

# Knapsack Problem

Solved using genetic algorithm

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15767

Mutation Probability: 0.1 | Crossover Probability: 0.8

Item No.	1	2	3	4	5	6	7	8	9	10
Weight	7	12	3	4	9	6	11	15	6	1
Value	14	2	12	14	8	3	10	2	8	9

Max Weight: 52

## 1. Randomly generated population (First Iteration)

Genotype		Phenotype	
Ch1	0010010110	Ch1	30
Ch2	1010001001	Ch2	22
Ch3	0111011010	Ch3	42
Ch4	0100010111	Ch4	40
Ch5	1101010010	Ch5	35
Ch6	1011011000	Ch6	31
Ch7	1100101100	Ch7	54
Ch8	1011111011	Ch8	47
Ch9	0100100111	Ch9	43
Ch10	0010010100	Ch10	24
Ch11	1000100010	Ch11	22
Ch12	1111011001	Ch12	44
Ch13	0010110110	Ch13	39
Ch14	1011101010	Ch14	40
Ch15	1100111100	Ch15	60
Ch16	1110111001	Ch16	49
Ch17	0110011001	Ch17	33
Ch18	0011010101	Ch18	29
Ch19	1101101001	Ch19	44
Ch20	1011010101	Ch20	36

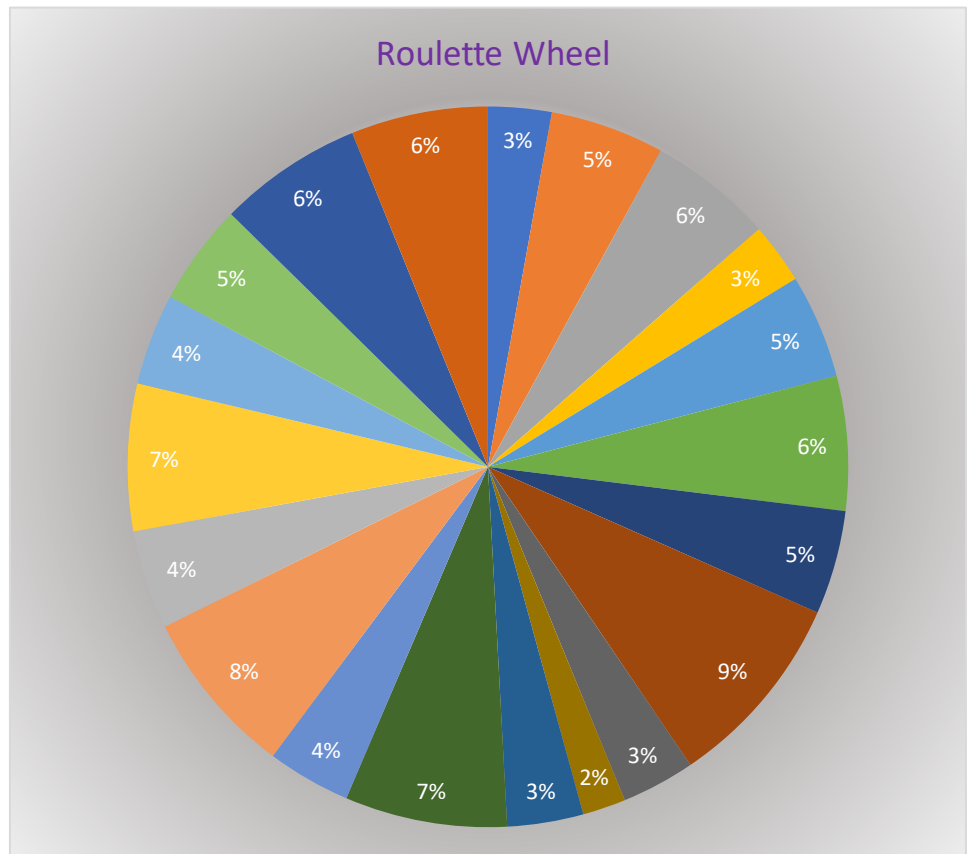
If the **weight** of the backpack is exceeded 52, we have to mutate this individual by changing the genotype.

Ch7	1100100011	35
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Ch15	1100110011	47
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## 2. Adaptation Function of chromosomes

F(Ch1)	25	3%
F(Ch2)	45	5%
F(Ch3)	49	6%
F(Ch4)	24	3%
F(Ch5)	41	5%
F(Ch6)	53	6%
F(Ch7)	41	5%
F(Ch8)	78	9%
F(Ch9)	29	3%
F(Ch10)	17	2%
F(Ch11)	30	3%
F(Ch12)	64	7%
F(Ch13)	33	4%
F(Ch14)	66	8%
F(Ch15)	39	4%
F(Ch16)	58	7%
F(Ch17)	36	4%
F(Ch18)	40	5%
F(Ch19)	57	6%
F(Ch20)	54	6%
F(sum)	877	100%



$$p(Ch_i) = \frac{F(Ch_i)}{\sum_{i=1}^{20} F(Ch_i)} \cdot 100\%$$

## 3. 20 randomly picked percentage values from roulette wheel spin

%	41	5	90	80	62	28	39	98	21	59	46	92	51	48	68	76	30	17	26	58
F(Ch)	8	2	19	16	14	6	8	20	5	13	10	19	12	11	14	16	7	4	6	13

## 4. Crossover

For each pair we generate random numbers from the range [0-1]. If the number is lower than probability of crossover: 0.8, then there will be a crossover, additionally for each pair subject to crossover, we generate random crossover points from [1-10]

Chromosome Pairs	Ch8 Ch2	Ch19 Ch16	Ch14 Ch6	Ch8 Ch20	Ch5 Ch13	Ch10 Ch19	Ch12 Ch11	Ch14 Ch16	Ch7 Ch4	Ch6 Ch13
Random Number	0.19	0.58	0.92	0.48	0.23	0.04	0.31	0.85	0.6 1	0.20
Crossover Point	5	7	x	3	2	6	8	x	2	4

1 <sup>st</sup> Pair of Parents	
Ch8	101111 <b>1011</b>
Ch2	101000 <b>1001</b>

1 <sup>st</sup> Pair of Children		
Ch1	1011101001	35
Ch2	1010011011	34

2 <sup>nd</sup> Pair of Parents	
Ch19	110 <b>1101001</b>
Ch17	111 <b>10111001</b>

2 <sup>nd</sup> Pair of Children		
Ch3	1100111001	46
Ch4	1111101001	47

3 <sup>rd</sup> Pair of Parents	
Ch14	1011101010
Ch6	1011011000

3 <sup>rd</sup> Pair of Children		
Ch5	1011101010	40
Ch6	1011011000	31

4 <sup>th</sup> Pair of Parents	
Ch8	1011111 <b>1011</b>
Ch20	1011010 <b>101</b>

4 <sup>th</sup> Pair of Children		
Ch7	1011111101	<b>56</b>
Ch8	1011010011	27

5 <sup>th</sup> Pair of Parents	
Ch5	11010100 <b>10</b>
Ch13	00101101 <b>10</b>

5 <sup>th</sup> Pair of Children		
Ch9	1101010010	35
Ch10	0010110110	39

6 <sup>th</sup> Pair of Parents	
Ch10	00100 <b>10100</b>
Ch19	1101 <b>101001</b>

6 <sup>th</sup> Pair of Children		
Ch11	0010101001	24
Ch12	1101010100	44

7 <sup>th</sup> Pair of Parents	
Ch12	111 <b>1011001</b>
Ch11	10 <b>00100010</b>

7 <sup>th</sup> Pair of Children		
Ch13	1100100010	34
Ch14	1011011001	32

8 <sup>th</sup> Pair of Parents	
Ch14	1011101010
Ch16	1110111001

8 <sup>th</sup> Pair of Children		
Ch15	1011101010	40
Ch16	1110111001	49

9 <sup>th</sup> Pair of Parents	
Ch7	11001000 <b>11</b>
Ch4	01000101 <b>11</b>

9 <sup>th</sup> Pair of Children		
Ch17	1100100011	35
Ch18	0100010111	40

10 <sup>th</sup> Pair of Parents	
Ch6	101101 <b>1000</b>
Ch13	001011 <b>10110</b>

10 <sup>th</sup> Pair of Children		
Ch19	1011010110	41
Ch20	0010111000	29

## 5. First offspring population (Second Iteration)

For each individual child, after crossing, we randomize a number from 0 to 1. The mutation is subject to those individuals for which the drawn number is lower than the probability of mutation: 0.1. If there are individuals to be mutated, we draw random integers from the range [1-10] to set mutation point.

Genotype	
Ch1	1011101001
Ch2	1010011011
Ch3	1100011001
Ch4	0111101001
Ch5	1011101010
Ch6	1011011000
Ch7	1011111101
Ch8	1011010011
Ch9	1101010010
Ch10	0010110110
Ch11	0010101001
Ch12	1101010100
Ch13	1100100010
Ch14	1011011001
Ch15	1011101010
Ch16	1110111001
Ch17	1100100011
Ch18	0100010111
Ch19	1011010110
Ch20	0010111000

Phenotype	
Ch1	35
Ch2	34
Ch3	46
Ch4	47
Ch5	40
Ch6	31
Ch7	56
Ch8	27
Ch9	35
Ch10	39
Ch11	24
Ch12	44
Ch13	34
Ch14	32
Ch15	40
Ch16	49
Ch17	35
Ch18	40
Ch19	41
Ch20	29

Random	
0.47	
0.12	
0.95	
0.08	4
0.89	
0.83	
0.76	3
0.30	
0.95	
0.51	
0.16	
0.37	
0.55	
0.62	
0.44	
0.24	
0.44	
0.54	
0.31	
0.04	2

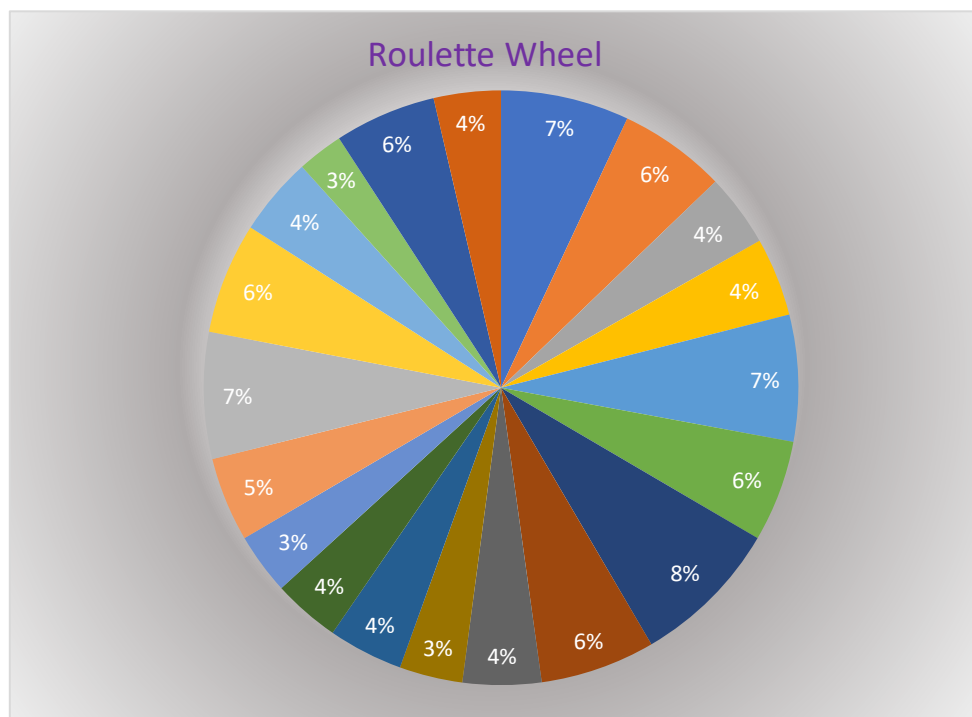
Ch4	0110101001	43
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Ch7	1011111011	47
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Ch20	0110111000	41
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## 6. Adaptation functions for second generation chromosomes

F(Ch1)	67	7%
F(Ch2)	56	6%
F(Ch3)	38	4%
F(Ch4)	41	4%
F(Ch5)	66	7%
F(Ch6)	53	6%
F(Ch7)	78	8%
F(Ch8)	60	6%
F(Ch9)	41	4%
F(Ch10)	33	3%
F(Ch11)	39	4%
F(Ch12)	35	4%
F(Ch13)	32	3%
F(Ch14)	44	5%
F(Ch15)	66	7%
F(Ch16)	58	6%
F(Ch17)	41	4%
F(Ch18)	24	3%
F(Ch19)	53	6%
F(Ch20)	35	4%
F(sum)	960	100%



## 7. 20 randomly picked percentage values from roulette wheel spin

%	59	25	50	85	32	48	19	74	27	9	66	92	51	44	38	81	20	63	79	13
F(Ch)	9	5	19	17	6	8	4	16	5	2	14	19	9	8	7	16	4	12	16	2

## 8. Crossover

For each pair we generate random numbers from the range [0-1]. If the number is lower than probability of crossover: 0.8, then there will be a crossover, additionally for each pair subject to crossover, we generate random crossover points from [1-10]

Chromosome Pairs	Ch9 Ch5	Ch19 Ch17	Ch6 Ch8	Ch4 Ch16	Ch5 Ch2	Ch14 Ch19	Ch9 Ch8	Ch7 Ch16	Ch4 Ch12	Ch16 Ch2
Random Number	0.99	0.32	0.51	0.41	0.56	0.34	0.17	0.93	0.83	0.88
Crossover Point	x	3	6	8	5	9	2	x	x	x

1 <sup>st</sup> Pair of Parents	
Ch9	1101010010
Ch5	1011101010
2 <sup>nd</sup> Pair of Parents	
Ch19	1011010 <b>110</b>
Ch17	1100100 <b>011</b>
3 <sup>rd</sup> Pair of Parents	
Ch6	1011 <b>011000</b>
Ch8	1011 <b>010011</b>
4 <sup>th</sup> Pair of Parents	
Ch4	0 <b>110101001</b>
Ch16	11 <b>10111001</b>
5 <sup>th</sup> Pair of Parents	
Ch5	10111 <b>01010</b>
Ch2	10100 <b>11011</b>
6 <sup>th</sup> Pair of Parents	
Ch14	101101 <b>1001</b>
Ch19	1011010 <b>110</b>
7 <sup>th</sup> Pair of Parents	
Ch9	<b>1101010010</b>
Ch8	<b>1011010011</b>
8 <sup>th</sup> Pair of Parents	
Ch7	1011111011
Ch16	1110111001
9 <sup>th</sup> Pair of Parents	
Ch4	0110101001
Ch12	1101010100
9 <sup>th</sup> Pair of Parents	
Ch16	1110111001
Ch2	1010011011

1 <sup>st</sup> Pair of Children	
Ch1	1101010010
Ch2	1011101010
2 <sup>nd</sup> Pair of Children	
Ch3	1011010011
Ch4	1100100110
3 <sup>rd</sup> Pair of Children	
Ch5	1011010011
Ch6	1011011000
4 <sup>th</sup> Pair of Children	
Ch7	0110111001
Ch8	1110101001
5 <sup>th</sup> Pair of Children	
Ch9	1011111011
Ch10	1010001010
6 <sup>th</sup> Pair of Children	
Ch11	1011011010
Ch12	1011010101
7 <sup>th</sup> Pair of Children	
Ch13	1101010010
Ch14	1011010011
8 <sup>th</sup> Pair of Children	
Ch15	1011111011
Ch16	1110111001
9 <sup>th</sup> Pair of Children	
Ch17	0110101001
Ch18	1101010100
10 <sup>th</sup> Pair of Children	
Ch19	1110111001
Ch20	1010011011

## 9. Second offspring population (Third Iteration)

For each individual child, after crossing, we randomize a number from 0 to 1. The mutation is subject to those individuals for which the drawn number is lower than the probability of mutation: 0.1. If there are individuals to be mutated, we draw random integers from the range [1-10] to set mutation point.

Genotype		Phenotype		Random					Adaptation Function	
Ch1	1101010010	Ch1	35	0.85					F(Ch1)	41
Ch2	1011101010	Ch2	40	0.16					F(Ch2)	66
Ch3	1011010011	Ch3	27	0.58					F(Ch3)	60
Ch4	1100100110	Ch4	49	0.20					F(Ch4)	38
Ch5	1011010011	Ch5	27	0.37					F(Ch5)	60
Ch6	1011011000	Ch6	31	0.89					F(Ch6)	53
Ch7	0110111001	Ch7	42	0.38					F(Ch7)	44
Ch8	1110101001	Ch8	43	0.64					F(Ch8)	55
Ch9	1011111011	Ch9	47	0.70					F(Ch9)	78
Ch10	1010001010	Ch10	27	0.07	8	Ch10	1010001110	42	F(Ch10)	46
Ch11	1011011010	Ch11	37	0.75					F(Ch11)	61
Ch12	1011010101	Ch12	36	0.08	5	Ch12	1011110101	45	F(Ch12)	62
Ch13	1101010010	Ch13	35	0.64					F(Ch13)	41
Ch14	1011010011	Ch14	27	0.82					F(Ch14)	60
Ch15	1011111011	Ch15	47	0.68					F(Ch15)	78
Ch16	1110111001	Ch16	49	0.13					F(Ch16)	58
Ch17	0110101001	Ch17	36	0.14					F(Ch17)	41
Ch18	1101010100	Ch18	44	0.73					F(Ch18)	35
Ch19	1110111001	Ch19	49	0.66					F(Ch19)	58
Ch20	1010011011	Ch20	34	0.57					F(Ch20)	56
									F(sum)	1091

## 10. Result for fittest individual chromosome

Through observing from 3 iterations of populations we can determine that the fittest individual without overloading the knapsack is: **1011111011** with the weight of **47** and a value of **78**.