximate elements of the $\dot{S}\dot{S}$.

Definition 2.2. *The intersection of couple of $\dot{S}\dot{S}$s $(\tilde{F}, C), (\mathbb{L}, D)$ across a shared universal set M is the $\dot{S}\dot{S}$ $(\mathbb{K}, E)$, where $E = C \cap D$, and for all $\omega \in E$, $\mathbb{K}(\omega) = \tilde{F}(\omega)$ or $\mathbb{L}(\omega)$, (due to the fact that both the set are same). We write $(\tilde{F}, C)\ddot{\cap}(\mathbb{L}, D) = (\mathbb{K}, E)$.*

Definition 2.3. *Suppose $(\tilde{F}, C)$ and $(\mathbb{L}, D)$ be a couple of $\dot{S}\dot{S}$s across a shared universal set M. The extended intersection of $(\tilde{F}, C)$ and $(\mathbb{L}, D)$ is indicated to be the $\dot{S}\dot{S}$ $(\mathbb{K}, E)$, where $E = C \cup D$ and for all $\omega \in E$,*

$$\mathbb{K}(\omega) = \left\{ \begin{array}{ll} \tilde{F}(\omega) & \text{if } \omega \in C \backslash D \\ \mathbb{L}(\omega) & \text{if } \omega \in D \backslash C \\ \tilde{F}(\omega) \cap \mathbb{L}(\omega) & \text{if } \omega \in C \cap D \end{array} \right\}$$

This connection is indicated by $(\tilde{F}, C) \sqcap_{\varepsilon} (\mathbb{L}, D) = (\mathbb{K}, E)$.

Definition 2.4. *Let $(\tilde{F}, C)$ and $(\mathbb{L}, D)$ be two $\dot{S}\dot{S}$s across a shared universal set M such that $C \cap D \neq \emptyset$. The restricted intersection of $(\tilde{F}, C)$ and $(\mathbb{L}, D)$ is notated by $(\tilde{F}, C) \cap (\mathbb{L}, D)$, and is defined as $(\tilde{F}, C) \cap (\mathbb{L}, D) = (\mathbb{K}, E)$, where $E = C \cap D$ and for all $q \in E, \mathbb{K}(q) = \tilde{F}(q) \cap \mathbb{L}(q)$.*

Definition 2.5. *If $(\tilde{F}, C)$ and $(\mathbb{L}, D)$ are two $\dot{S}\dot{S}$s across a shared universal set M, then $(\tilde{F}, C)$ and $(\mathbb{L}, D)$ denoted by $(\tilde{F}, C) \wedge (\mathbb{L}, D)$ is indicated by $(\tilde{F}, C) \wedge (\mathbb{L}, D) = (\mathbb{K}, C \times D)$, where $\mathbb{K}(x), y) = \mathbb{G}(x) \cap \mathbb{L}(y)$ for all $(x, y) \in C \times D$.*

Definition 2.6. *If $(\tilde{F}, C)$ and $(\mathbb{L}, P)$ are two $\dot{S}\dot{S}$s across a shared universal set M, then $(\tilde{F}, C)$ or $(\mathbb{L}, D)$ denoted by $(\tilde{F}, C) \vee (\mathbb{L}, D)$ is indicated by $(\tilde{F}, C) \vee (\mathbb{L}, D) = (\mathbb{K}, C \times D)$, where $\mathbb{K}(x), y) = \tilde{F}(x) \cup \mathbb{L}(y)$ for all $(x, y) \in C \times D$.*

For more definitions and results about $\dot{S}\dot{S}$ see [7]. While for ranked $\dot{S}\dot{S}$ see [9].

2.2. Ranked Soft Groups

This section introduces the structure of ranked soft groups (RSGs), providing essential definitions, examples. The concept draws inspiration from two separate foundations: the soft group framework introduced by Aktas and Cagman in 2007 [10], and the ranked soft set formulation proposed by Garcia in 2023 [9]. By merging these perspectives, the new structure become more capable of handling parametric uncertainty with embedded importance levels. To enhance the clarity and continuity of the present work, selected definitions and results have been adapted, with proper acknowledgment, from the foundational article [11]. These references provide necessary background and support for the development of our main results.

Definition 2.7. *Suppose that* $\mathbb{G}$ *be a group with binary operation "* $\cdot$ *",* E *be some collection of parameters,* $\tilde{F} : E \to \mathcal{P}(\mathbb{G})$ *be a* $\dot{S}\dot{S}$ *over* $\mathbb{G}$*, i.e., for each parameter* $e \in E$*,* $\tilde{F}(e)$ *is subgroup of* $\mathbb{G}$*,* $r : E \to R$ *be a ranking function assigning a real-valued importance to each parameter. Then the triplet* $(\tilde{F}, E, r)$ *is called RSG for the group* $\mathbb{G}$*.*

Example 2.1. *Let* $\mathbb{G} = (\mathbb{Z}_6, +)$*, the group of integers modulo 6. Let us* $E = \{e_1, e_2, e_3, e_4\}$ *be some collection of parameters which measure the order of the subgroup with*

- $\tilde{F}(e_1) = \{0\}$*, a subgroup of* $\mathbb{Z}_6$*,*
- $\tilde{F}(e_2) = \{0, 3\}$*, also a subgroup of* $\mathbb{Z}_6$*,*
- $\tilde{F}(e_3) = \{0, 2, 4\}$*, also a subgroup of* $\mathbb{Z}_6$*,*
- $\tilde{F}(e_4) = \mathbb{Z}_6$*, also a subgroup of* $\mathbb{Z}_6$*,*
- *Ranking function:* $r(e_1) = 1, r(e_2) = 2, , r(e_3) = 3, r(e_4) = 6.$

Then the triplet $(\tilde{F}, E, r)$ *is a RSG over* $\mathbb{Z}_6$*.*

Note: The above example illustrates a RSG that is not a fuzzy soft group. This distinction highlights that RSGs form a broader class of structures, capable of modeling scenarios where fuzzy membership degrees are either unavailable or inappropriate.

In the next section, we explore the substructures of RSGs, such as sub-RSGs and normalistic ranked soft subgroups. These concepts allow us to analyze the internal composition of RSGs and understand how structural properties are preserved within their subsets.

Definition 2.8. *A triple* (H, B, r') *is called a subRSG of RSG* $(\tilde{F}, E, r)$ *over group* $\mathbb{G}$ *if:*

1. $B \subseteq E$
2. $H(\omega)$ *is a subgroup of* $\tilde{F}(\omega)$ *for all* $(\omega) \in B$*,*
3. $r'(\omega) \leq r(\omega)$ *for all* $(\omega) \in B$*.*

Definition 2.9. *Suppose* (H_1, B_1, r'_1) *and* (H_2, B_2, r'_2) *be two sub-RSGs of an RSG* $(\tilde{F}, E, r)$ *for the group* $\mathbb{G}$*. Their intersection is defined as the triple* (H, B, r')*, where:*

- $B = B_1 \cap B_2$*,*
- $H(\omega) = H_1(\omega) \cap H_2(\omega)$ *for all* $(\omega) \in B$*,*
- $r'(\omega) = \min\{r'_1(\omega), r'_2(\omega)\}$ *for all* $(\omega) \in B$*.*

Definition 2.10. *Let* (H_1, B_1, r'_1) *and* (H_2, B_2, r'_2) *be two sub-RSGs of a RSG* $(\tilde{F}, E, r)$ *for the group* $\mathbb{G}$*. Their union is defined as the triple* (H, B, r')*, where:*

- $B = B_1 \cup B_2$*,*
- $H(\omega) = H_1(\omega) \cup H_2(\omega)$ *for all* $(\omega) \in B$*,*
- $r'(\omega) = \max\{r'_1(\omega), r'_2(\omega)\}$ *for all* $(\omega) \in B$*.*

Definition 2.11. *Let* $(\tilde{F}, E, r)$ *be an RSG over a group* $\mathbb{G}$*, the support of the RSG is defined as:* $\operatorname{supp}(\tilde{F}, E, r) = \{\tilde{F}(e) \neq \emptyset\,,\ r(e) > 0,\ for\ all\ e \in E\}$*.*

Remarks: If $r(e,x)=0$, it means the element x has no relevance or weight in the group context under parameter e. Where $supp(\tilde{F},E,r)$ gives the active or effective part of the RSG the pairs where the ranked soft structure matters. The null RSG is an RSG with an empty support, and an RSG $(\tilde{F},E,r)$ is non-null if supp$(\tilde{F},E,r)\neq 0$.

Theorem 2.1. *Let (H_1,B_1,r'_1) and (H_2,B_2,r'_2) be two sub-RSGs of an RSG (F,E,r) for the group $\mathbb{G}$. Then their intersection is also subRSG for the group $\mathbb{G}$, if it is non-null.*

2.2.1. RSGs Homomorphism and Normalistic RSGs

This section expands on the classical notion of group homomorphisms to the concept of RSG homomorphisms. These mappings preserve both the algebraic structure of groups and the layered soft information associated with ranked parameters. Such homomorphisms allow us to study how RSGs relate to one another under structure-preserving transformations, enabling a deeper analysis of their morphic behavior and categorical properties.

Definition 2.12. *Let $(\tilde{F}_1,E_1,r_1)$ be an RSG over a group $\mathbb{G}_1$, and $(\tilde{F}_2,E_2,r_2)$ be an RSG over a group $\mathbb{G}_2$. A triple (ϕ,ψ,ρ) is called an RSG homomorphism from $(\tilde{F}_1,E_1,r_1)$ to $(\tilde{F}_2,E_2,r_2)$ if:*

1. *$\phi:\mathbb{G}_1\to\mathbb{G}_2$ is a group homomorphism,*
2. *$\psi:E_1\to E_2$ is a mapping between parameter sets,*
3. *$\rho:\mathbb{R}\to\mathbb{R}$ is a function satisfying $\rho(r_1(e))\leq r_2(\psi(e))$ for every $e\in E_1$,*
4. *for all $e\in E_1$, $\phi(\tilde{F}_1(e))\subseteq\tilde{F}_2(\psi(e))$.*

Let $(\tilde{F},E,r)$ be a RSG over a group $\mathbb{G}$. A sub-RSG (H,B,r') of $(\tilde{F},E,r)$ is called a ranked soft normal subgroup (RSNS) of $(\tilde{F},E,r)$ if for every $(\omega)\in B$, $H(\omega)$ is a normal subgroup of $\tilde{F}(\omega)$, i.e., $gH(\omega)g^{-1}\subseteq H(\omega)\quad$ for every $g\in F(\omega)$. Equivalently, $gH(\omega)g^{-1}=H(\omega)$ for every $g\in F(\omega)$ and $(\omega)\in B$.

Definition 2.13. *Let $(\tilde{F},E,r)$ be a RSG over a group $\mathbb{G}$. Then $(\tilde{F},E,r)$ is called a normalistic RSG (NRSG) over $\mathbb{G}$ if $F(e)\trianglelefteq\mathbb{G}\quad$ for every $e\in Supp(\tilde{F},E,r)$, where $\trianglelefteq$ stands for normal subgroup.*

Theorem 2.2. *Suppose that $\mathbb{G}$ be a group, and let us $(\tilde{F},E,r)$ be a NRSG over $\mathbb{G}$. Let $B\subseteq E$ and define $r_B=r|_B$ (the restriction of r to B). If $(\tilde{F},B,r_B)$ is non-null, i.e., there exists $b\in B$ such that $\tilde{F}(b)\neq\emptyset$, then $(\tilde{F},B,r_B)$ is also a normalistic RSG over $\mathbb{G}$.*

Definition 2.14. *Suppose that $(\tilde{F}_1,E_1,r_1)$ and $(\tilde{F}_2,E_2,r_2)$ be normalistic RSGs for the groups $\mathbb{G}_1$ and $\mathbb{G}_2$, respectively. Define their product as the triple $(\tilde{F},E_1\times E_2,r)$ for the group $\mathbb{G}_1\times\mathbb{G}_2$, where:*

- *$\tilde{F}(e_1,e_2)=\tilde{F}_1(e_1)\times\tilde{F}_2(e_2)$ for every $(e_1,e_2)\in E_1\times E_2$,*
- *$r(e_1,e_2)=\min\{r_1(e_1),r_2(e_2)\}$.*

Then $(\tilde{F},E_1\times E_2,r)$ is called the product RSG of $(\tilde{F}_1,E_1,r_1)$ and $(\tilde{F}_2,E_2,r_2)$.

If each $\tilde{F}_1(e_1)\trianglelefteq\mathbb{G}_1$ and $\tilde{F}_2(e_2)\trianglelefteq\mathbb{G}_2$, then $\tilde{F}(e_1,e_2)=\tilde{F}_1(e_1)\times\tilde{F}_2(e_2)\trianglelefteq\mathbb{G}_1\times\mathbb{G}_2$, so the product we can see in the next theorem is also a normalistic RSG.

Theorem 2.3. *Let $(\tilde{F},A,r_1)$ and (H,B,r_2) be two normalistic RSGs for the groups $\mathbb{G}_1$ and $\mathbb{G}_2$, respectively.*

Define their product as $(\tilde{F}\times H,A\times B,r)$ over $\mathbb{G}_1\times\mathbb{G}_2$, where:

- *$(\tilde{F}\times H)((\omega),b)=\tilde{F}(\omega)\times H(b)$ for every $(\omega,b)\in A\times B$,*
- *$r(a,b)=\min\{r_1(\omega),r_2(b)\}$.*

If the product $\dot{S}\dot{S}$ is non-null, i.e., there exists $(\omega,b)\in A\times B$ such that $\tilde{F}(\omega)\neq\emptyset$ and $H(b)\neq\emptyset$, then $(\tilde{F}\times H,A\times B,r)$ is a normalistic RSG over $\mathbb{G}_1\times\mathbb{G}_2$.

Theorem 2.4. *Let* $(\tilde{F}_i, A_i, r_i)$ *be normalistic RSGs over groups* $\mathbb{G}_i$ *for* $i = 1, 2, 3$. *Then the product is associative up to isomorphism:* $((\tilde{F}_1, A_1, r_1) \times (\tilde{F}_2, A_2, r_2)) \times (\tilde{F}_3, A_3, r_3) \cong (\tilde{F}_1, A_1, r_1) \times ((\tilde{F}_2, A_2, r_2) \times (\tilde{F}_3, A_3, r_3))$ *as normalistic RSGs over* $\mathbb{G}_1 \times \mathbb{G}_2 \times \mathbb{G}_3$.

Theorem 2.5. *Let* $(\tilde{F}, A, r)$ *be a normalistic RSG over a group* $\mathbb{G}_1$, *and let* $\phi : \mathbb{G}_1 \to \mathbb{G}_2$ *be a group homomorphism. Define a new* $\dot{S}\dot{S}$ $\phi(\tilde{F}) : A \to \mathcal{P}(\mathbb{G}_2)$ *by* $\phi(\tilde{F})(\omega) = \phi(\tilde{F}(\omega)) = \{\phi(g) \mid g \in \tilde{F}(\omega)\},$ *for every* $(\omega) \in A$. *Then the triple* $(\phi(\tilde{F}), A, r)$ *is a normalistic RSG over* $\mathbb{G}_2$.

Theorem 2.6. *Let* $(\tilde{F}, A, r)$ *and* (H, B, s) *be RSGs for the groups* $\mathbb{G}_1$ *and* $\mathbb{G}_2$, *respectively, and let* $\phi : \mathbb{G}_1 \to \mathbb{G}_2$ *be a group homomorphism. Suppose that for each* $(\omega) \in A$, $\phi(\tilde{F}(\omega)) \subseteq H(\omega)$ *and* $r(\omega) \leq s(\omega)$. *Define the kernel* $\dot{S}\dot{S}$ $\ker(\phi) : A \to \mathcal{P}(\mathbb{G}_1)$ *by:* $\ker(\phi)(\omega) = \{g \in \tilde{F}(\omega) \mid \phi(g) = e_{\mathbb{G}_2}\}$, *where* $e_{\mathbb{G}_2}$ *is the identity in* $\mathbb{G}_2$. *Then the triple* $(\ker(\phi), A, r)$ *is a normalistic RSG over* $\mathbb{G}_1$.

Theorem 2.7. *Let* $\mathbb{G}$ *be a group, and let* $N \trianglelefteq \mathbb{G}$ *be a fixed normal subgroup of* $\mathbb{G}$. *Let* ω *be a nonempty set of parameters, and let* $\tilde{F} : A \to \mathcal{P}(\mathbb{G})$ *be defined by* $\tilde{F}(\omega) = N,$ *for every* $(\omega) \in A$. *Let* $r : A \to \mathbb{R}$ *be any ranking function. Then the triple* $(\tilde{F}, A, r)$ *is a normalistic RSG over* $\mathbb{G}$.

3. Ranked Soft Algebra for Genetic Systems: Toward Intelligent Trait Prediction

In the context of genetic modeling, the Ranked Soft Group (RSG) provides a flexible algebraic structure to represent gene behavior influenced by environmental and biological parameters.

- **Group** $\mathbb{G}$**:** Represents a set of genes or gene expressions. The group operation models interactions such as gene recombination, mutation, or functional binding among genes.
- **Parameter set** E**:** Represents external or internal biological factors influencing gene expression, such as age, temperature, nutrition, chemical exposure, or epigenetic modifications.
- **Soft set** $\tilde{F} : E \to \mathcal{P}(\mathbb{G})$**:** For each parameter $e \in E$, $\tilde{F}(e)$ is the set of genes that are expressed, active, or relevant under the condition represented by e. This allows uncertainty or partial membership due to biological variability.
- **Ranking function** $r : E \to [0, 1]$**:** Assigns a degree of influence or importance to each parameter. For example, nutritional factors might have a higher rank ($r = 0.9$) on a specific gene set than ambient temperature ($r = 0.4$).

Hence, an RSG $(\tilde{F}, E, r)$ models a genetic system where genes are affected by multiple, unequally important factors. This ranked and parameterized representation captures:

- The contextual activation or suppression of genes,
- Varying influence of environmental and biological parameters,
- The uncertainty and variability inherent in genetic data.

Such a structure is particularly valuable in applications like trait prediction, genetic disease modeling, personalized treatment planning, and understanding gene–environment interactions in complex biological systems.

3.1. Application to Genetic Breeding

In Dutch cow breeding systems, advanced genetic evaluation models consider multiple traits simultaneously. The RSG framework provides:

- A soft decision-making model where each trait is treated as a flexible set, not crisp inclusion/exclusion.
- A ranking mechanism r to prioritize traits such as milk production over less urgent traits like coat color.
- A group-like structure where trait-preserving breeding combinations are tracked, enhancing intelligent pairing decisions.

This ranked soft algebra allows breeders to balance trade-offs, such as slightly lowering milk yield to drastically improve disease resistance, guided by the ranking r.

3.2. Sub-Ranked Soft Group in Dutch Cow Breeding

Definition 3.1. *Let $(\tilde{F}, E, r)$ be a Ranked Soft Group (RSG) over a group $\mathbb{G}$, representing the genetic structure of a cow population.*

A triple $(\tilde{H}, B, s)$ is called a sub-Ranked Soft Group (sub-RSG) of $(\tilde{F}, E, r)$ if:

1. *$B \subseteq E$, i.e., the parameter set is a subset of the original trait parameters.*
2. *$s : B \to [0, 1]$ is a ranking function such that $s(b) \leq r(b)$ for all $b \in B$.*
3. *For each $b \in B$, $\tilde{H}(b) \subseteq \tilde{F}(b)$ and $\tilde{H}(b)$ is closed under the operation $\cdot$, i.e., $\forall x, y \in \tilde{H}(b) \Rightarrow x \cdot y \in \tilde{H}(b)$.*

Then, $(\tilde{H}, B, s)$ is a sub-RSG of $(\tilde{F}, E, r)$.

3.3. Example in Cow Breeding

Let $\mathbb{G}$ be the set of Holstein-Friesian cows in the Netherlands.

Suppose:

- $E = \{\text{Milk Yield}, \text{Disease Resistance}, \text{Fertility}\}$,
- $r(\text{Milk Yield}) = 0.9$, $r(\text{Disease Resistance}) = 0.8$, $r(\text{Fertility}) = 0.7$,
- $\tilde{F}$ assigns to each trait a set of cows having high levels of that trait.

Now define a sub-RSG $(\tilde{H}, B, s)$ as follows:

- $B = \{\text{Milk Yield}, \text{Fertility}\} \subseteq E$,
- $s(\text{Milk Yield}) = 0.85$, $s(\text{Fertility}) = 0.6$,
- $\tilde{H}(e) \subseteq \tilde{F}(e)$ for $e \in B$, and for all $x, y \in \tilde{H}(e)$, $x \cdot y \in \tilde{H}(e)$.

Then $(\tilde{H}, B, s)$ represents a subgroup of cows prioritized for milk and fertility traits only, with relatively lower importance rankings than the full RSG.

3.4. Homomorphism Between Ranked Soft Groups in Cow Breeding

Definition 3.2. *Let $(\tilde{F}_1, E_1, r_1)$ and $(\tilde{F}_2, E_2, r_2)$ be two Ranked Soft Groups over groups $\mathbb{G}_1$ and $\mathbb{G}_2$ respectively, where $\cdot_1$ and $\cdot_2$ are the binary operations on $\mathbb{G}_1$ and $\mathbb{G}_2$.*

A pair of mappings (ϕ, ψ) is called a Ranked Soft Group Homomorphism from $(\tilde{F}_1, E_1, r_1)$ to $(\tilde{F}_2, E_2, r_2)$ if:

1. *$\phi : \mathbb{G}_1 \to \mathbb{G}_2$ is a group homomorphism, i.e., for all $x, y \in \mathbb{G}_1$,*

$$\phi(x \cdot_1 y) = \phi(x) \cdot_2 \phi(y).$$

2. *$\psi : E_1 \to E_2$ is a mapping between parameter sets (traits) such that for each $e \in E_1$,*

$$\phi(\tilde{F}_1(e)) \subseteq \tilde{F}_2(\psi(e)).$$

3. *The ranking functions respect the inequality: for all $e \in E_1$,*

$$r_1(e) \leq r_2(\psi(e)).$$

3.5. Interpretation in Cow Breeding

- $\mathbb{G}_1, \mathbb{G}_2$: Two herds (e.g., in two different regions or farms).
- E_1, E_2: Sets of breeding traits (milk, health, calving ease, etc.).
- ϕ: A genetic compatibility mapping — e.g., mapping local cows to national database profiles.
- ψ: Matching of traits (e.g., local “milk quality” maps to national “milk yield”).
- The image of trait-based group members in one herd must fall within the corresponding trait set in the other.
- Rankings may improve (e.g., $r_2(\psi(e)) \geq r_1(e)$) when traits are more emphasized in target herd.

Numerical Example: RSG Homomorphism in Dutch Cow Breeding

Let $\mathbb{G}_1 = \{C_1, C_2, C_3\}$ represent a local cow population (e.g., Friesland farm), and $\mathbb{G}_2 = \{D_1, D_2, D_3, D_4\}$ a national-level breeding population.

Let $E_1 = \{e_1, e_2\}$ and $E_2 = \{e_1, e_2, e_3\}$ be sets of traits:

- e_1: Milk Yield (Liters/day)
- e_2: Disease Resistance (Score: 0–10)
- e_3: Fertility (Conception Rate %)

Ranked Soft Group 1 over $\mathbb{G}_1$

Trait	**Soft Set $\tilde{F}_1(e)$**	**Ranking $r_1(e)$**
e_1 (Milk Yield)	$\{C_1, C_2\}$	0.8
e_2 (Disease Resistance)	$\{C_2, C_3\}$	0.6

Ranked Soft Group 2 over $\mathbb{G}_2$

Trait	**Soft Set $\tilde{F}_2(e)$**	**Ranking $r_2(e)$**
e_1 (Milk Yield)	$\{D_1, D_2, D_3\}$	0.9
e_2 (Disease Resistance)	$\{D_2, D_3, D_4\}$	0.8
e_3 (Fertility)	$\{D_1, D_4\}$	0.7

Define Homomorphism

- $\phi : \mathbb{G}_1 \to \mathbb{G}_2$ defined as:

$$\phi(C_1) = D_1, \quad \phi(C_2) = D_2, \quad \phi(C_3) = D_3$$

- $\psi : E_1 \to E_2$ defined as:

$$\psi(e_1) = e_1, \quad \psi(e_2) = e_2$$

Verification of RSG Homomorphism

1. **Group Homomorphism:** ϕ preserves the group operation (breeding logic assumed consistent).
2. **Soft Set Condition:**

$$\phi(\tilde{F}_1(e_1)) = \{D_1, D_2\} \subseteq \tilde{F}_2(e_1)$$

$$\phi(\tilde{F}_1(e_2)) = \{D_2, D_3\} \subseteq \tilde{F}_2(e_2)$$

3. **Ranking Condition:**

$$r_1(e_1) = 0.8 \leq 0.9 = r_2(\psi(e_1))$$

$$r_1(e_2) = 0.6 \leq 0.8 = r_2(\psi(e_2))$$

Hence, (ϕ, ψ) defines a valid RSG homomorphism from $(\tilde{F}_1, E_1, r_1)$ to $(\tilde{F}_2, E_2, r_2)$ in the context of Dutch cow breeding systems.

Definition 3.3. *Let $(\tilde{F}, E, r)$ be a Ranked Soft Group (RSG) over a group $\mathbb{G}$. A triple $(\tilde{H}, B, s)$ is called a* ***normal sub-Ranked Soft Group (normal sub-RSG)*** *of $(\tilde{F}, E, r)$ if:*

1. *$B \subseteq E$, and $s : B \to [0, 1]$ with $s(b) \leq r(b)$ for all $b \in B$,*
2. *For each $b \in B$, $\tilde{H}(b)$ is a subgroup of $\tilde{F}(b)$ under the operation $\cdot$,*
3. *For all $g \in \tilde{F}(b)$ and $h \in \tilde{H}(b)$, the conjugate $g \cdot h \cdot g^{-1} \in \tilde{H}(b)$,*

i.e., $\tilde{H}(b) \trianglelefteq \tilde{F}(b)$ for all $b \in B$.

Example: Normal Sub-RSG in Dutch Cow Breeding

Let $\mathbb{G} = \{C_1, C_2, C_3, C_4\}$ represent a herd of cows.

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Let the parameter set be $E = \{e_1, e_2\}$ where:

- e_1: Milk Yield (Liters/day)
- e_2: Disease Resistance (Score: 0–10)

Define a Ranked Soft Group $(\tilde{F}, E, r)$ over $\mathbb{G}$:

Trait	**Soft Set $\tilde{F}(e)$**	**Ranking $r(e)$**
e_1	$\{C_1, C_2, C_3\}$	0.9
e_2	$\{C_2, C_3, C_4\}$	0.8

Now define a substructure $(\tilde{H}, B, s)$ as:

Trait	**Soft Set $\tilde{H}(b)$**	**Ranking $s(b)$**
e_1	$\{C_2, C_3\}$	0.8
e_2	$\{C_3, C_4\}$	0.7

Assume:

- Each $\tilde{H}(b)$ is a subgroup of $\tilde{F}(b)$ under cow breeding compatibility,
- For each $g \in \tilde{F}(b)$ and $h \in \tilde{H}(b)$, the conjugate $g \cdot h \cdot g^{-1} \in \tilde{H}(b)$.

Then $(\tilde{H}, B, s)$ is a **normal sub-RSG** of $(\tilde{F}, E, r)$.

Why Normal Sub-RSGs Matter in Cow Breeding

In the context of structured cow breeding programs, especially in highly regulated environments such as the Netherlands, normal sub-Ranked Soft Groups (normal sub-RSGs) play a vital role in modeling controlled and stable subpopulations. Their importance can be summarized as follows:

1. **Trait Invariance under Breeding Operations:** Normal sub-RSGs are closed under conjugation within the parent RSG, ensuring that important genetic traits (e.g., disease resistance or calving ease) remain stable even when subjected to complex breeding combinations.
2. **Nucleus Herd Modeling:** Elite breeding programs often involve isolated high-performing herds called nucleus herds. These can be modeled as normal sub-RSGs, where the trait structure is preserved and the group remains stable under internal breeding logic.
3. **Selective Isolation for Genetic Conservation:** Traits that are at risk of dilution (e.g., rare resistance genes or environmental adaptation) can be maintained within a normal sub-RSG, ensuring that these traits do not vanish from the overall breeding pool.
4. **Filtered Trait-Based Selection:** Normal sub-RSGs provide a foundation for creating breeding filters—selecting animals only from subgroups where traits meet certain ranking thresholds and exhibit structural closure.
5. **Computational Simplification:** Working within normal sub-RSGs allows breeders and algorithms to limit genetic evaluations and optimizations to smaller, well-behaved substructures, thus reducing complexity.
6. **Stability in Genetic Algorithms and AI Models:** When integrated into AI-assisted trait prediction systems, normal sub-RSGs define safe regions of the data where predictive stability is guaranteed, improving model robustness.

In summary, normal sub-RSGs support robust and intelligent breeding strategies by preserving genetic structure, enforcing trait security, and facilitating modular selection architectures within ranked soft algebraic frameworks.

Conclusion

In this work, we have introduced and developed the theory of *Ranked Soft Groups (RSGs)* as a powerful algebraic framework for modeling trait-based structures in real-world decision systems, with particular focus on genetic selection in Dutch cow breeding.

We first defined the RSG as a soft set-valued structure equipped with a ranking function, allowing the representation of parameterized subpopulations of cows evaluated over traits such as milk yield, disease resistance, and fertility. This ranking mechanism enables prioritization of traits based on breeding objectives, facilitating soft decision-making under uncertainty.

We extended this framework by defining sub-RSGs and normal sub-RSGs. These substructures represent genetically stable sub-herds with specific trait constraints and closure properties. In particular, normal sub-RSGs preserve trait structures under internal breeding logic and conjugation, making them ideal for modeling nucleus herds or elite subgroups within larger populations.

The concept of RSG homomorphisms was then introduced to formally capture structure-preserving maps between two ranked soft group systems. Through a detailed numerical example, we demonstrated how local herds can be mapped into national-level genetic databases while respecting trait mappings and rankings, enabling intelligent data integration and model transfer.

The proposed RSG framework supports advanced applications such as:

- intelligent breeding selection,
- modular trait filtering,
- preservation of rare or critical traits,
- and trait-priority-driven optimization.

Overall, Ranked Soft Groups offer a natural and mathematically rigorous setting for solving complex genetic selection problems where traits are uncertain, ranked, and interdependent. This structure not only strengthens theoretical understanding but also paves the way for AI-assisted breeding models, contributing to sustainable and intelligent genetic advancement in agriculture.

Conflicts of Interest: The authors declare there is no conflict of interest.

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