Sistemas de Inteligencia Artificial
TP2: Algoritmos Genéticos

Equipo

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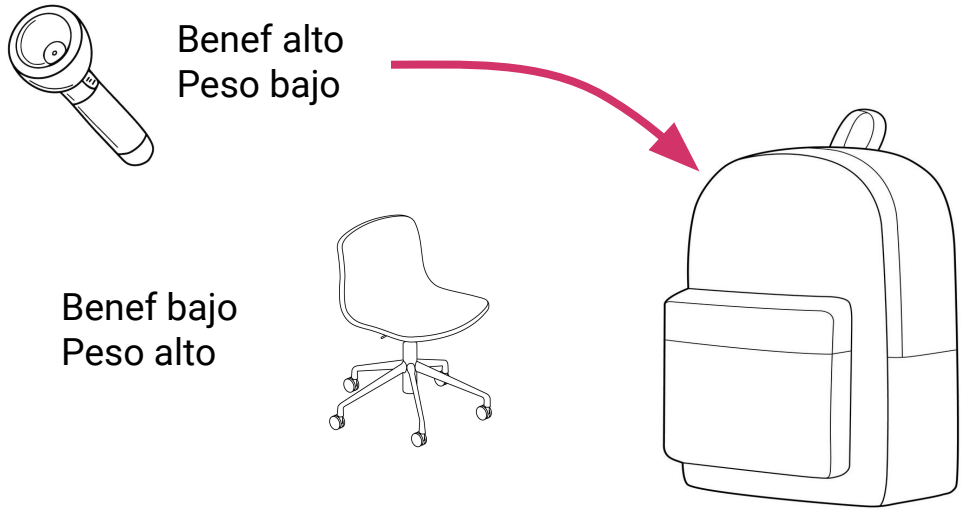
Problema de la Mochila

Dado un conjunto de *n* elementos, cada uno tiene asociado un peso y un beneficio. La mochila tiene un peso máximo y una cantidad tope de elementos. La idea es decidir qué elementos poner en la mochila, de manera de obtener el máximo beneficio posible.



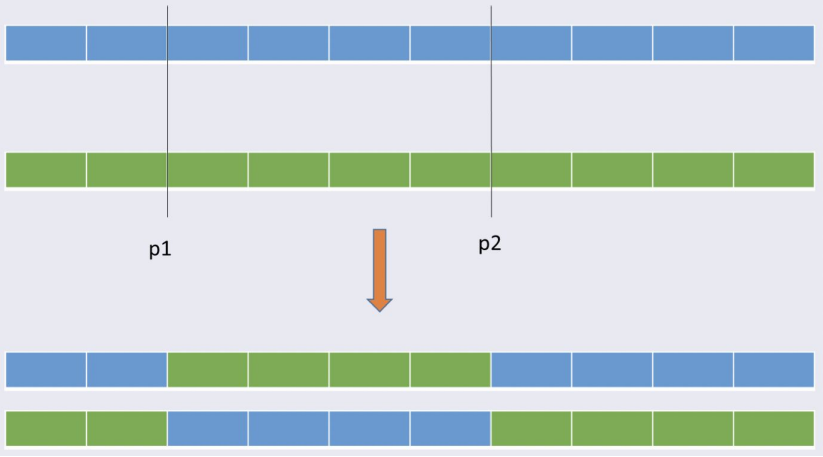
Función de Fitness

$$f(i) = \begin{cases} absWeight + benefits(i) & Valid \\ absWeight - weight(i) & Invalid \end{cases}$$

Representación binaria

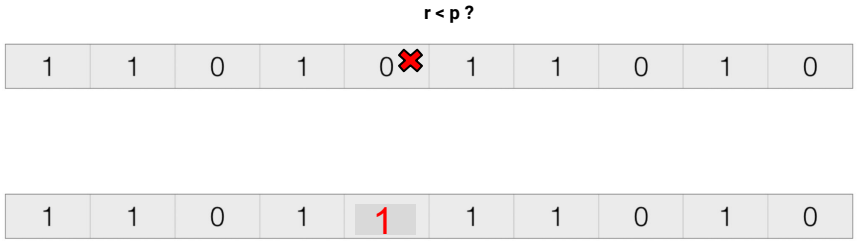
Los cromosomas de un individuo están representados por un *array* binario, en donde cada componente indica si el elemento está o no en la mochila.

Métodos de Cruza



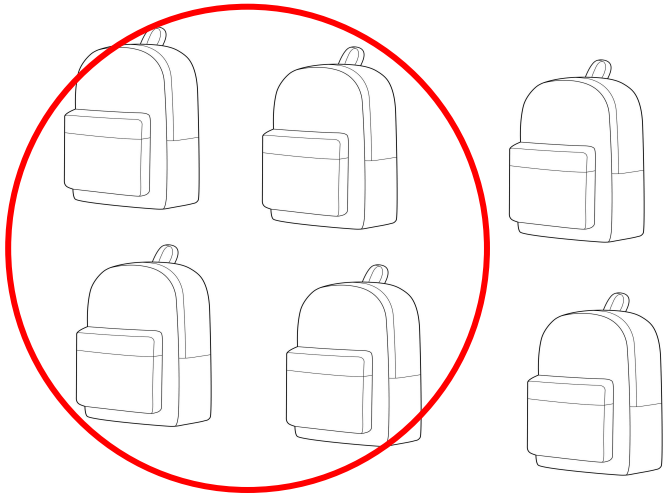
- Simple
- Múltiple
- Uniforme

Mutación



- Probabilidad *p*

Métodos de Selección



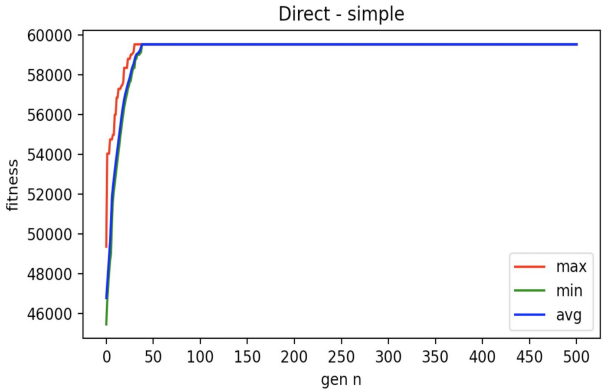
- Elitista
- Ruleta
- Rank
- Torneo
- Truncado
- Boltzmann

Comparación de Algoritmos

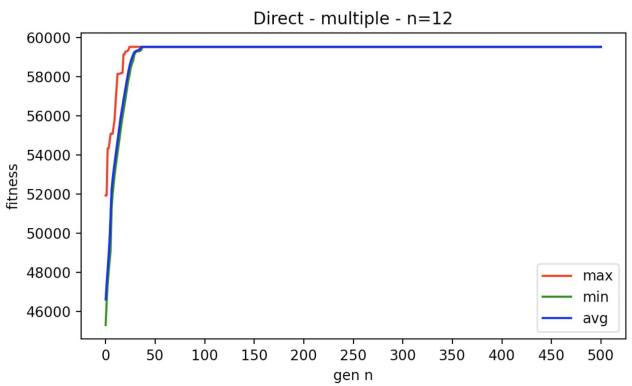
Gráficos

Selección Elite

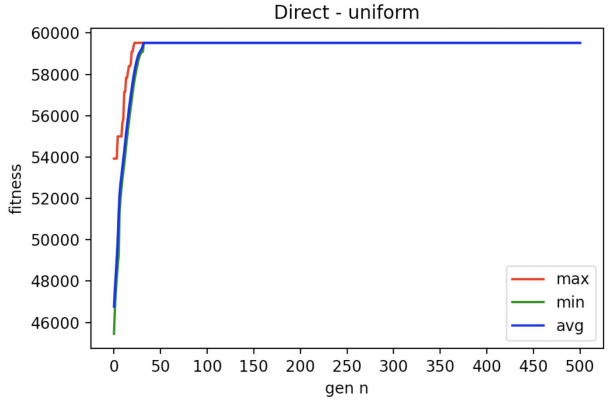
Sol benefit: 9147 - sol weight: 985



Sol benefit: 9147 - sol weight: 985



Sol benefit: 9147 - sol weight: 985

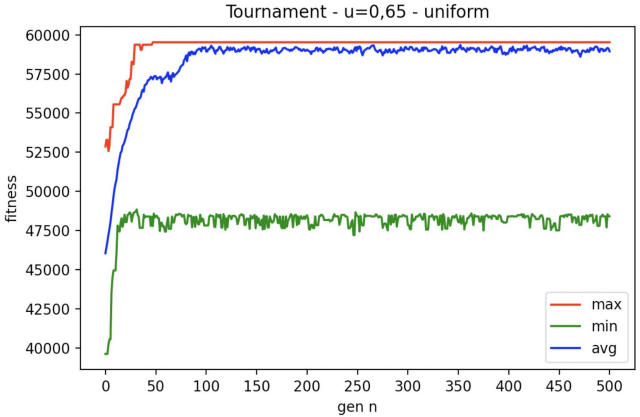


Comparación de métodos de cruza

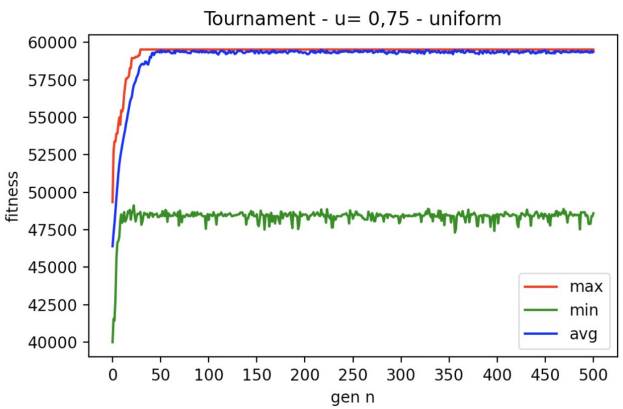
Probabilidad de mutación p = 0,001

Selección por Campeonatos

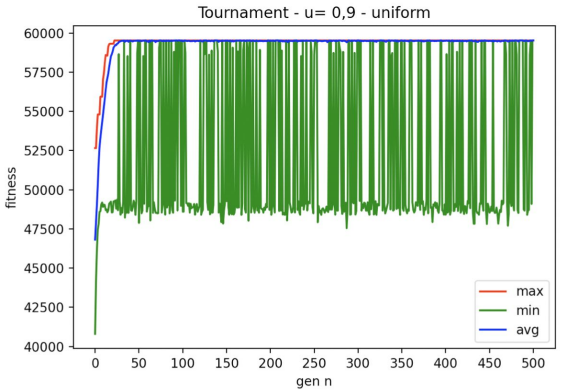
Sol benefit: 9147 - sol weight: 985



Sol benefit: 9147 - sol weight: 985



Sol benefit: 9147 - sol weight: 985

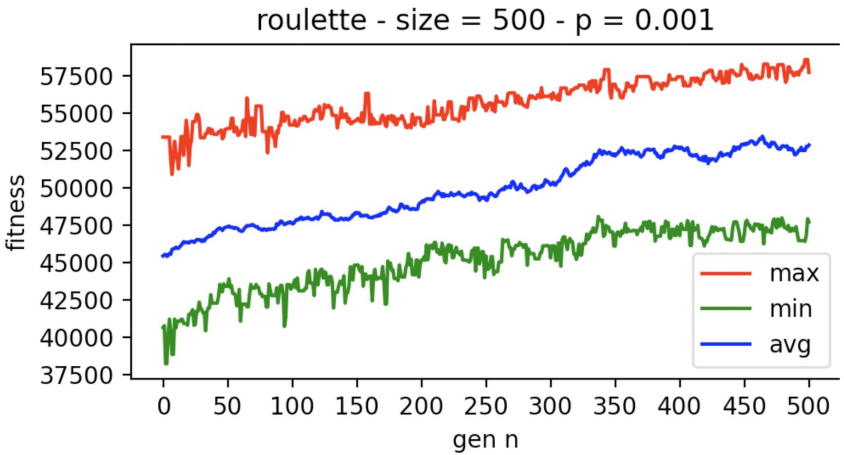


Comparación de ***u***

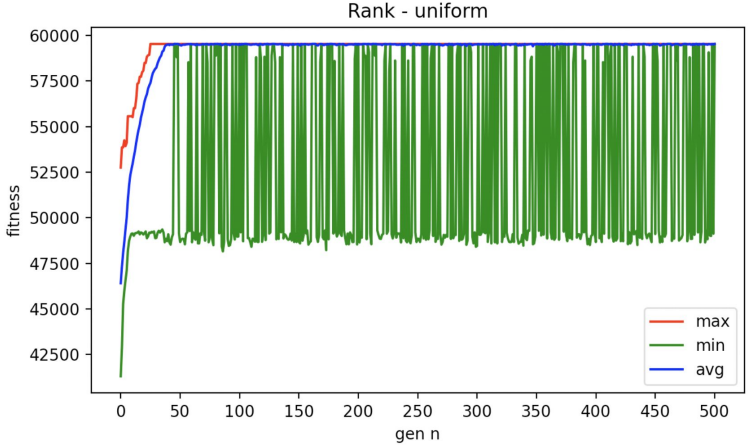
Probabilidad de mutación p = 0,001

Selección Roulette vs Rank

Sol benefit: 7324 - sol weight: 964



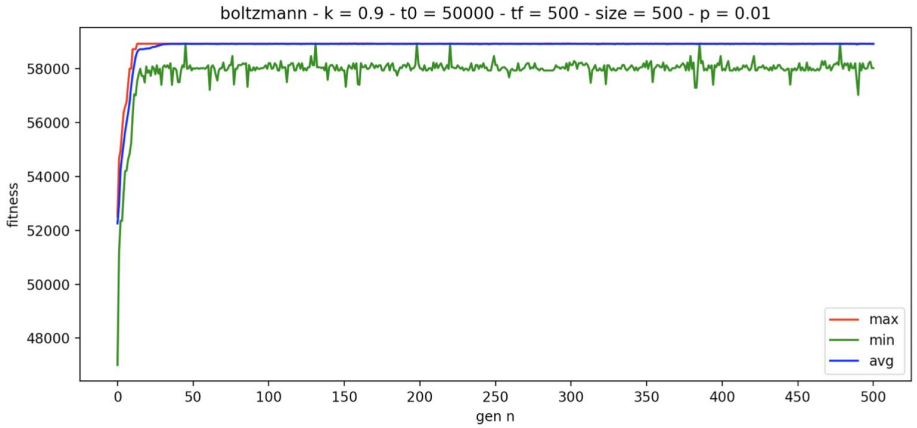
Sol benefit: 9147 - sol weight: 985



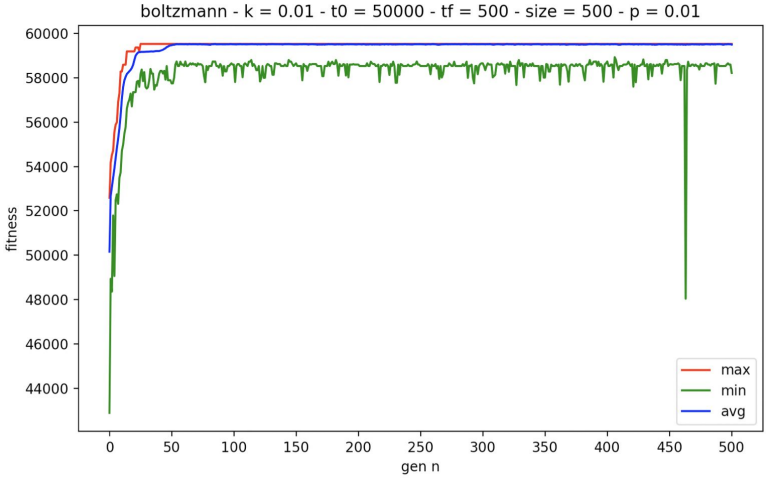
Podemos notar como se acerca
el promedio al máximo en rank

Selección Boltzmann

Sol benefit: 8544 - sol weight: 990



Sol benefit: 9147 - sol weight: 985

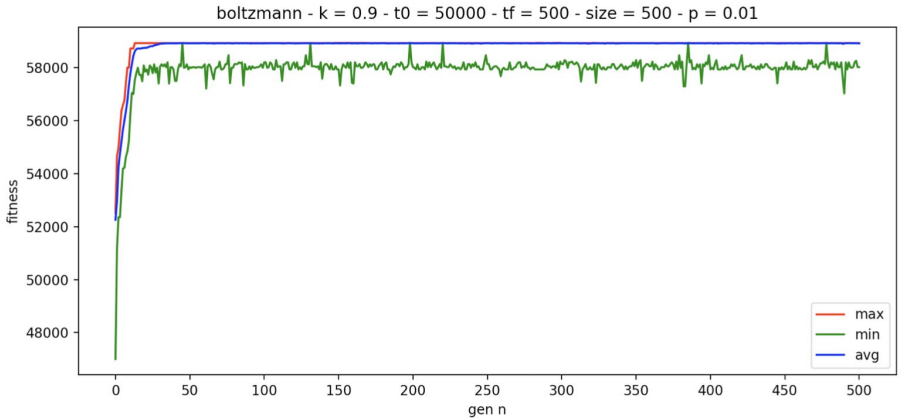


Comparación ***k***

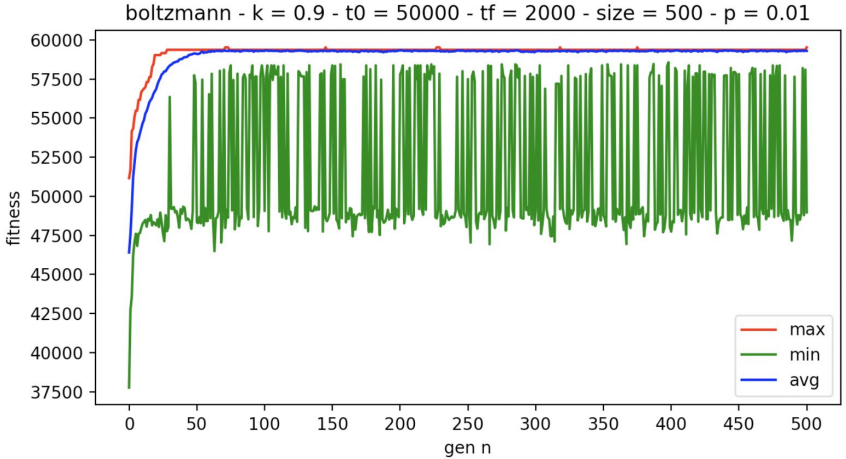
Probabilidad de mutación p = 0,01

Selección Boltzmann

Sol benefit: 8544 - sol weight: 990



Sol benefit: 9147 - sol weight: 985

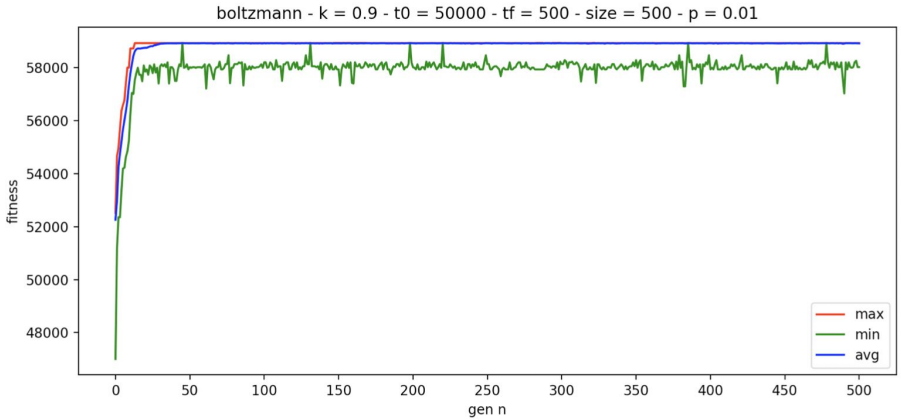


Comparación t_f

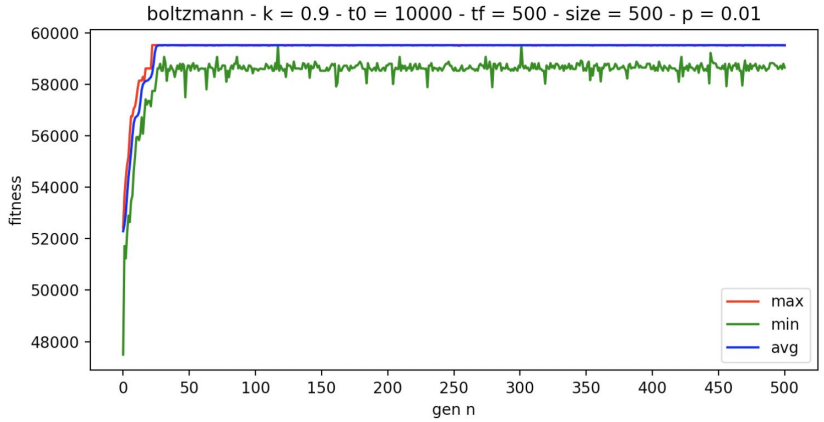
Probabilidad de mutación p = 0,01

Selección Boltzmann

Sol benefit: 8544 - sol weight: 990



Sol benefit: 9147 - sol weight: 985

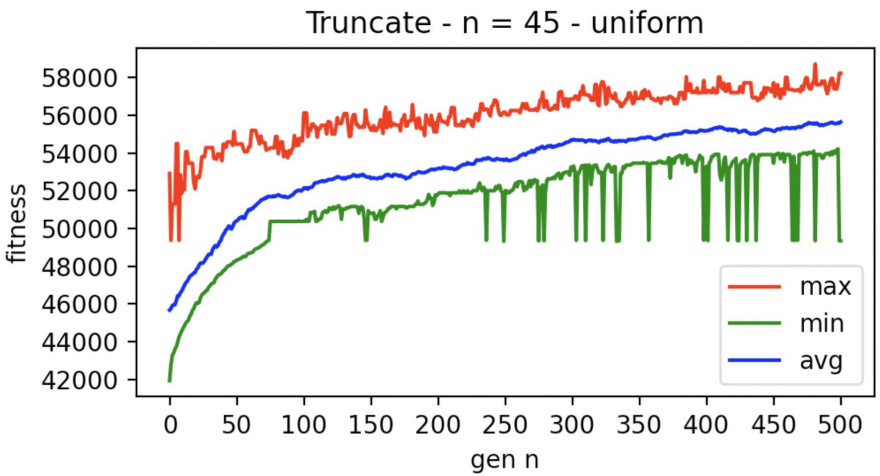


Comparación t_0

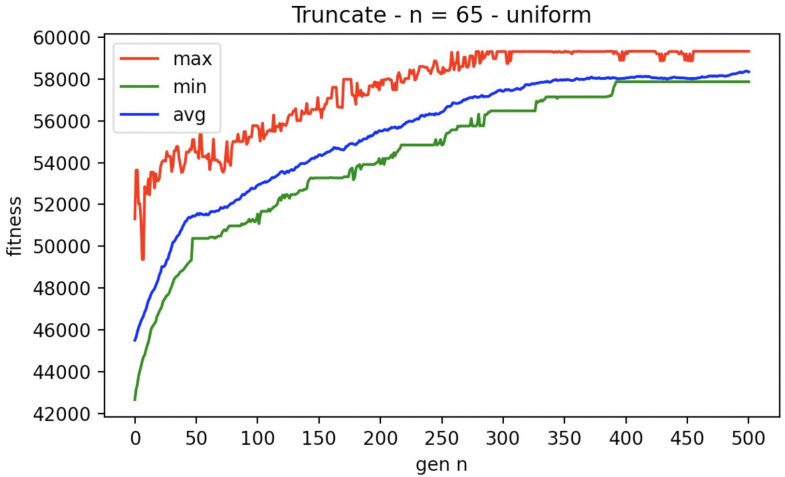
Probabilidad de mutación p = 0,001

Selección truncada

Sol benefit: 7858 - sol weight: 831



Sol benefit: 8940 - sol weight: 969



Comparación ***n***

Conclusiones

https://github.com/srosati/SIA/tree/master/TP2