

Mutations in finite groups

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1 Introduction

One generally studies the different types of algebraic structures from the equivalence relation “being isomorphic”, thus establishing a series of invariants and canonical models for each equivalence class under the mentioned relation. The main goal of this paper is to study how we can minimally quantify, by means of certain parameters, the degree of non-isomorphy between two given groups of the same order, i.e., to study the degree of invariance between two distinct equivalence classes under the relation “being isomorphic” in the category of finite groups.

The search of an efficient estimator of the qualification “non-isomorphic groups”, which allow us to know if they are “hardly or nearly” isomorphic, has led us to define the concept of mutation, which, formalized in the category of internal Ω -algebras, is widely studied in this paper in the category of finite groups.

We present the concept and the results relative to mutations, according with the three stages their study has taken us chronologically. First of all, from the comparative analysis of pairs of similar structures having underlying sets of the same cardinality, i.e., groups of the same small order, 4,6,8, etc., it arises the concept of mutation, as being a bijection maximally satisfying the homomorphy condition, in order to minimize the number of times one has to mutate the group law to get an isomorphism from the given map.

It is also worth noting that the concept of mutation furthermore lets us rapidly check whether two given distinct presentation correspond to the same group.

Once introduced the concept of mutation between non-isomorphic groups and dealt with its properties we obtain in a second stage the evolutive chains in the sets

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of non-isomorphic groups of order up to 16. The concept of evolutive chain aims toward minimizing the number of germs and mutating zones for the length of links in the chain, this length being related to the amount of mutating surface. We thus aim towards the least abrupt way of evolving from a given group to another group of the same order.

Finally, in the third stage, we study the way mutations between groups of higher order may be constructed, this constructions being related to certain parameters, thus rapidly obtaining the set and table of germs.

2 Mutation (First stage)

2.1. Given two finite groups of the same order we study which minimum changes (hereby the term mutation) we have to perform to the group's law to obtain another group's structure.

To illustrate this concept, let us first consider an example: consider the bijection $h: C_6 \rightarrow D_3$ given by $h(1) = 1, h(x) = z, h(x^2) = y, h(x^3) = y^2, h(x^4) = y^2z, h(x^5) = yz$, where $C_6 = \langle x/x^6 = 1 \rangle$ and $D_3 = \langle y, z/y^3 = z^2 = 1, y^z = y^2 \rangle$ and the following table

C_6/D_3	1/1	x/z	x^2/y	x^3/y^2	x^4/y^2z	x^5/yz
1/1	1/1	x/z	x^2/y	x^3/y^2	x^4/y^2z	x^5/yz
x/z	x/z	$x^2/1$	x^3/y^2z	x^4/yz	x^5/y	$1/y^2$
x^2/y	x^2/y	x^3/yz	x^4/y^2	$x^5/1$	$1/z$	x/y^2z
x^3/y^2	x^3/y^2	x^4/y^2z	$x^5/1$	$1/y$	x/yz	x^2/z
x^4/y^2z	x^4/y^2z	x^5/y^2	$1/yz$	x/z	$x^2/1$	x^3/y
x^5/yz	x^5/yz	$1/y$	x/z	x^2/y^2z	x^3/y^2	$x^4/1$

From this picture we may deduce that the homomorphy condition is verified by only 15 pairs out of a total number of 36 (a pair $(a, b) \in C_6$ is said to verify the homomorphy condition with respect to h provided $h(ab) = h(a)h(b)$.) For instance $1 = h(x^3)h(x^2) \neq h(x^3x^2) = yz$ thus (x^3, x^2) does not verify the homomorphy condition. Therefore we make a local modification of the group structure, only for the pair (x^3, x^2) in order to get the homomorphy condition for (x^3, x^2) and the new law $*$ thus defined. In other words, $*$ is defined as follows:

$$x^3 * x^2 = \begin{cases} \zeta x^3 x^2 \\ x^3 \zeta x^2 \\ x^3 x^2 \zeta \end{cases}$$

with ζ to be determined. Thus, we aim to find a $\zeta \in C_6$ verifying $h(x^3 * x^2) = h(x^3)h(x^2)$, where $*$ denotes one of the three latter alternatives. In the present case the three possibilities lead to the same, by choosing $\zeta = x$.

In the following table we see the different elements ζ which are necessary to obtain the homomorphy condition for each pair of elements of C_6 .

Our objective is to find the bijection between both groups which maximizes the homomorphy condition. And to do so we make the following

Definition 2.2 Let G, M be semigroups such that $|G| = |M|$. A bijection $h: G \rightarrow M$ is a similarity from G to M when one of the sets

$$\begin{aligned} CH(h) &= \{t \in G : h(tg) = h(t)h(g) \forall g \in G\} \\ CV(h) &= \{c \in G : h(gc) = h(g)h(c) \forall g \in G\} \end{aligned}$$

is non-empty.

Notation 2.3 In the situation of the latter definition we shall call $CH(h)$ (resp. $CV(h)$) the horizontal field (resp. the vertical field) of the given similarity. We denote by $\mathcal{S}(G, M)$ the set of all the similarities between both structures. We denote by $\mathcal{S}^H(G, M)$ (resp. $\mathcal{S}^V(G, M)$, resp. $\mathcal{S}^C(G, M)$) the set of horizontal (resp. vertical, resp. crossed) similarities from G to M given by the condition $CH(h) \neq \emptyset$ (resp. $CV(h) \neq \emptyset$, resp. $CH(h) \neq \emptyset \neq CV(h)$).

Proposition 2.4 *If $h \in \mathcal{S}^H(G, M)$ then $CH(h)$ is a stable part with respect to the product in G . Similarly, if $h \in \mathcal{S}^V(G, M)$ then $CV(h)$ is a stable part with respect to the product in G and thus if $h \in \mathcal{S}^C(G, M)$ then $CH(h)$ and $CV(h)$ are stable parts with respect to the product in G .*

Proof. Let $t_1, t_2 \in CH(h)$. It easily follows that

$$h(t_1t_2g) = h(t_1)h(t_2g) = h(t_1)h(t_2)h(g) = h(t_1t_2)h(g)$$

hence $t_1t_2 \in CH(h)$. The proof of the rest of the proposition is similar \square

Proposition 2.5 (i) *If $h \in \mathcal{S}^H(G, M)$ then $h(CH(h))$ is a stable part with respect to the law in M .*

(ii) *If $h \in \mathcal{S}^V(G, M)$ then $h(CV(h))$ is a stable part with respect to the law in M .*

(iii) *If $h \in \mathcal{S}^C(G, M)$ then $h(CH(h))$ and $h(CV(h))$ are stable parts with respect to the law in M .*

Proof. (i) If $v_1, v_2 \in h(CH(h))$ then there exists $t_1, t_2 \in CH(h)$ such that $h(t_i) = v_i$ ($i = 1, 2$). Then $v_1v_2 = h(t_1)h(t_2) = h(t_1t_2) \in h(CH(h))$, by applying (2.4). \square

Definition 2.6 Given $h \in \mathcal{S}(G, M)$ we shall say that h is e -invariant if $1_G \in CH(h) \cap CV(h)$.

We shall assume throughout that G and M are finite groups with $|G| = |M|$.

Lemma 2.7 Given $h \in \mathcal{S}(G, M)$ then

- (i) $h(1_G) = 1_M$
- (ii) h is e -invariant.
- (iii) $h(t^{-1}) = h(t)^{-1}$, $\forall t \in CH(h)$
- (iv) $h(c^{-1}) = h(c^{-1})$, $\forall c \in CV(h)$

Proof. (i) We shall assume $h \in CH(h)$, the other alternative may be dealt with symmetrically.

Let $t \in CH(h)$, $h(t) = h(t1_G) = h(t)h(1_G)$, hence $h(1_G) = 1_M$. The rest of the Lemma follows easily from (i). \square

Theorem 2.8 If $h \in \mathcal{S}(G, M)$ then

- (i) $CH(h) \leq G$
- (ii) $CV(h) \leq G$
- (iii) $h(CH(h)) \leq M$
- (iv) $h(CV(h)) \leq M$
- (v) $CH(h) \cong h(CH(h))$
- (vi) $CV(h) \cong h(CV(h))$

Proof. (i) Let $T = CH(h)$ and $t \in T$. It follows from (2.7)(iii) that $h(t^{-1})h(t) = 1_M = h(t^{-1}t)$ whence, given $g \in G$ and considering $g = t^2x$, we get

$$h(t^{-1}g) = h(t^{-1}t^2x) = h(tx)h(t^{-1})h(t)h(tx) = h(t^{-1})h(t^2x) = h(t^{-1})h(g)$$

Therefore $t^{-1} \in CH(h)$. This, together with (2.4), yields the result.

(iii) and (v) Let $V = h(CH(h))$. By definition of $CH(h)$, $h|_{CH(h)}: CH(h) \rightarrow V$ is a group homomorphism, hence an isomorphism, as it is a bijection.

The rest of the result may be proved symmetrically. \square

After this result it makes sense the following

Definition 2.9 A group R is said to be a similarity kernel from G to M if there exist $T \leq G$ and $V \leq M$ such that $T \cong R \cong V$.

Notation 2.10 We denote by $SK(G, M)$ the set of similarity kernels from G to M . Clearly the trivial group is a member of $SK(G, M)$.

Definition 2.11 Let $R \in SK(G, M)$. An element of the set $\{(f, (T, V)) : R \cong T \cong V\}$ is called a first factor of the R -similarity from G to M .

Definition 2.12 Let $(f_i, (T_i, V_i))$ be first R_i -similarity factors from G to M ($i = 1, 2$). We denote $(f_1, (T_1, V_1)) \leq (f_2, (T_2, V_2))$ if

- (i) R_1 is isomorphic to a subgroup of R_2 .

(ii) $f_2|_{T_1} = f_1$

It easily follows that this defines a partial order. Therefore, we may establish the following

Definition 2.13 An element $R \in SK(G, M)$ is said to be maximal if it is a maximal element in the set $SK(G, M)$ provided with the latter partial order.

Definition 2.14 Given $R \in SK(G, M)$, a domain (resp. codomain) of a second R -similarity factor from G to M is a right transversal of $T \cong R$ (resp. $V \cong R$) in G (resp. M) containing 1_G (resp. 1_M).

Notation 2.15 Should no confusion arise we shall denote $(T|G) = \{g_1, \dots, g_k\}$ with $g_1 = 1_G$ (resp. $(V|M) = \{m_1, \dots, m_k\}$ with $m_1 = 1_M$) the domain (resp. codomain) of a second R -similarity factor from G to M .

Furthermore, we shall denote $(T|G)^* = \{g_2, \dots, g_k\}$ and $(V|M)^* = \{m_2, \dots, m_k\}$.

Proposition 2.16 Let $R \in SK(G, M)$ and $h \in \mathcal{S}(G, M)$. If $(T|G) = \{g_1, \dots, g_k\}$ with $g_1 = 1_G$ then $\{h(g_1), \dots, h(g_n)\}$, with $h(g_1) = 1_M$ is a right transversal of V in M .

Proof. Straightforward. \square

Definition 2.17 With the foregoing notation a second similarity factor from G to M is a bijection $\phi: (T/G) \rightarrow (V/M)$ such that $\phi(g_1) = m_1$.

Theorem 2.18 (Construction method for f^ϕ)

Let R be a maximal element in $SK(G, M)$, $f: T \rightarrow V$ a first R -similarity factor and $\phi: (T/G) \rightarrow (V/M)$ a second R -similarity factor. Then there exists a unique similarity h from G to M verifying:

- (i) $CH(h) = T$,
- (ii) $h(t) = f(t), \forall t \in T$
- (iii) $h(g_i) = \phi(g_i), (1 \leq i \leq k)$.

Proof. Define $f^\phi: G \rightarrow M$ by $f^\phi(g) = f(t)\phi(g_i)$ where $g = tg_i$. If $t' \in T, g \in G$, then

$$f^\phi(t'g) = f^\phi(t'tg_i) = f(t't)\phi(g_i) = f(t')f(t)\phi(g_i) = f^\phi(t')f^\phi(g)$$

Since $g \in G$ has been chosen arbitrarily, it follows that $T \subseteq CH(f^\phi)$. In particular f^ϕ is a similarity.

Now (2.8) yields $CH(f^\phi) \leq G, f^\phi(CH(f^\phi)) \leq M$ and $CH(f^\phi) \stackrel{g}{\cong} f^\phi(CH(f^\phi))$, where g is induced by f^ϕ , hence $g|_T = f^\phi|_T = f$. We deduce from these facts and the maximality of the given element $(f, (T, V))$ that $CH(f^\phi) = T$. The other assertions may be easily proven from the definition of f^ϕ (since $g_1 = 1!$). \square

Definition 2.19 In the conditions of the latter theorem, the map associated to the first R -similarity factor $(f, (T, V))$ and the second R -similarity factor ϕ is called the mutation from G to M associated to T and V .

Note 2.20 Given a mutation between two groups a comparative analysis of the product tables of both groups leads us to consider the existence of zones where the homomorphy condition is satisfied (horizontal field, vertical field and, eventually, other non-mutating zones) and other zones where this condition does not hold. In these ones we study which minimum changes in the multiplication table of G lead to obtaining that of M , after the following

Proposition 2.21 *Let h be a similarity from G to M with $T = CH(h)$, $V = h(T)$, $(T/G) = \{g_1, \dots, g_k\}$ ($g_1 = 1_G$) and $(V/M) = \{m_1, \dots, m_k\}$ ($m_1 = 1_M$). Given g_i ($1 \leq i \leq k$) and $x \in G$, there exists $\zeta = \zeta_i^x \in G$ verifying $h(g\zeta x) = h(g)h(x)$ $\forall g \in Tg_i$*

Proof. Let $g, g' \in Tg_i$ with $g = tg_i$, $g' = t'g_i$ ($t, t' \in T$). Assume that ζ, ζ' verify $h(g\zeta x) = h(g)h(x)$ and $h(g'\zeta'x) = h(g')h(x)$. Considering $t'' = t't^{-1} \in T$ it follows that $h(g'\zeta'x) = h(g')h(x) = h(t'g_i)h(x) = h(t''tg_i)h(x) = h(t'')(h(tg_i)h(x)) = h(t'')(h(g)h(x)) = h(t'')h(g\zeta x) = h(t''g\zeta x) = h(g'\zeta x)$. Since h is one-to-one we get $g'\zeta'x = g'\zeta x$, thus $\zeta = \zeta'$. \square

Definition 2.22 In the situation of the latter proposition we shall say that $\zeta = \zeta_i^x$ verifies the germ condition of the mutation from G to M at level 2 in the field (Tg_i, x) , with respect to h and we shall write $\zeta = Germ_h(Tg_i, x)$.

It thus makes sense to analyze under which hypothesis there exists coincidence of germs. In this direction, we establish the following proposition, whose proof is routine.

Proposition 2.23 *Let h be a similarity from G to M with $CH(h) = T$, $h(T) = V$. If $C = CV(h)$ then $Germ_h(Tg_i, x) = Germ_h(Tg_i, xc)$, for each $c \in C$, $x \in G$ and $g_i \in (T/G)$.*

Definition 2.24 In the situation of (2.23) we shall write

$$Germ_h(Tg_i, xC) = Germ_h(Tg_i, x)$$

and, denoting by $(G/C) = \{x_1 = 1_G, \dots, x_r\}$ a left transversal of C in G ,

$$\begin{aligned} Germ(h) &= \{Germ_h(Tg_i, x_j C) : g_i \in (T/G), x_j \in (G/C)\} \\ Germ^*(h) &= Germ(h) \setminus \{1_G\} \end{aligned}$$

Remark 2.25 It is worth noting that, given a similarity h from G to M then we have $Germ_h(T, xC) = Germ_h(Ty, C) = 1_G$, for each $x, y \in G$, where $T = CH(h)$ and $C = CV(h)$.

Remark 2.26 Likewise it is worth mentioning that, if $g, g' \in (T/G)$ ($T = CH(f^\phi)$) are such that $\phi(gg') = \phi(g)\phi(g')$ then it appears an non-mutating zone in $(Tg, g'C)$, since $Germ_h(Tg, g'C) = 1_G$. Therefore, it is important to define the second similarity factor ϕ respecting the homomorphy condition as far as possible.

Definition 2.27 Once defined the concept of germs at level 2 of a similarity h , one may analogously define the germs at level 1 and 3 as follows:

We say that ζ is a germ at level 1 of the similarity h in the zone (g_i, x_j) and denote $\zeta = Germ_h^1(g_i, x_j)$, if $h(\zeta g_i x_j) = h(g_i)h(x_j)$. Similarly, we say that ζ' is a germ at level 3 of the similarity h in the zone (g_i, x_j) and denote $\zeta' = Germ_h^3(g_i, x_j)$ if $h(g_i x_j \zeta') = h(g_i)h(x_j)$

Remark 2.28 To study the similarities we shall mainly use germs at level 2 for simplicity's sake, since $Germ_h(g_i, x_j) = Germ(Tg_i, x_j C)$, but, at level 1,

$$Germ_h^1(tg_i, x_j C) = Germ_h^1(g_i, x_j C)^{t^{-1}},$$

and at level 3,

$$Germ_h^3(Tg_i, x_j c) = Germ_h^3(Tg_i, x_j)^c.$$

Proposition 2.29 Given a similarity h from G to M with $T = CH(h)$, $C = CV(h)$, if $\zeta = Germ_h(Tg_i, x_j C)$ then $\zeta = g_i^{-1}h^{-1}(h(g_i)h(x_j))x_j^{-1}$

Proof. The proof is easily obtained from the definitions. \square

Definition 2.30 Given the mutation f^ϕ from G to M associated to T and V , we shall say that it is a mutation of order s if $|Germ^*(f^\phi)| = s$. If $s = 1$ then we shall say that it is a simple mutation.

Definition 2.31 Following Definition 2.24 we construct the table of germs of the mutation f^ϕ as sketched in the following picture

		$x_1 C$	\cdots	$x_j C$	\cdots	$x_r C$	
Tg_1		1_G	\cdots	1_G	\cdots	1_G	
\vdots		\cdots	\cdots	\cdots	\cdots	\cdots	
Tg_i		1_G	\cdots	ζ_i^j	\cdots	ζ_i^r	
\vdots		\cdots	\cdots	\cdots	\cdots	\cdots	
Tg_k		1_G	\cdots	ζ_k^j	\cdots	ζ_k^r	

where $\zeta_i^j = Germ_{f^\phi}(Tg_i, x_j C)$. We associate to this table the following matrix of germs of the mutation:

$$(\zeta_i^j)_{\substack{1 \leq j \leq r \\ 1 \leq i \leq k}} \in Mat(|G : T| \times |G : C|, G)$$

and the mutation's system, with indeterminates (ζ_i^j) given by

$$g_i \zeta_i^j x_j = (f^\phi)^{-1}(f^\phi(g_i) f^\phi(x_j))$$

$$2 \leq i \leq k, 2 \leq j \leq r.$$

Definition 2.32 We call unit area, of height $|T|$ and base $|C|$, of the mutation f^ϕ , to each of the zones $Tg_i \times x_j C$ of its table of germs.

We shall call mutating area of f^ϕ to each unit area such that the germ in this area is not the identity of G .

Remark 2.33 The fact that the mutating zone of f^ϕ , with $T = CH(f^\phi)$ and $C = CV(f^\phi)$ are product of right classes of G modulo T by left classes of G modulo C gives us an “economical” test for the construction of isomorphisms, since this may eventually allow us to easily check whether two given groups are isomorphic or not by the construction of the corresponding mutation. As an example, by just finding three germs, we easily obtain that $D_3 \times C_2 \cong D_6$.

Consider the groups G , generated by the matrices $A = \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix}$ and $B = \begin{bmatrix} 0 & i \\ i & 0 \end{bmatrix}$, with the group law being given by the product of matrices, and $M = \langle i, j, k/i^2 = j^2 = k^2 = -1 \rangle$ and the cork screw law. Both groups have order 8. Furthermore $G \geq T = \langle A \rangle \stackrel{f}{\cong} C_4 \cong \langle i \rangle = V \leq M$, where $f: \langle A \rangle \rightarrow \langle i \rangle$ is defined by mapping $A \mapsto i$. We choose $(T/G) = \{I, B\}$ and $(V/M) = \{1, j\}$, $\phi(I) = 1$, $\phi(B) = j$. We thereby get a mutation $f^\phi: G \rightarrow M$. Since $CH(f^\phi) = \langle A \rangle$, $CV(f^\phi) \leq G$ and the germ is unique in each of the mutating zones, it is enough to check the homomorphy condition in the following cases:

$$\begin{aligned} f^\phi(BA) &= f^\phi(B)f^\phi(A) \\ f^\phi(BB) &= f^\phi(B)f^\phi(B) \end{aligned}$$

to conclude that f^ϕ is an isomorphism. Therefore G and M are distinct presentations of the quaternion group $Q_8 = \langle a, b/a^4 = 1, a^2 = b^2, a^b = a^{-1} \rangle$.

Towards the minimization of the number of germs of a mutation we consider the following

Definition 2.34 Given a mutation f^ϕ from G to M associated to T and V , we shall say that f^ϕ is a principal mutation of first order if T and V have maximum order verifying $T \cong V$.

Considering T, V proper subgroups of maximum order of G and M , respectively, and $f: T \rightarrow M$ a non-isomorphism, if there exists $K \leq T$ and $K' \leq V$ such that $g: K \rightarrow K'$ is an isomorphism and there exists a second K -similarity factor φ such that $f = g^\varphi$, then we shall say that $f^\phi = (g^\varphi)^\phi$ is a principal mutation of second order.

We may similarly define higher order principal mutations.

Definition 2.35 Given a mutation f^ϕ from G to M associated to T and V , if neither T nor V have maximum order verifying the condition $T \cong V$ nor its order is a divisor of the order of the proper isomorphic subgroups of G and M of maximum order as such, then we shall say that f^ϕ is a secondary mutation of first order. According to (2.34) one may define higher order secondary mutations.

Proposition 2.36 *Given a mutation f^ϕ from G to M (principal or secondary) of first order, associated to T and V , if there exists $K \leq G$ and $K' \leq M$ such that $|K| = |K'|$, $K \geq T$, $K' \geq V$, we may consider f^ϕ as a mutation of second order $(f^\varphi)^\delta$ where $f^\varphi: K \rightarrow K'$.*

In this situation, the germs of the mutation of first order and those of the one of second order coincide.

Proof. Let $\{x_i\}_{i=1}^k$ (resp. $\{y_j\}_{j=1}^r$, resp. $\{z_i\}_{i=1}^k$, resp. $\{w_j\}_{j=1}^r$) be a right transversal of K in G (resp. of T in K , resp. of K' in M , resp. V in K'). Then it may be easily checked that $\{y_j x_i\}$ (resp. $\{w_j z_i\}$) is a right transversal of T in G (resp. of V in M). Furthermore, given $g \in G$, $g = kx_i = ty_j x_i$, and then one has: $f^\phi(g) = f^\phi(ty_j x_i) = f(t)\phi(y_j x_i)$ and $(f^\varphi)^\delta(g) = (f^\varphi)^\delta(ty_j x_i) = f^\varphi(ty_j)\delta(x_i) = f(t)\varphi(y_j)\delta(x_i)$ hence, by defining $\phi(y_j x_i) = w_j z_i$ and $\varphi(y_j) = w_j$, then it follows that $f^\phi = (f^\varphi)^\delta$ thereby obtaining the equality of their mutating zones and their germs. \square

Remark 2.37 According to the latter proposition, to minimize the number of germs of a mutation we have to construct the second similarity factor such that the mutation be of maximum order. Normally, given two groups, a principal mutation of order one will be constructed, for easiness' sake, forcing the second similarity factor to respect the homomorphi condition at maximum, which is equivalent to the principal mutation being of maximum order.

Remark 2.38 Regarding to the convenience of the mutation being principal or secondary, in most of the cases the principal one will give less number of germs and less mutating surface than the secondary one. But there are some instances wher the secondary mutations has less number of germs and less mutating surface than in the case of the principal one. For instance, given the groups of order 12 C_{12} and A_4 , we may construct a maximal mutation from th cyclic subgroup of order 3 and obtain a matrix of germs 4×6 with 7 germs and 84 mutating zones. Nevertheless, if we construct the secondary mutation from a cyclic subgroup of order 2 and forcing it to be of maximum order considering the subgroup of order 4 in C_{12} and the product of two cyclic subgroups of order 2 of A_4 , one obtains a matrix of germs 6×12 but with only 3 germs and 80 mutating areas.

We now study the product of similarities and, consequently, the germs in this product. The following proposition may be easily proven

Proposition 2.39 *Given a R -similarity h from G to M and h' a R' -similarity from G' to M' then $h \times h'$ is a $(R \times R')$ -similarity from $G \times G'$ to $M \times M'$ which will be called the similarity product of h and h' . Furthermore $CH(h \times h') = CH(h) \times CH(h')$ and $CV(h \times h') = CV(h) \times CV(h')$.*

Remark 2.40 The previous remark may be easily extended to arbitrary sets of R_i -similarities $\{h_i\}$, thus yielding a $\coprod R_i$ -similarity $\coprod h_i$.

Proposition 2.41 *Let h be a R -similarity from G to M and h' a R' -similarity from G' to M' , with $T = CH(h)$, $T' = CH(h')$, $C = CV(h)$ and $C' = CV(h')$. If $\zeta = \text{Germ}_h(Tg, xC)$ and $\zeta' = \text{Germ}_{h'}(T'g', x'C')$ then*

$$(\zeta, \zeta') = \text{Germ}_{h \times h'}((T \times T')(g, g'), (x, x')(C \times C')).$$

Proof. Straightforward from (2.39) and the definitions. \square

We now deal with semidirect products.

Proposition 2.42 *Given groups $G = T \times_{\alpha} H$ and $M = V \times_{\beta} K$, with $T \stackrel{f}{\cong} V$ and $H \cong K$ then there exists a mutation f^{ϕ} from G to M such that $CH(f^{\phi}) = T$ and $H \subseteq CV(f^{\phi})$.*

Proof. We consider $f: T \rightarrow V$ as first similarity factor, H (resp. K) as a right transversal of T (resp. V) in G (resp. M) and $\phi: H \rightarrow K$ as second similarity factor. Obviously, $CH(f^{\phi}) = T$; on the other hand, given $h \in H$, $g = th'$, with $t \in T$, $h' \in H$.

$$f^{\phi}(gh) = f^{\phi}(th'h) = f(t)\phi(h'h) = f(t)\phi(h')\phi(h) = f^{\phi}(th')f^{\phi}(h) = f^{\phi}(g)f^{\phi}(h)$$

thus $h \in CV(f^{\phi})$. \square

3 Evolutive chains (Second stage)

3.1. Once obtained the germ matrices we have considered in the set $\mathfrak{Gr}(n)$ of the non-isomorphic groups of a certain order n , what we have called an evolutive chain, since this is related to the minimum condition on the lengths of the links of the chain, these lengths being given by the number of germs in the corresponding mutation. We search how to pass from one to another structure with minimum number of steps in germs and mutating zones.

In the set $\mathfrak{Gr}(16)$, in which there exist 14 non-isomorphic groups, we have split the evolutive chain in four subchains. We have used the fact that, given a mutation between two groups, if the image of the center of the first group is contained in the center of the other, some more non-mutating zones eventually appear, to decompose the study of $\mathfrak{Gr}(16)$ in 4 subchains, attending to the structure of the centers in the non-abelian case. These 4 subchains are minimal, since each link has length one, i.e., the mutations have a unique germ.

We finally cite a subchain which relates the different elements in this partition and give the number of germs of each of its mutations.

The evolutive chains may be represented in the following picture, in which the

numbers under the arrows stand for the number of germs, are the following:

n	Evolutionary chain in $\mathfrak{Gr}(n)$
4	$C_4 \xrightarrow{1} C_2 \times C_2$
6	$C_6 \xrightarrow{3} D_3$
8	$C_8 \xrightarrow{1} C_4 \times C_2 \xrightarrow{1} C_2 \times C_2 \times C_2 \xrightarrow{1} D_4 \xrightarrow{1} Q_8$
9	$C_9 \xrightarrow{1} C_3 \times C_3$
10	$C_{10} \xrightarrow{5} D_5$
12	$D_6 \xrightarrow{1} DC_3 \xrightarrow{2} C_{12} \xrightarrow{1} C_6 \times C_2 \xrightarrow{3} A_4$
14	$C_{14} \xrightarrow{7} D_7$
16	G abelian
	$C_{16} \xrightarrow{1} C_8 \times C_2 \xrightarrow{1} C_4 \times C_2 \xrightarrow{1} C_4 \times C_2 \times C_2 \xrightarrow{1} C_2 \times C_2 \times C_2 \times C_2$
	$Z(G) \cong C_4$ $M_{16} \xrightarrow{1} (C_4 \times C_2) \times_{\alpha} C_2$
	$Z(G) \cong C_2 \times C_2$ $(C_4 \times C_2) \times_{\beta} C_2 \xrightarrow{1} D_4 \times C_2 \xrightarrow{1} Q_8 \times C_2 \xrightarrow{1} C_4 \times_{\alpha} C_4$
	$Z(G) \cong C_2$ $Q_{16} \xrightarrow{1} SD_{16} \xrightarrow{1} D_8$
$C_8 \times C_2 \xrightarrow{1} M_{16} \xrightarrow{3} Q_8 \times C_2 \xrightarrow{1} Q_{16}$	

3.2 Evolutionary chain in $\mathfrak{Gr}(6)$

As an example and to contrast it with the one considered in Section 1 let us consider the evolutionary chain in $\mathfrak{Gr}(6)$.

Given the set $\mathfrak{Gr}(6) = \{C_6, D_3\}$ we consider the chain of mutations from C_6 to D_3 . Let

$$G = C_6 = \langle x/x^6 = 1 \rangle = \{1, x, x^2, x^3, x^4, x^5\}$$

$$M = D_3 = \langle y, z/y^3 = z^2 = 1, y^z = y^{-1} \rangle = \{1, y, y^2, z, yz, y^2z\}$$

In the set $\Delta = \{(T, V)/T \leq C_6, V \leq D_3, T \cong V\}$ the pair $(\langle x^2 \rangle, \langle y \rangle)$ has maximal order.

We consider the isomorphism $f: \langle x^2 \rangle \rightarrow \langle y \rangle$ given by $x^2 \mapsto y$ as first C_3 -similarity factor and extend it to a bijection $f^\phi: C_6 \rightarrow D_3$ via a second C_3 -similarity factor ϕ of domain (resp. codomain) a right transversal of $\langle x^2 \rangle$ (resp. $\langle y \rangle$) in C_6 (resp. D_3) given by $\phi: \{1_G, x\} \rightarrow \{1_M, z\}$, $\phi(1_G) = 1_M$, $\phi(x) = z$. Hence $f^\phi(x^{2i+j}) = f(x^{2i})\phi(x^j) = y^i z^j$ ($0 \leq i \leq 2, 0 \leq j \leq 1$). According to the definition, the mutation from C_6 to D_3 is

$$f^\phi \downarrow \begin{array}{|c|c|c|c|c|c|} \hline 1_G & x^2 & x^4 & x & x^3 & x^5 \\ \hline 1_M & y & y^2 & z & yz & y^2z \\ \hline \end{array}$$

Hence we have $T = CH(f^\phi) = \langle x^2 \rangle \cong C_3$ and $C = CV(f^\phi) = \langle x^3 \rangle \cong C_2$ and the following table of germs

	C	xC	x^2C
T	1_G	1_G	1_G
Tx	1_G	x^4	x^2

Germs = $\{x^2, x^4\}$
Number of germs = 2
Number of mutating areas = 2
Surface unit of mutating area = 6
Surface of mutating zone = 12
(out of a total amount of 36)

It is worth pointing out that there only exist two distinct germs of the identity and they are exactly the generators of the horizontal field. Furthermore, the mutating zone has 12 units and the bijection constructed in (2) has 21.

With regards to the inverse mutation of this one, we point out that the number of germs is also 2, a coincidence that occurs in all the mutations we have studied in $\mathfrak{Gr}(n)$, $n \leq 16$.

4 Parametrized mutations (Third stage)

The analysis of the mutations studied for the groups of order ≤ 16 , suggested us a generalized study, which we call parametrized mutations, since the germs are determined by arithmetical conditions which obviously involve the parameters of the order of the group.

4.1 The general case

Let

$$G = C_{p^n} = \langle x/x^{p^n} = 1 \rangle = \{x^i : 0 \leq i \leq p^n - 1\}$$

and

$$M = C_p \times \dots \times C_p = \langle a_0, \dots, a_{n-1} / a_i^p = 1, a_i a_j = a_j a_i, 0 \leq i, j \leq n - 1 \rangle =$$

$$\{a_0^{i_0} \dots a_{n-1}^{i_{n-1}} : 0 \leq i_0, \dots, i_{n-1} \leq p - 1\}$$

The pair $(\langle x^{p^{n-1}} \rangle, \langle a_{n-1} \rangle)$ is maximal in the set $\Delta = \{(T, V) : T \leq C_{p^n}, V \leq C_p \times \dots \times C_p, T \cong V\}$. Consider the isomorphism $f: \langle x^{p^{n-1}} \rangle \longrightarrow \langle a_{n-1} \rangle$ as first C_p -similarity factor, given by $f(x^{p^{n-1}}) = a_{n-1}$. This isomorphism can be extended to a bijection

$$f^\phi: C_{p^n} \longrightarrow C_p \times \dots \times C_p$$

via a second C_p -similarity factor ϕ between a right transversal \mathcal{A} of T in G and a right transversal \mathcal{B} of V in M , which is defined as follows: consider the sets

$$\begin{aligned} \mathcal{A} &= \{x^{i_{n-2}p^{n-2}+\dots+i_1p+i_0} : 0 \leq i_0, \dots, i_{n-2} < p\} \\ \mathcal{B} &= \{a_{n-2}^{i_{n-2}} \cdots a_1^{i_1} a_0^{i_0} : 0 \leq i_0, \dots, i_{n-2} < p\} \end{aligned}$$

The map ϕ is defined to be the map $\mathcal{A} \rightarrow \mathcal{B}$ for which

$$\phi(x^{i_{n-2}p^{n-2}+\dots+i_1p+i_0}) = a_{n-2}^{i_{n-2}} \cdots a_1^{i_1} a_0^{i_0}$$

Therefore

$$f\phi(x^{i_{n-1}p^{n-1}+\dots+i_1p+i_0}) = a_{n-1}^{i_{n-1}} \cdots a_1^{i_1} a_0^{i_0}$$

for every $0 \leq i_0, \dots, i_{n-1} < p$. Hence, one has $T = CH(f\phi) = \langle x^{p^{n-1}} \rangle \cong C_p$ and, since both are abelian, $C = CV(f\phi) = T$.

Given $a, b \in \mathcal{A}$, with

$$\begin{aligned} a &= x^{i_{n-2}p^{n-2}+\dots+i_1p+i_0} \\ b &= x^{j_{n-2}p^{n-2}+\dots+j_1p+j_0} \end{aligned}$$

then the area $Ta \times bC$ is mutating if and only if there exists some k ($0 \leq k \leq n-2$), such that $i_k + j_k \geq p$. If there exists a unique such k , then germ in the cited mutating area is

$$Germ_{f\phi}(Ta, bC) = x^{p^n - p^{k+1}}$$

Given $a, b \in \mathcal{A}$, considering the set $\mathcal{K} = \{k : i_k + j_k \geq p\}$, one has

$$Germ_{f\phi}(Ta, bC) = \prod_{k \in \mathcal{K}} x^{p^n - p^{k+1}}$$

Hence, since the former germs are distinct for distinct cardinalities of \mathcal{K} and distinct $k \in \mathcal{K}$ one has:

if $|\mathcal{K}| = 1$ then there exist $n - 1$ distinct germs

if $|\mathcal{K}| = 2$ then there exist $\binom{n-1}{2}$ distinct germs

.....

if $|\mathcal{K}| = n - 1$ then there exists $\binom{n-1}{n-1=1}$ germ.

Whence the total number of germs in the mutation $f\phi$, different from the identity of G , is

$$\binom{n-1}{1} + \cdots + \binom{n-1}{n-1} = 2^{n-1} - 1$$

Therefore one has that the set of germs, including the identity of G is:

$$Germ(f\phi) = \{x^{p^n - (s_1p + \dots + s_{n-1}p^{n-1})} : 0 \leq s_1, \dots, s_{n-1} \leq 1\}$$

Regarding the inverse mutation $(f^\phi)^{-1}$, let $V = f^\phi(T) = \langle a_{n-1} \rangle$ and $D = f^\phi(C) = V$. Given a mutating area $V f^\phi(a) \times f^\phi(b) D$, where

$$\begin{aligned} f^\phi(a) &= a_{n-2}^{i_{n-2}} \cdots a_1^{i_1} a_0^{i_0} \\ f^\phi(b) &= a_{n-2}^{j_{n-2}} \cdots a_1^{j_1} a_0^{j_0} \end{aligned}$$

We consider the set

$$\begin{aligned} \mathcal{K}' &= \{k : i_k + j_k \geq p \vee (i_k + j_k = p - 1 \wedge i_{k-1} + j_{k-1} \geq p) \vee \\ &\quad (i_k + j_k = i_{k-1} + j_{k-1} = p - 1 \wedge i_{k-2} + j_{k-2} \geq p) \vee \\ &\quad \dots \vee (i_k + j_k = i_{k-1} + j_{k-1} = \dots = i_1 + j_1 = p - 1 \wedge i_0 + j_0 \geq p)\} \end{aligned}$$

In this situation, one has

$$Germ_{(f^\phi)^{-1}}(V f^\phi(a), f^\phi(b) D) = \prod_{k \in \mathcal{K}'} a_{k+1}$$

thus the set of germs of the inverse mutation is

$$Germ((f^\phi)^{-1}) = \{a_{n-1}^{s_{n-1}} \cdots a_1^{s_1} : 0 \leq s_1, \dots, s_{n-1} \leq 1\}$$

from where one deduces that the number of distinct germs of $(f^\phi)^{-1}$, which are distinct from the identity of $C_p \times \dots \times C_p$ is $2^{n-1} - 1$, which coincides with the number of germs of f^ϕ .

4.2 Mutation between C_{16} and $C_2 \times C_2 \times C_2 \times C_2$

We now study the particular case $p = 2, n = 4$, in order to get a clearer vision of the germ tables of the mutation and its inverse.

Let $G = C_{16} = \langle x/x^{16} = 1 \rangle$ and

$$\begin{aligned} M &= C_2 \times C_2 \times C_2 \times C_2 = \\ &\langle a, b, c, d/a^2 = b^2 = c^2 = d^2 = 1, a^b = a, a^c = a, a^d = a, b^c = b, b^d = b, c^d = c \rangle \end{aligned}$$

The element $(\langle x^8 \rangle, \langle d \rangle)$ is maximal in the set

$$\Delta = \{(T, V) : T \leq C_{16}, V \leq C_2 \times C_2 \times C_2 \times C_2, T \cong V\}$$

Consider the isomorphism $f: \langle x^8 \rangle \rightarrow \langle d \rangle$ as first C_2 -similarity factor, which is given by $f(x^8) = d$. This isomorphism extends to a bijection

$$f^\phi: C_{16} \rightarrow C_2 \times C_2 \times C_2 \times C_2$$

via a second C_2 -similarity factor ϕ . As seen before, ϕ is given by

$$\phi: \{1_G, x, \dots, x^7\} \rightarrow \{1_M, a, b, c, ab, ac, bc, abc\}$$

given by $\phi(x^{4i_2+2i_1+i_0}) = c^{i_2} b^{i_1} a^{i_0}$ ($0 \leq i_0, i_1, i_2 < 2$) thus

$$f^\phi(x^{8i_3+4i_2+2i_1+i_0}) = f(x^{8i_3})\phi(x^{4i_2+2i_1+i_0}) = d^{i_3} c^{i_2} b^{i_1} a^{i_0}$$

($0 \leq i_0, i_1, i_2, i_3 < 2$) This is represented in the following picture

$$f^\phi \downarrow \begin{array}{|c|c|c|c|c|c|c|c|} \hline 1_G & x^8 & x & x^9 & x^2 & x^{10} & x^3 & x^{11} \\ \hline 1_M & d & a & ad & b & bd & ab & abd \\ \hline \end{array}$$

$$f^\phi \downarrow \begin{array}{|c|c|c|c|c|c|c|c|} \hline x^4 & x^{12} & x^5 & x^{13} & x^6 & x^{14} & x^7 & x^{15} \\ \hline c & cd & ac & acd & bc & bcd & abc & abcd \\ \hline \end{array}$$

Hence one has $T = CH(f^\phi) = \langle x^8 \rangle \cong C_2$ and, since both are abelian, $C = CV(f^\phi) = T$ and the germ table is as follows

	C	x^2C	x^4C	x^6C	x^8C	$x^{10}C$	$x^{12}C$	$x^{14}C$
T	1_G	1_G	1_G	1_G	1_G	1_G	1_G	1_G
Tx	1_G	x^{14}	1_G	x^{14}	1_G	x^{14}	1_G	x^{14}
Tx^2	1_G	1_G	x^{12}	x^{12}	1_G	1_G	x^{12}	x^{12}
Tx^3	1_G	x^{14}	x^{12}	x^{10}	1_G	x^{14}	x^{12}	x^{10}
Tx^4	1_G	1_G	1_G	1_G	x^8	x^8	x^8	x^8
Tx^5	1_G	x^{14}	1_G	x^{14}	x^8	x^6	x^8	x^6
Tx^6	1_G	1_G	x^{12}	x^{12}	x^8	x^8	x^4	x^4
Tx^7	1_G	x^{14}	x^{12}	x^{10}	x^8	x^6	x^4	x^2

*Germ*s= $\{x^2, x^4, x^6, x^8, x^{10}, x^{12}, x^{14}\}$

Frequencies= $1, 3, 3, 9, 3, 9, 9$

Number of germs= 7

Number of mutating areas= 37

Surface unit of mutating area= 4

Surface of mutating zone= 148

(out of a total amount of 256)

If $V = D = f^\phi(T) \cong C_2$ one has the following table of germs for the inverse mutation:

	D	aD	bD	abD	cD	acD	bcD	$abcD$
V	1_M	1_M	1_M	1_M	1_M	1_M	1_M	1_M
Va	1_M	b	1_M	bc	1_M	b	1_M	bcd
Vb	1_M	1_M	c	c	1_M	1_M	cd	cd
Vab	1_M	bc	c	bc	1_M	bcd	cd	bcd
Vc	1_M	1_M	1_M	1_M	d	d	d	d
Vac	1_M	b	1_M	bcd	d	bd	d	bcd
Vbc	1_M	1_M	cd	cd	d	d	cd	cd
$Vabc$	1_M	bcd	cd	bcd	d	bcd	cd	bcd

*Germ*s= $\{b, c, bc, d, bd, cd, bcd\}$

Frequencies= $3, 3, 3, 9, 1, 9, 9$

Number of germs= 7

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