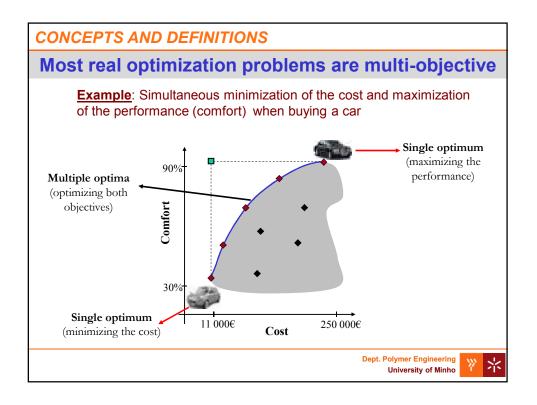
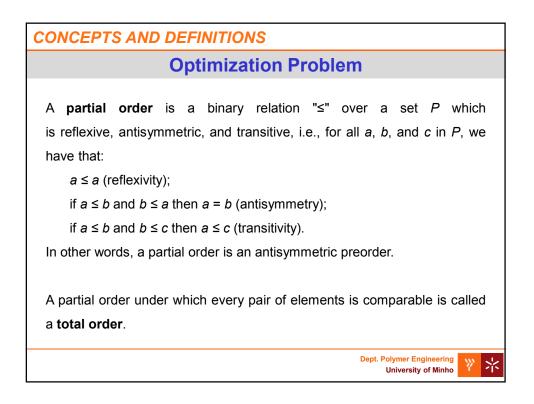
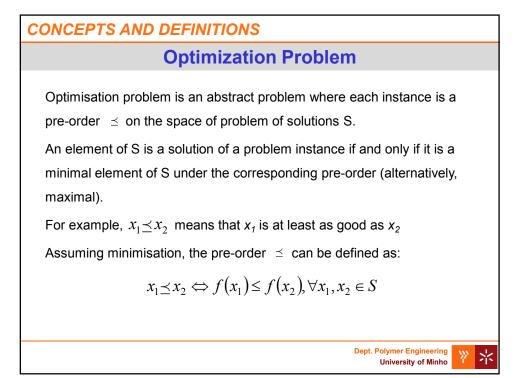
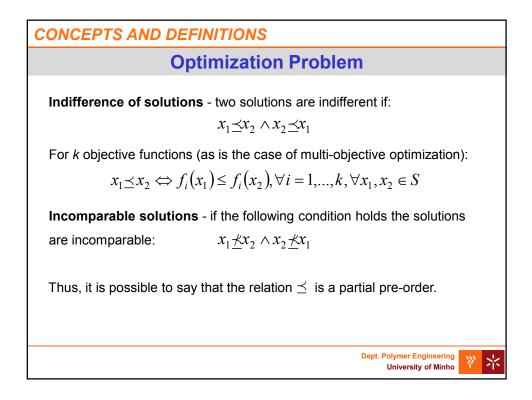


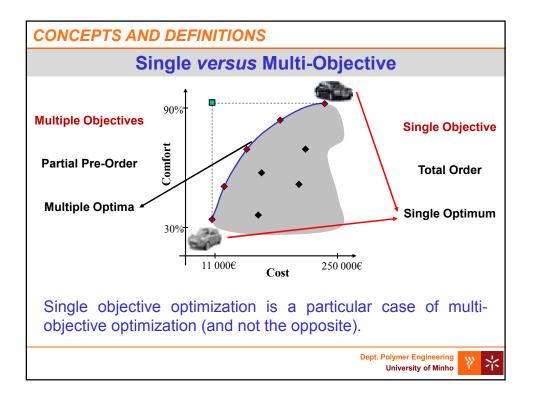
OUTLINE	
	Concepts and Definitions
	Classical Methods
	EMO Methods
	State-of-the-art EMO
	≻ NSGA-II
	> RPSGA
	Application Example
	Niching and Speciation
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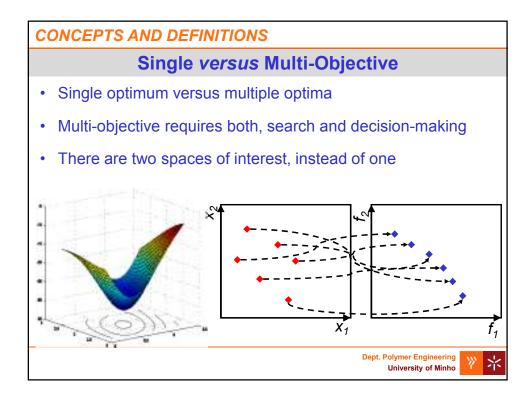


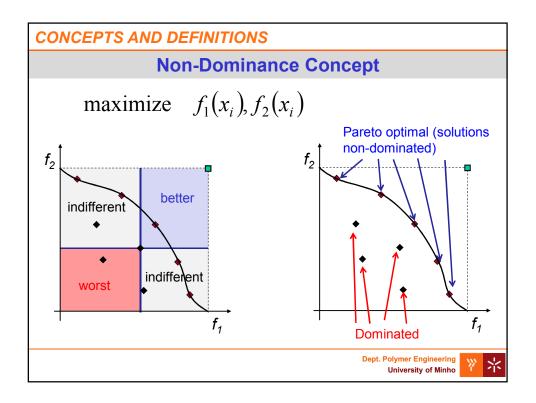


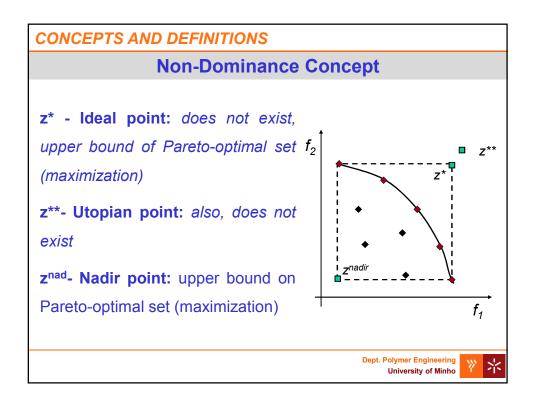


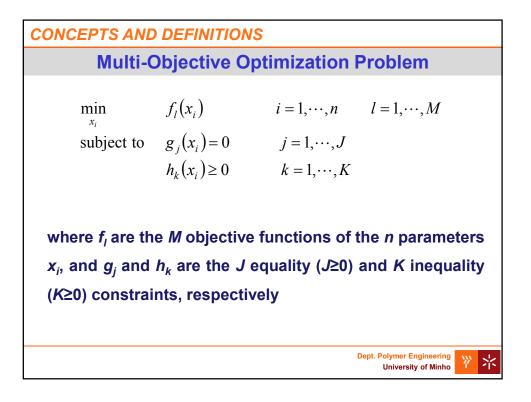


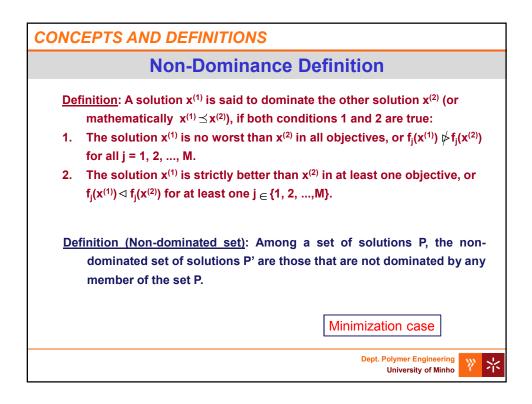






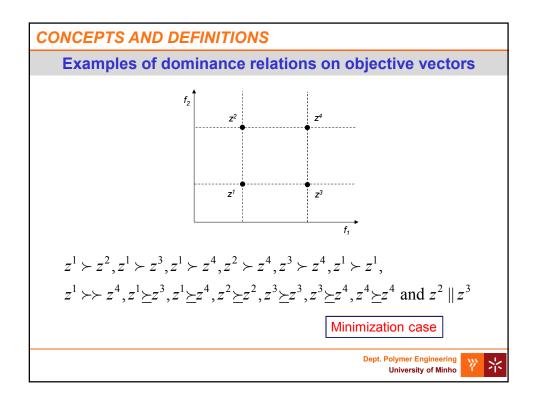


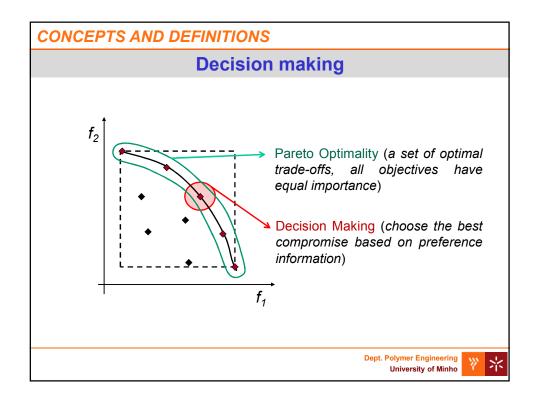


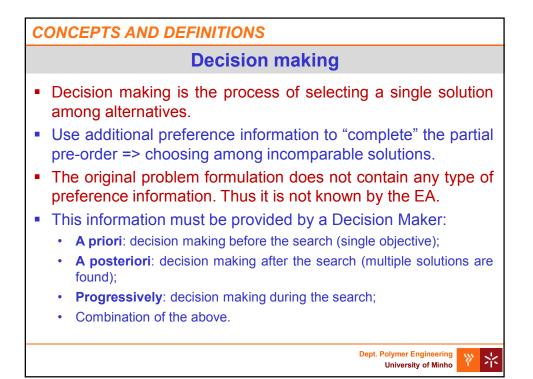


Ν	on-Domi	nance Definition
		coximation sets. The relations \prec , $\prec \prec$, \triangleleft , and \preceq are define ¹ and $A \triangleleft B$ is defined as $B \triangleright A$.
relation		objective vectors
strictly dominates	$z^1 \succ z^2$	z^1 is better than z^2 in all objectives
dominates	$x^1 \succ x^2$	x^1 is not worse than x^2 in all objectives and better in at least one objective
better		
weakly dominates	$z^1 \succeq z^2$	z^1 is not worse than z^2 in all objectives
incomparable	$z^1 z^2$	neither z^1 weakly dominates z^2 nor z^2 weakly dominates z^1
		Minimization case
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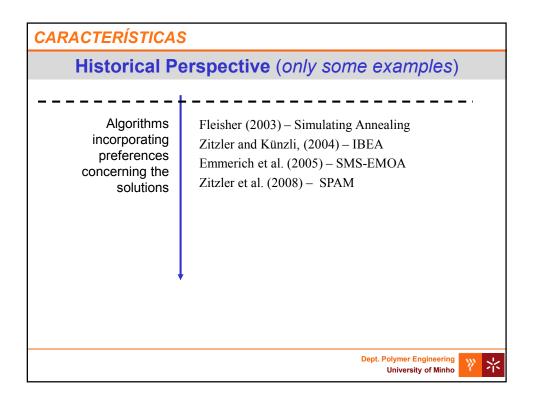
No	n-Domiı	nance Definition
relation		approximation sets
strictly dominates	$A \succ \succ B$	every $z^2 \in B$ is strictly dominated by at least one $z^1 \in A$
dominates	$A \succ B$	every $z^2 \in B$ is dominated by at least one $z^1 \in A$
better	$A \triangleright B$	every $z^2 \in B$ is weakly dominated by at least one $z^1 \in A$ and $A \neq B$
weakly dominates	$A \succeq B$	every $z^2 \in B$ is weakly dominated by at least one $z^1 \in A$
incomparable	A B	neither A weakly dominates B nor B weakly dominates A
		Minimization case

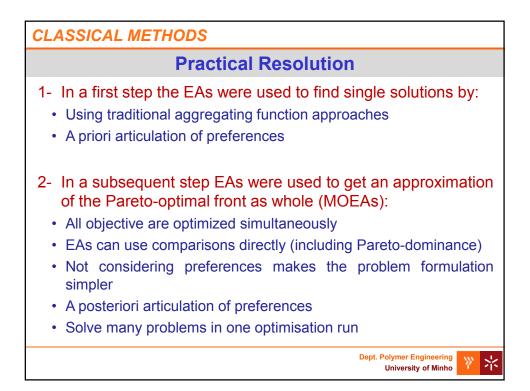


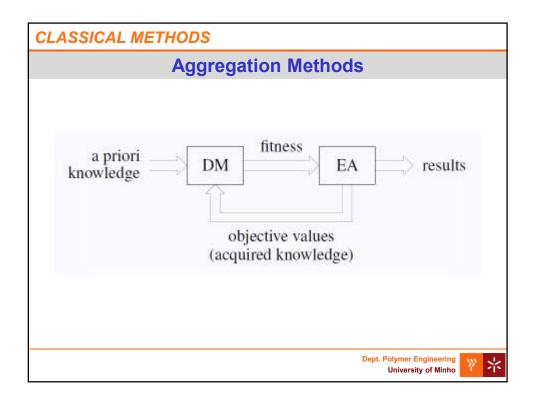


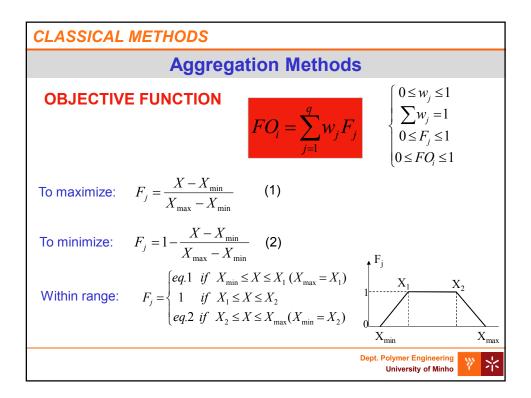


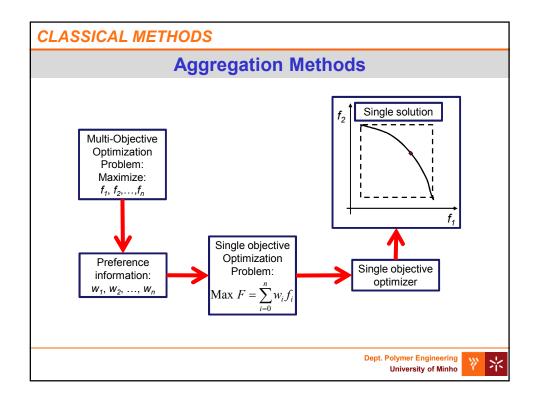
CARACTERÍSTICAS	5
Historical Pe	erspective (only some examples)
First algorithms	Schaffer (1985) – VEGA Kursawe (1990) –VOES
Classic algorithms	Fonseca and Fleming (1993) – MOGA Srinivas and Deb (1994) – NSGA Horn, Nafpliotis and Goldberg (1994) – NPGA
Elitist algorithms	Zitzler and Thiele (1999) – SPEA, (2001) – SPEA2 Deb and co-authors (2000) – NSGA-II Knowles and Corne (2000) – PAES, PESA
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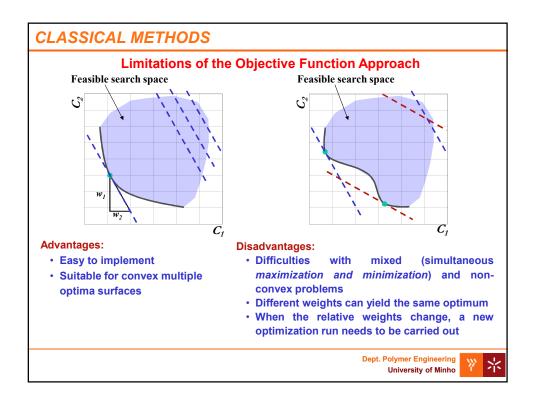


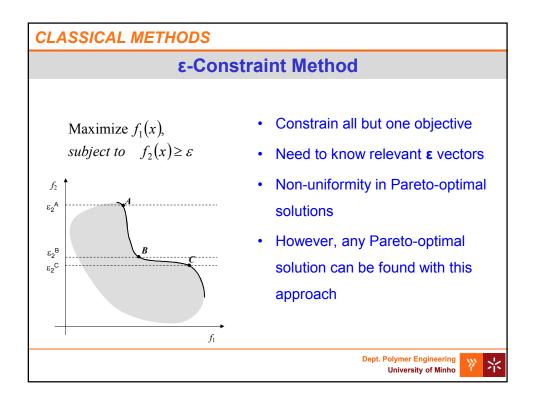


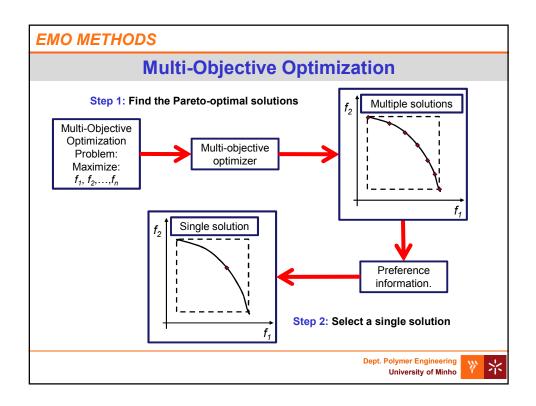


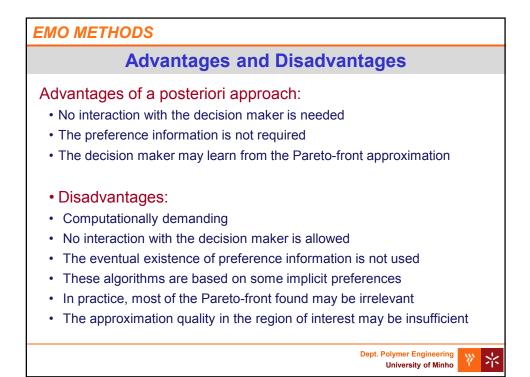


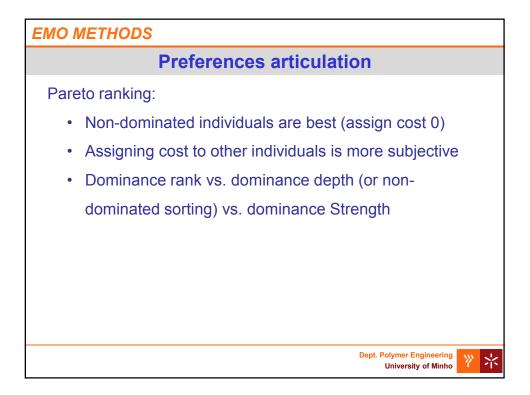


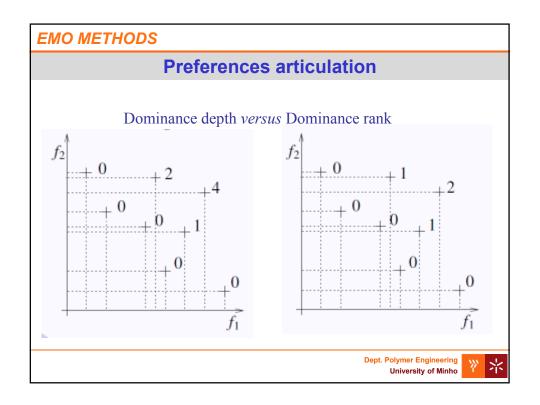


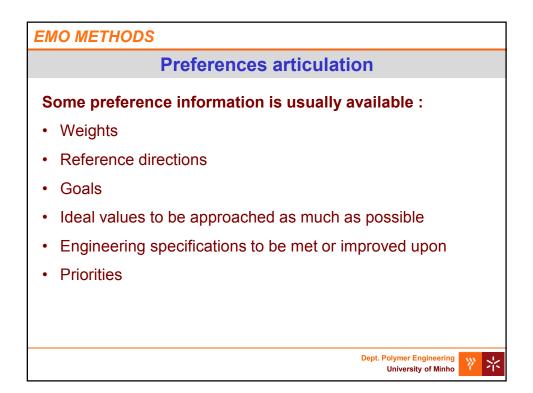


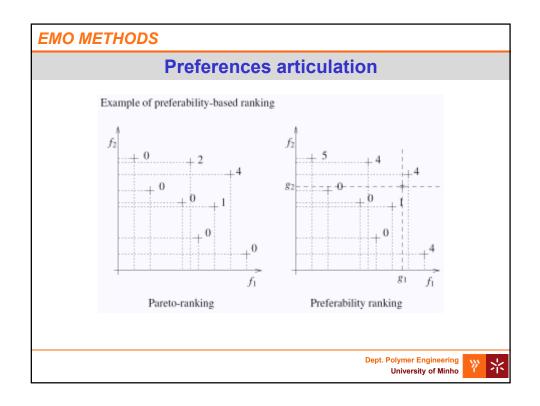




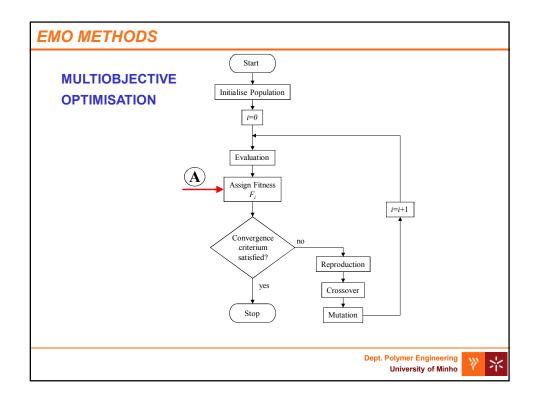


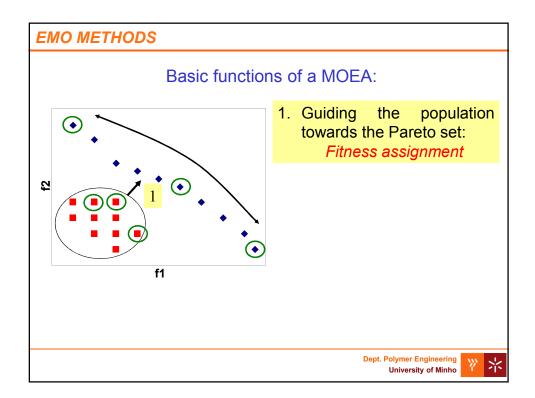


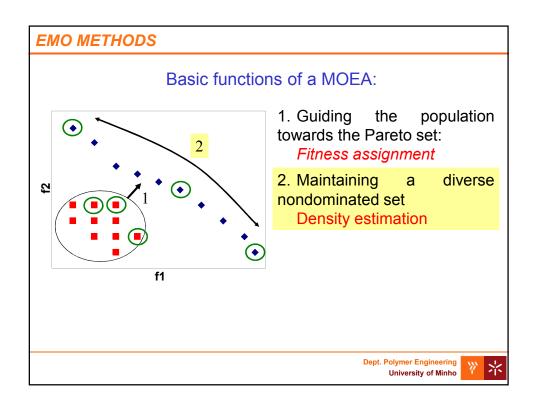


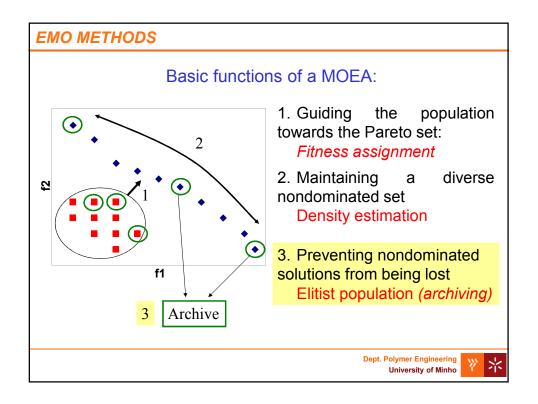


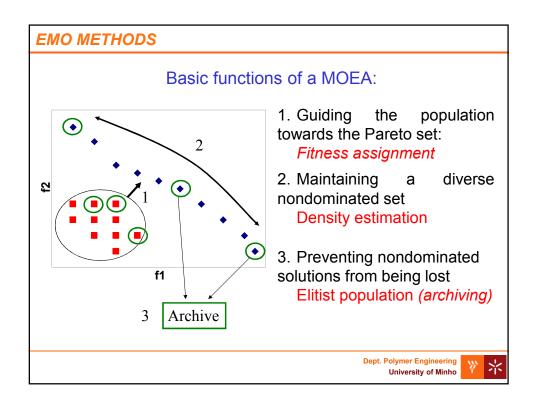
EMO METHODS
Preferences articulation
 1. All aggregations of the objectives: Weighted sum, minimax, Goal programming variants (goal + reference direction) Other comparison operators Guided dominance (Branke et al. 2001), lexicographic order
 2. Other MCDM techniques: ELECTRE (Benayoun, 1966), PROMETHEE (Brans and Vinke, 1985), GRIP (Figueira et al., 2009), etc.
Challenge:Allow the DM to state its preferences easily
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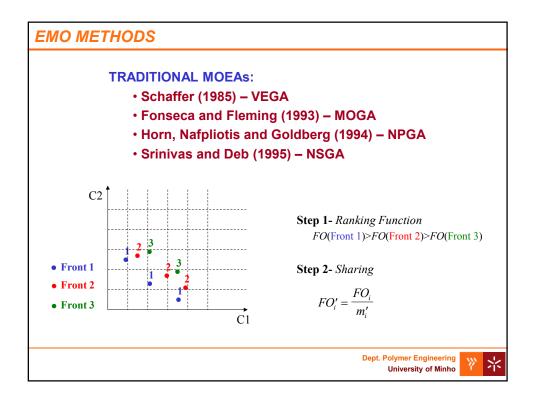


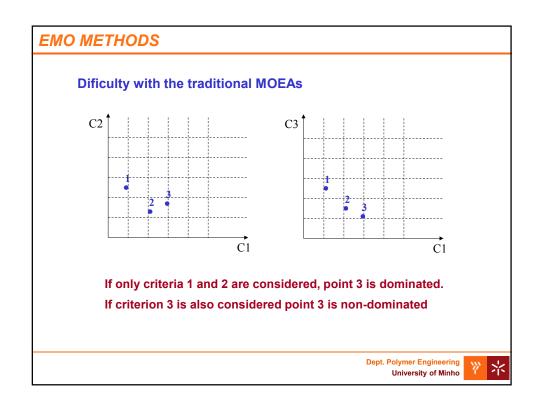


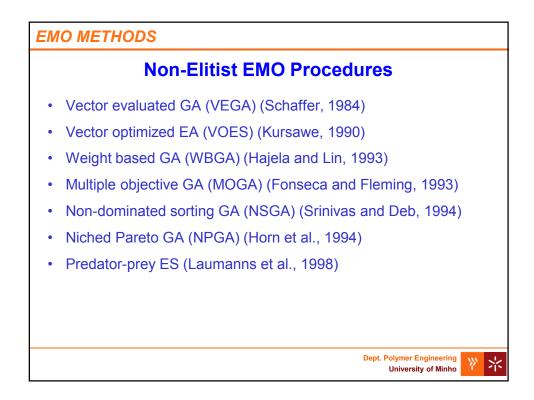












EMO METHODS

Elitist EMO Methods

- Distance-based Pareto GA (DPGA) (Osyczka and Kundu, 1995)
- Thermodynamical GA (TDGA) (Kita et al., 1996)
- Strength Pareto EA (SPEA) (Zitzler and Thiele, 1998)
- Non-dominated sorting GA-II (NSGA-II) (Deb et al., 1999)
- Pareto-archived ES (PAES) (Knowles and Corne, 1999)
- Multi-objective Messy GA (MOMGA) (Veldhuizen and Lamont, 1999)
- Other methods: Pareto-converging GA, multi-objective micro-GA, elitist MOGA with co-evolutionary sharing

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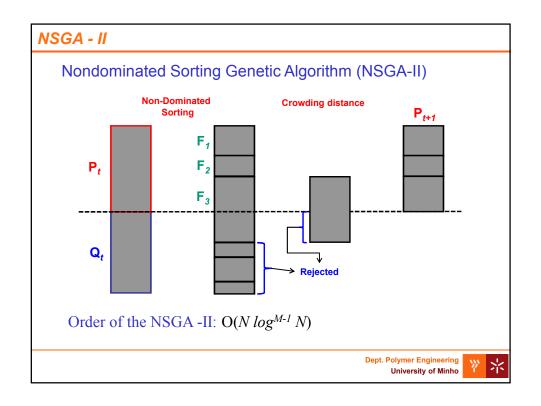
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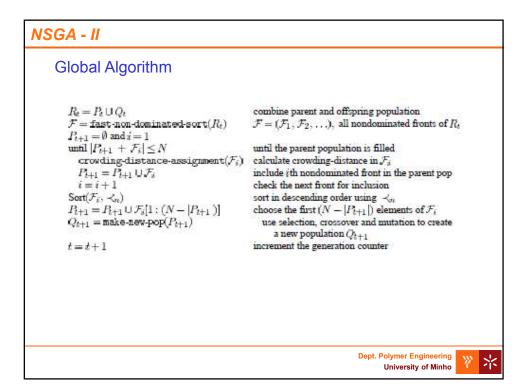
 EMO METHODS

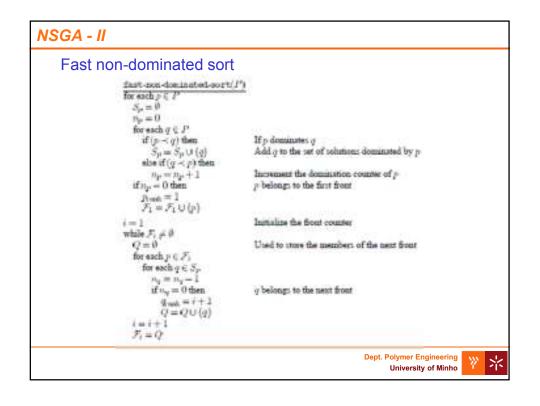
 Nondominated Sorting Genetic Algorithm (NSGA-II):

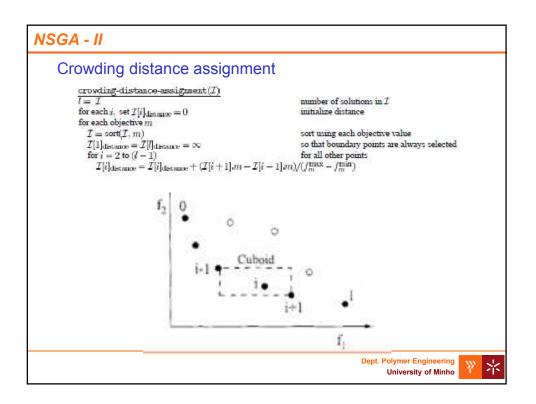
 Kalyanmoy Deb, Amrit Pratap, Sameer Agarwal and T. Meyarivan

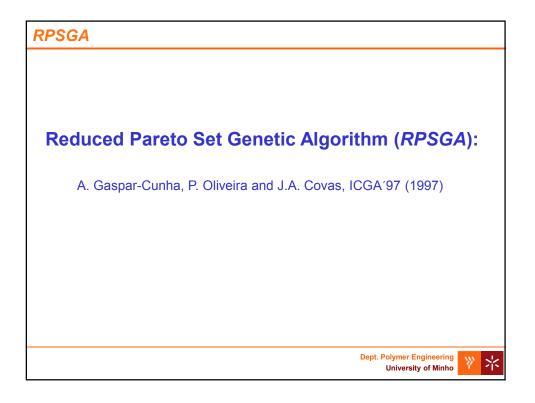
 IEEE TRANSACTIONS ON EVOLUTIONARY COMPUTATION, VOL. 6, NO. 2, APRIL 2002

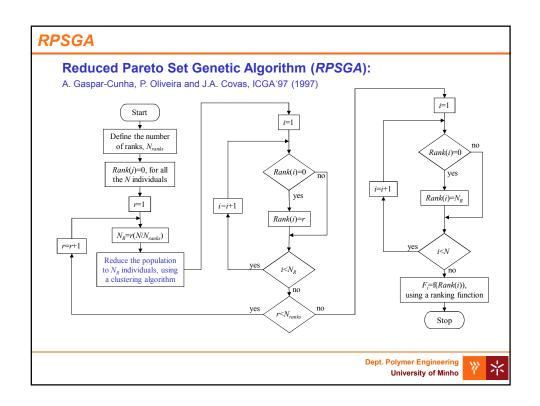


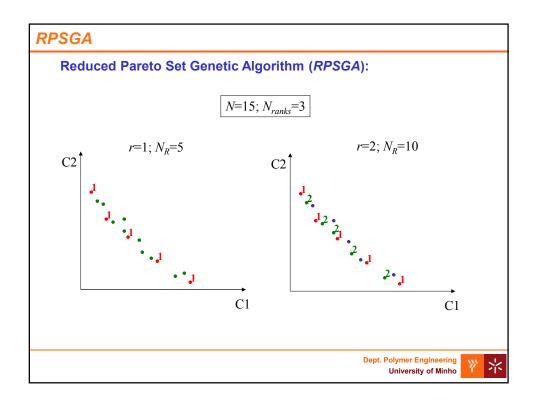


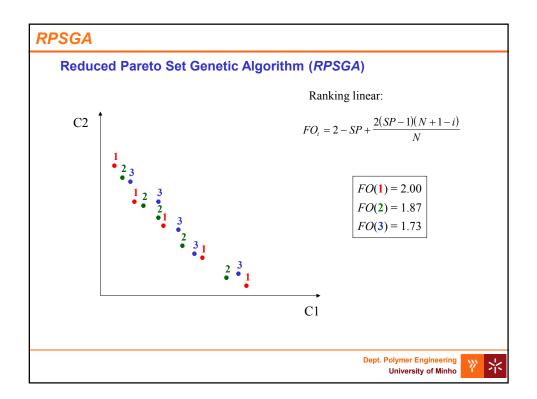


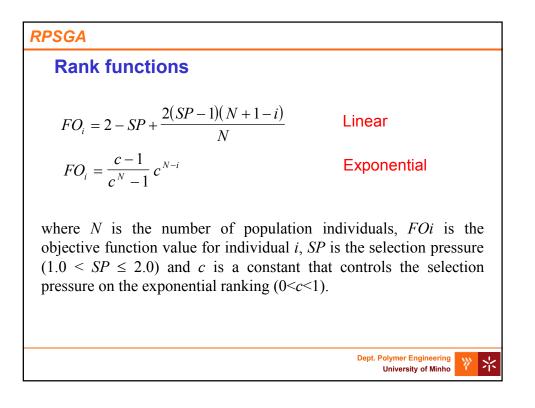


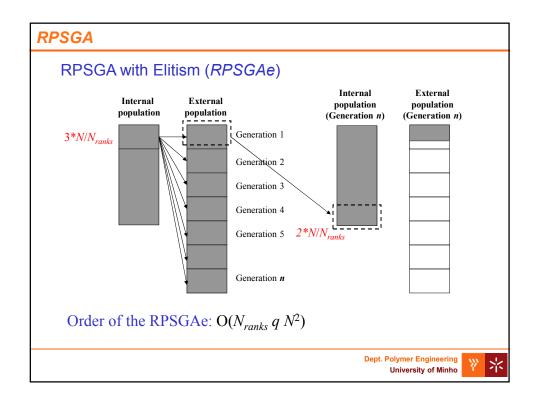


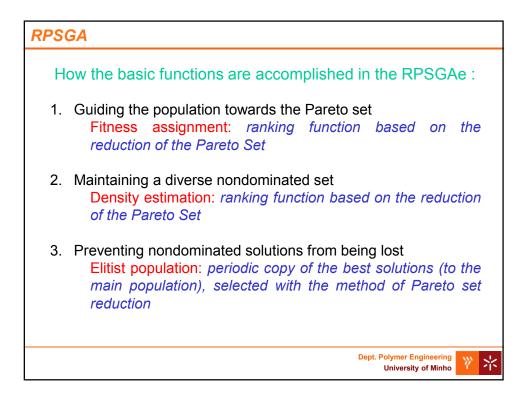


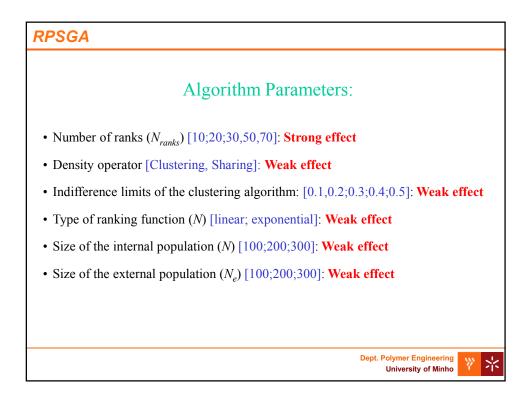


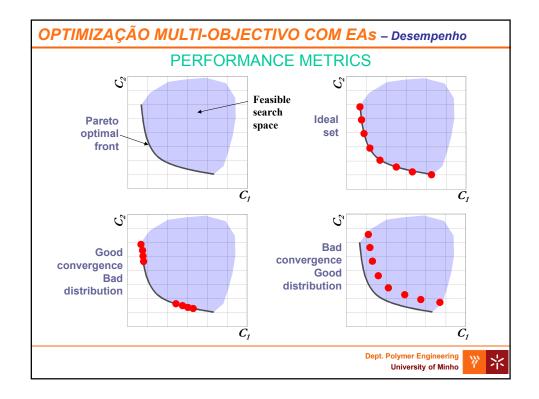


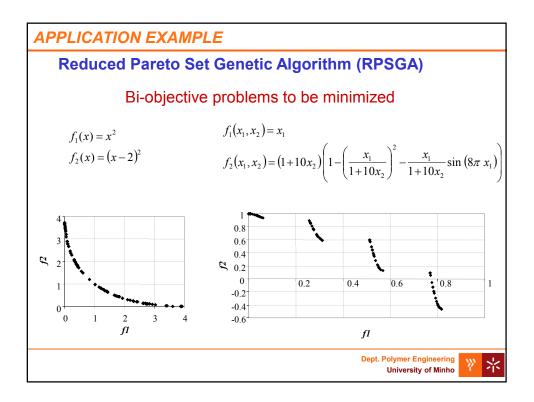


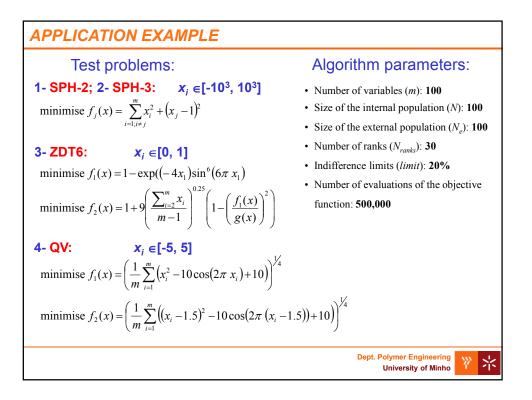


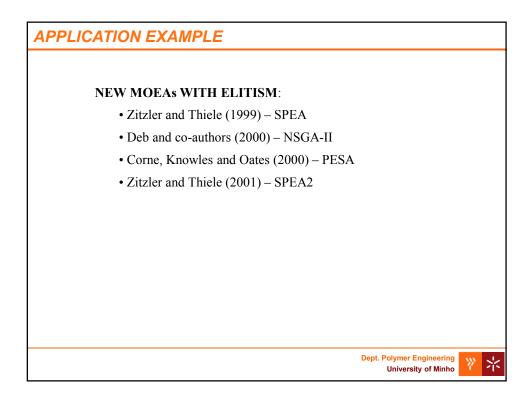




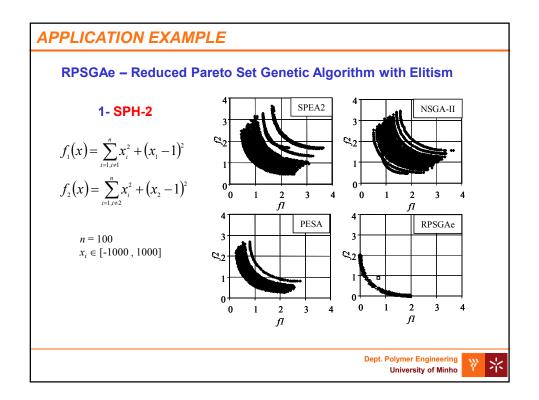


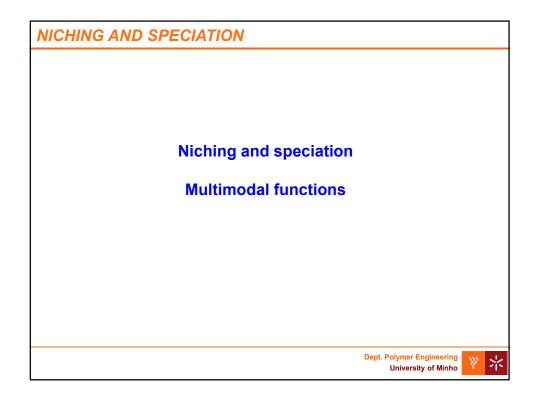


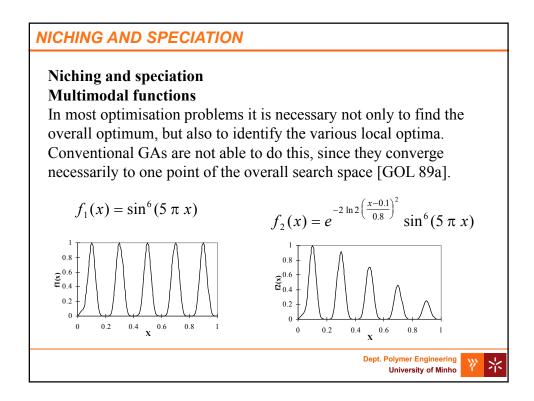




omparative	study:			
 Statistica 	al comparison an	alysis		
• 30 runs	for each problem	using different s	seed values	
esults (for e	each algorithm	n) [.]		
	f the Pareto from		algorithm is not	beaten by the of
e			e	5
Percentage o	f the Pareto from	tier in which the	algorithm beats a	all the others
	PESA	NSGA-II	SPEA2	RPSGAe
SPH-2	[0; 0]	[0; 0]	[0; 0]	[100; 100]
SPH-2 SPH-3	[0; 0] [0; 0]	[0; 0] [0; 0]	[0; 0] [0; 0]	
			L / J	[100; 100]
SPH-3	[0; 0] [0; 0]	[0; 0]	[0; 0] [43.3; 0]	[100; 100] [56.6; 56.5
SPH-3 ZDT6 QV	[0; 0] [0; 0] [35.3; 31.5]	[0; 0] [43.5; 0.1] [29.1; 7.3]	[0; 0] [43.3; 0] [61.2; 35.9]	[100; 100] [56.6; 56.5 [0; 0]
SPH-3 ZDT6 QV	[0; 0] [0; 0]	[0; 0] [43.5; 0.1] [29.1; 7.3]	[0; 0] [43.3; 0] [61.2; 35.9]	[100; 100] [56.6; 56.5 [0; 0]
SPH-3 ZDT6 QV	[0; 0] [0; 0] [35.3; 31.5]	[0; 0] [43.5; 0.1] [29.1; 7.3]	[0; 0] [43.3; 0] [61.2; 35.9]	[100; 100] [56.6; 56.5 [0; 0]







NICHING AND SPECIATION

If GAs are applied repeatedly to determine of the maximum of the first function, they converge indifferently to any single peak. This happens because the population cannot have an infinite dimension, as assumed by the schemata theory. The problem is designated by "genetic drift" and can cause the accumulation of errors as the search proceeds [GOL 87]. However, convergence to a single peak is not desirable in functions with various similar maxima. Generally, when the search space has local maxima with different values, it will be interesting that convergence occurs to the peak with the greatest value, but also that a determined number of individuals converge for each individual peak. This is particularly important in the case of complex functions, as it provides the characterisation of their topography.

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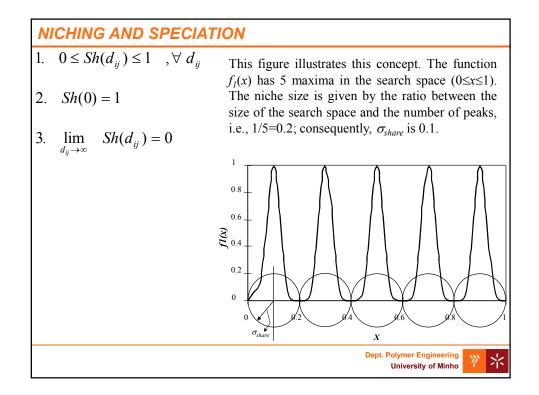
NICHING AND SPECIATION

In order to deal with the above, the concepts of **niching** and **speciation** of natural evolution should be introduced in a population of chromosomes. This is based on the idea of forming stable populations of organisms by creating separated niches where they are forced to **share** the available resources [GOL 87, DEB 89].

$$Sh(d_{ij}) = \begin{cases} 1 - \left(\frac{d_{ij}}{\sigma_{share}}\right)^{\alpha}, & \text{if } d_{ij} < \sigma_{share} \\ 0, & \text{otherwise} \end{cases}$$

sharing function, $Sh(d_{ij})$, where α is a constant and σ_{share} is the radius of a circumference defining the maximum distance between chromosomes, in order to form as many niches as the number of peaks on the search space.

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NICHING AND SPECIATION

Since the basic idea of sharing is that the objective function of an individual diminishes in the presence of its neighbours, the final objective function value (FO'_i) will result from the ratio between the initial evaluation (FO_i) and its niche count (m'_i) .

$$FO'_{i} = \frac{FO_{i}}{m'_{i}}$$
 $m'_{i} = \sum_{j=1}^{N} sh(d_{i_{j}})$

where m'_i is the sum of all the sharing functions related to this individual.

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The sharing function with himself $[sh(d_{ii})=1]$ will be also included.

NICHING AND SPECIATION

The distance between individuals can be determined in the real parameter space, (**phenotypic sharing**) or in the codified space (**genotype sharing**). The former will be adopted, since it has physical meaning and greater performance (according to Deb [DEB 89]). Two individuals ($X_i \ e \ X_j$) on a *p* dimensional space can be defined as:

$$X_{i} = \begin{bmatrix} x_{1,i}; x_{2,i}; \dots; x_{p,i} \end{bmatrix}$$
$$X_{j} = \begin{bmatrix} x_{1,j}; x_{2,j}; \dots; x_{p,j} \end{bmatrix}$$
$$d_{ij} = \sqrt{\sum_{k=1}^{p} (x_{k,i} - x_{k,j})^{2}}$$

The distance between them (d_{ij}) can be defined using the norm on a *p* dimensional space, using the Euclidean distance.

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NICHING AND SPECIATION

- Since in most optimisation problems the number of peaks is unknown, the use of the above methodology to define the value of σ_{share} , implies the use of a trial and error procedure.
- Sharing can be indistinctly applied in the space of the variables to optimise, or in the criteria space, depending on which niching is necessary. Generally it is applied in the criteria space, where the choice of the solution is carried out and where diversity along the Pareto frontier is required.

