In [1]:

```
import warnings
warnings.filterwarnings('ignore')
%matplotlib inline
import matplotlib.pyplot as plt
import math
import numpy as np
from tqdm import tqdm
np.random.seed(1234)
```

Individuals

- The base unit of an evolutionary algorithm (EA) is the individual.
- An individual represents a single solution to the problem we want to solve.
- Classic EAs often have binary individuals, where each gene is represented by a bit (0/1 value).

In [2]:

```
class Individual:

    def __init__(self, n: int):
        self.genes = np.random.randint(0, 2, (n,))
        self.fitness = -np.inf

    def __str__(self):
        return f'(Ind: {self.genes}, {self.fitness})'

    def __repr__(self):
        return str(self)
```

- Individual has binary genes and an integer fitness.
- A newly-initialized individual often has random genes.

In [3]:

```
ind = Individual(10)
ind
```

Out[3]:

```
(Ind: [1 1 0 1 0 0 0 1 1 1], -inf)
```

Objectives

- The objective function gives a value to our individual.
- The objective function can be designed so that it can **evaluate** the individual.
- The objective function value of an individual is often called the **fitness value** of that individual.
- The objective function does not need to be differentiable or continuous.

In [4]:

```
def onemax(i: Individual):
    return np.sum(i.genes)
```

- The OneMax function simply adds all the bits of the genotype of the individual.

In [5]:

```
ind.fitness = onemax(ind)
ind
```

Out[5]:

```
(Ind: [1 1 0 1 0 0 0 1 1 1], 6)
```

- The optimal solution for OneMax is the individual that has the genotype of all 1s.

- To be more general, we often define an **evaluate** function, which evaluate the fitness value of an individual.

In [6]:

```
def evaluate(ind: Individual, objective):
    ind.fitness = objective(ind)

evaluate(ind, onemax)
ind
```

Out[6]:

```
(Ind: [1 1 0 1 0 0 0 1 1 1], 6)
```

- Each time we evaluate the fitness value of an individual, we spend one evaluation function call.
- To be abstract from the exact runtime on specific hardware, we often use the **number of evaluations** as the computing cost/budget for EAs.

(1+1) Evolutionary Algorithm ~~~ (1+1)-EA

1. Initialize a random individual of n genes, i.e., a bitstring $x \in \{0;1\}^n$.
2. Repeat the following **mutation** step:
    A. Compute x' by flipping each bit x_i with probability p.
    B. Replace x by x' if $f(x') \geq f(x)$.

In [7]:

```
n = 20
```

In [8]:

```
parent = Individual(n)
evaluate(parent, onemax)
parent
```

Out[8]:

```
(Ind: [1 1 0 0 1 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0], 6)
```

In [9]:

```
def mutate(ind: Individual, mutation_rate=1.0/len(ind.genes)):
    new_genes = np.copy(ind.genes)
    for i in range(len(new_genes)):
        if np.random.rand() < mutation_rate:
            new_genes[i] = not ind.genes[i]
    child = Individual(len(ind.genes))
    child.genes = new_genes
    return child
```

- The **mutate** function create a **child/offspring** individual from a **parent** individual with the mutation probability of $\mathrm{p} = \frac{1}{\mathrm{n}}$.
- We scan through each gene in an individual.
- For each gene, we generate a random number $\mathrm{r} \in (0, 1)$.
- If $\mathrm{r} < \mathrm{p}$, we flip the gene value $0 \leftrightarrow 1$.

In [10]:

```
child = mutate(parent)
print("Parent :", parent)
print("Child  :", child)
print("Genes :", parent.genes == child.genes)
```

```
Parent : (Ind: [1 1 0 0 1 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0], 6)
Child  : (Ind: [1 1 1 0 1 0 0 1 0 0 0 0 0 0 1 0 1 1 0 0], -inf)
Genes : [ True  True False  True  True  True  True False  True  True
  True  True  True  True  True  True  True  True  True  True]
```

- Running this mutation function a few times.
- Each time, only one or two genes change because the mutation rate is set to $\mathrm{p} = \frac{1}{\mathrm{n}}$.

In [11]:

```
child = mutate(parent)
print("Parent :", parent)
print("Child  :", child)
print("Genes :", parent.genes == child.genes)
```

```
Parent : (Ind: [1 1 0 0 1 0 0 0 0
0 0 0 0 0 1 0 1 1 0 0], 6)
Child  : (Ind: [1 0 0 0 1 0 0 0 1
0 0 0 0 0 1 0 1 1 0 0], -inf)
Genes : [ True False  True  True
True  True  True  True False  Tru
e  True  True
  True  True  True  True  True  T
rue  True  True]
```

In [12]:

```
child = mutate(parent)
print("Parent :", parent)
print("Child  :", child)
print("Genes :", parent.genes == child.genes)
```

```
Parent : (Ind: [1 1 0 0 1 0 0 0 0
0 0 0 0 0 1 0 1 1 0 0], 6)
Child  : (Ind: [1 1 0 1 1 0 0 0 0
0 0 0 0 0 1 0 1 1 0 0], -inf)
Genes : [ True  True  True False
True  True  True  True  True  Tru
```

```
e  True  True
  True  True  True  True  True  T
rue  True  True]
```

- Each time, we replace the parent individual x by the child individual x' if the fitness of the offspring is better, i.e., $f(x') \geq f(x)$.

In [13]:

```
evaluate(child, onemax)
print(parent.fitness)
print(child.fitness)
if child.fitness >= parent.fitness:
    parent = child
parent.fitness
```

```
6
7
```

Out[13]:

```
7
```

- We simply run this mutation step over and over until we reach the solution we want or the certain **termination criterion** is met (e.g., the **maximum number of evaluations** are all spent).
- Let's just run for a few iterations.

In [14]:

```
parent = Individual(n)
for i in range(20):
    child = mutate(parent)
    evaluate(child, onemax)
    if child.fitness >= parent.fitness:
        parent = child
    # print(i, " ", parent.fitness)

print(parent.fitness, " / ", n)
```

```
19  /  20
```

- Let's code the (1+1)-EA.

In [15]:

```
def one_plus_one(ind_length: int, num_generations: int, objective):
    fits = np.zeros(num_generations)
    parent = Individual(ind_length)
    evaluate(parent, objective)

    for i in tqdm(range(len(fits))):
        child = mutate(parent)
        evaluate(child, objective)

        if child.fitness >= parent.fitness:
            parent = child

        fits[i] = parent.fitness
    return fits
```

- Since EAs are stochastic algorithm, it's difficult to guarantee their exact computational complexity.
- A common metric is the **expected number of generations** to each the optimal solution.
- The worst-case for a binary (1+1)-EA to converge is $O(n^n)$, but we often don't need to run that long to see convergence.
- For OneMax, the expected runtime for (1+1)-EA has been proven to be $O(n \log n)$ when the mutation rate is $p = \frac{1}{n}$.
  https://core.ac.uk/download/pdf/82100186.pdf

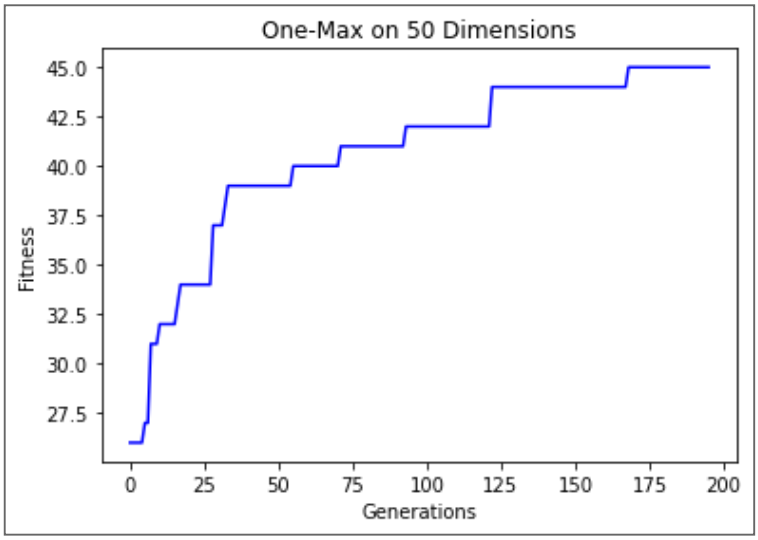
In [16]:

```
n = 50
fits = one_plus_one(n, int(np.round(n * np.log(n))), onemax)
print(fits[-1])
```

```
100%|██████████| 196/196 [00:00<00:00, 27996.31it/s]

45.0
```

In [17]:

```
plt.plot(fits, 'b')
plt.xlabel("Generations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions");
```


One-Max on 50 Dimensions
Fitness
Generations
45.0
42.5
40.0
37.5
35.0
32.5
30.0
27.5
0
25
50
75
100
125
150
175
200

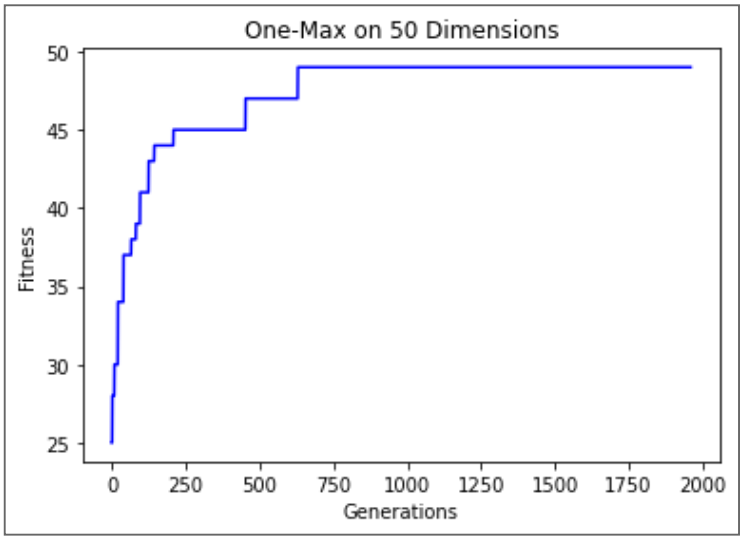
In [18]:

```
n = 50
fits = one_plus_one(n, int(np.round(n * np.log(n)))*10, onemax)
print(fits[-1])
```

```
100%|██████████| 1960/1960 [00:00<00:00, 33213.49it/s]

49.0
```

In [19]:

```
plt.plot(fits, 'b')
plt.xlabel("Generations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions");
```


One-Max on 50 Dimensions
Fitness
Generations
50
45
40
35
30
25
0
250
500
750
1000
1250
1500
1750
2000

- The **Leading Ones** problem is another benchmark function for EAs.
- The Leading Ones function counts the number of 1-bits from left to right, stopping when the first 0-bit is found.

$$f(x) = \sum_{i=1}^{n} \prod_{j=1}^{i} x_j$$

In [20]:

```
def leading_ones(ind: Individual):
    f = 0
    for i in range(len(ind.genes)):
        if not ind.genes[i]:
            f = i
            break
    return f
print(ind)
leading_ones(ind)
```

```
(Ind: [1 1 0 1 0 0 0 1 1 1], 6)
```

Out[20]:

2

Question: What is the expected runtime of (1+1)-EA on the Leading Ones problem?

(1+λ) Evolutionary Algorithm - (1+λ)-EA

- We made a small change to the (1+1)-EA: instead of generating one offspring individual each iteration (generation), we generate λ offspring individuals.
- These λ individuals can be called a **population**, and λ is the **population size**.

- For (1+λ)-EA, beside the mutation rate, the population size is another control parameter of the algorithm (i.e., hyperparameter).
- The expected runtime for (1+λ)-EA on OneMax is upper bounded by $O(n \log\log \lambda / \log \lambda)$ when λ is larger than $O(\log n \log\log n / \log\log\log n)$.
  https://www.sciencedirect.com/science/article/pi

- We modify one_plus_one function to create the one_plus_lambda function.
- We keep track of the best offspring individual to compare it with the parent individual in the next generation.

In [21]:

```
def one_plus_lambda(ind_length: int, num_generations: int, objective, λ: int):
    fits = np.zeros(num_generations)
    parent = Individual(ind_length)
    evaluate(parent, objective)

    for i in tqdm(range(len(fits))):
        population = [parent,]
        best = 0
        for j in range(1, λ):
            population.append(mutate(parent))
            evaluate(population[j], objective)
            if population[j].fitness > population[best].fitness:
                best = j
        if population[best].fitness >= parent.fitness:
            parent = population[best]
        fits[i] = parent.fitness
    return fits
```

In [22]:

```
n = 100
λ = int(round(np.log(n)*np.log(np.log(n))/np.log(np.log(np.log(n)))))
print(λ)
```

```
17
```

Let's round up λ=20 for the sake of simplicity.

In [23]:

```
λ = 20
```

In [24]:

```
n = 100
n_gens = 1000
fits_1 = one_plus_one(n, n_gens, onemax)
fits_λ = one_plus_lambda(n, n_gens, onemax, λ)
fits_1[-1], fits_λ[-1]
```

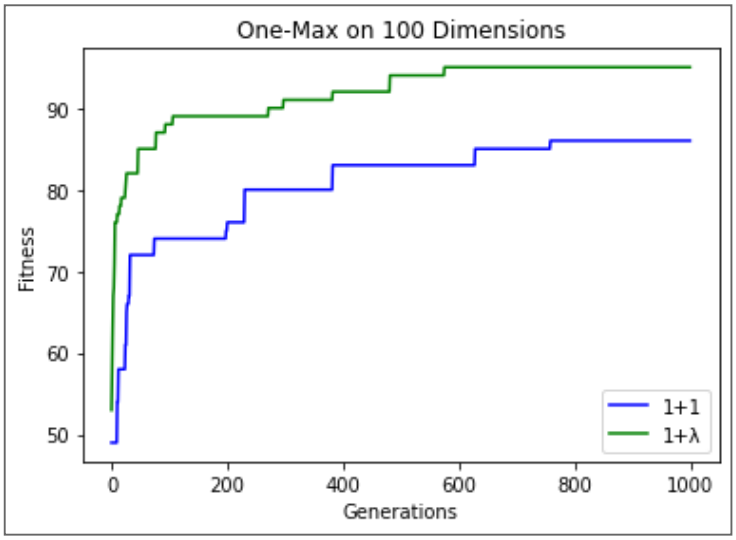
```
100%|                                                                                | 1000/1000 [00:00<00:00, 20403.19it/s]
100%|                                                                                | 1000/1000 [00:00<00:00, 1185.94it/s]
```

Out[24]:

```
(86.0, 95.0)
```

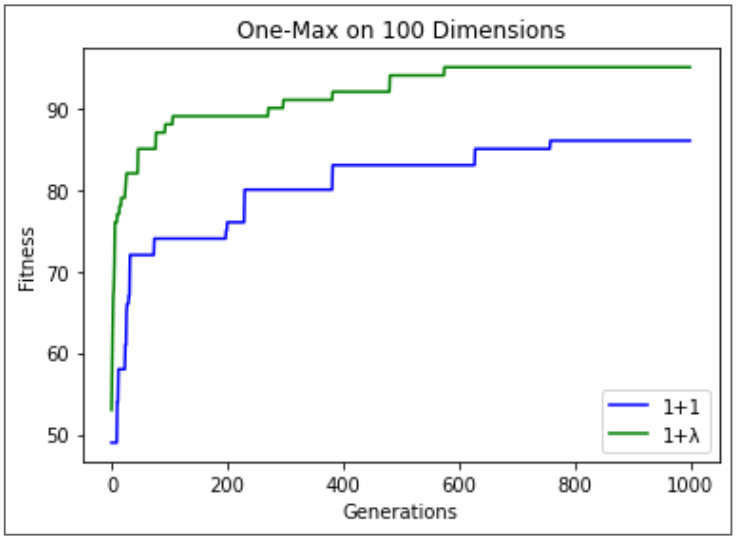
In [25]:

```
plt.plot(fits_1, label="1+1", color='b')
plt.plot(fits_λ, label="1+λ", color='g')
plt.xlabel("Generations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions")
plt.legend();
```


One-Max on 100 Dimensions
Fitness
Generations
90
80
70
60
50
0
200
400
600
800
1000
1+1
1+λ

In [26]:

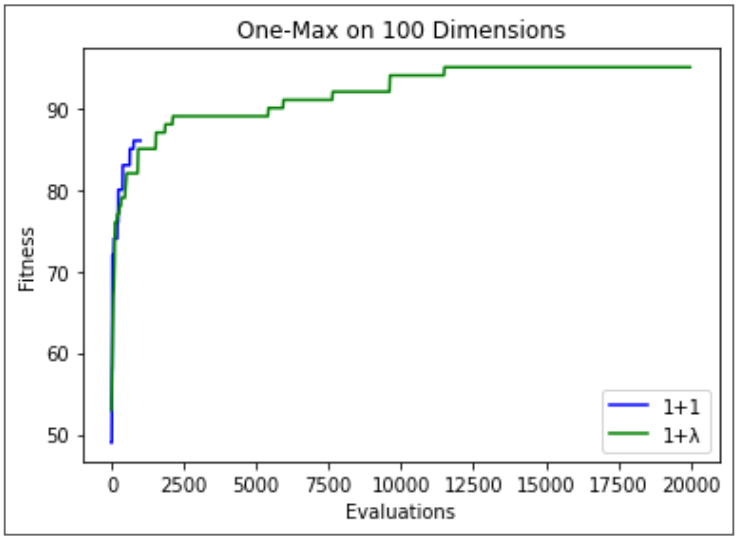
```
plt.plot(fits_1, label="1+1", color='b')
plt.plot(fits_λ, label="1+λ", color='g')
plt.xlabel("Generations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions")
plt.legend();
```



- (1+λ)-EA seems to be better than (1+1)-EA. But is this a fair comparison?
- (1+λ)-EA actually runs λ evaluation functions per generation, while (1+1)-EA only runs 1 evaluation function per generation.
- We need to plot the results base on the number of evaluations.

In [27]:

```
plt.plot(fits_1, label="1+1", color='b')
plt.plot(np.arange(1,n_gens*λ,λ), fits_λ, label="1+λ", color='g')
plt.xlabel("Evaluations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions")
plt.legend();
```



- We should give each algorithm the same number of function evaluations, like this:

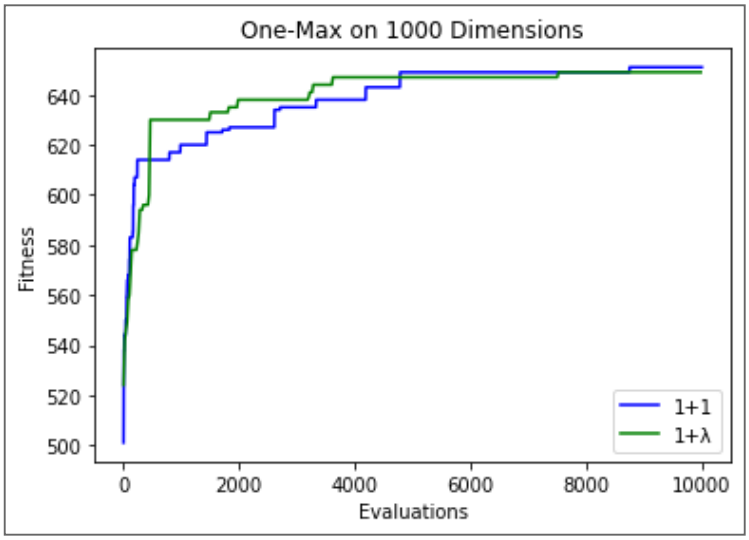
In [28]:

```
n = 1000
n_gens = 10000
fits_1 = one_plus_one(n, n_gens, onemax)
fits_λ = one_plus_lambda(n, int(n_gens/λ), onemax, λ)
```

```
100%|                                                                                | 10000/10000 [00:03<00:00, 3094.74it/s]
100%|                                                                                | 500/500 [00:03<00:00, 164.98it/s]
```

In [29]:

```
plt.plot(fits_1, label="1+1", color='b')
plt.plot(np.arange(1,n_gens,λ), fits_λ, label="1+λ", color='g')
plt.xlabel("Evaluations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions")
plt.legend();
```

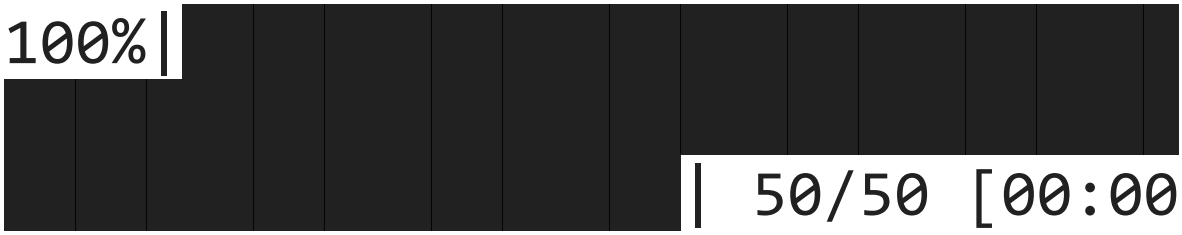


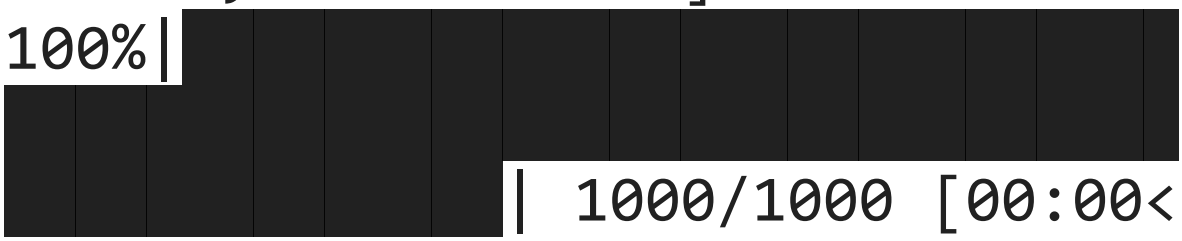
- Because EAs employ randomness in their operations, to assess the performance of EAs, we should run them multiple times.
- Let's run each algorithm 10 independent times.

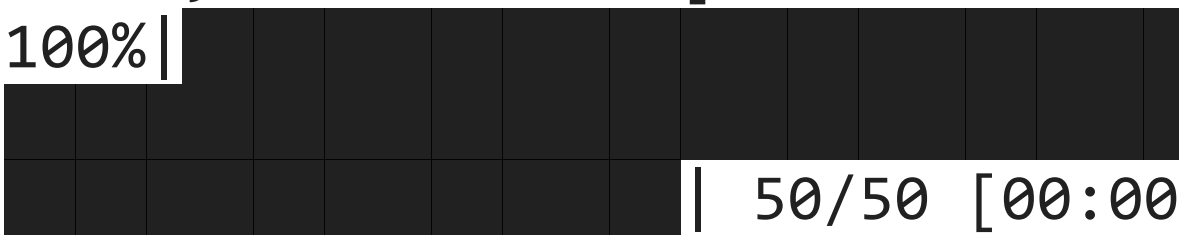
In [30]:

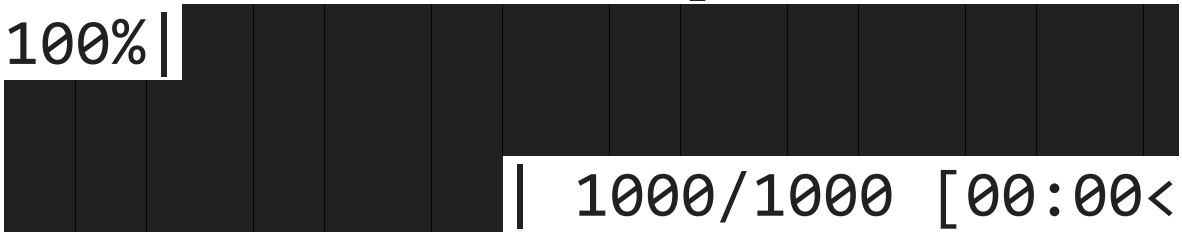
```
n_trials = 10
n = 100
n_gens = 1000

fits_1 = np.zeros((n_gens, n_trials))
fits_λ = np.zeros((int(n_gens/λ), n_trials))

for i in range(n_trials):
    fits_1[:, i] = one_plus_one(n, n_gens, onemax)
    fits_λ[:, i] = one_plus_lambda(n, int(n_gens/λ), onemax, λ)
```

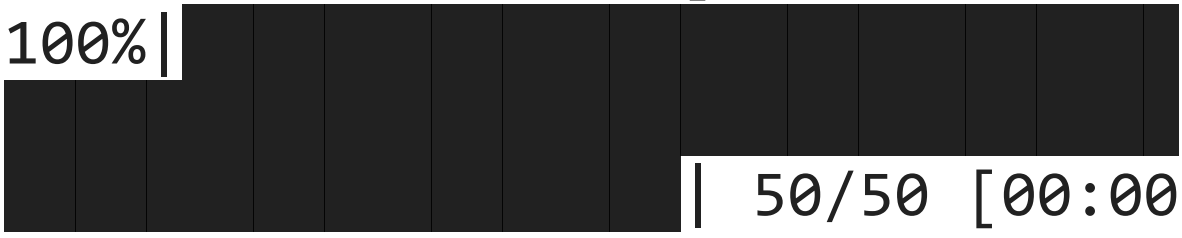
```
100%|| 1000/1000 [00:00<00:00, 22061.70it/s]
100%|| 50/50 [00:00<00:00, 1190.14it/s]
100%|| 1000/1000 [00:00<00:00, 22217.36it/s]
```

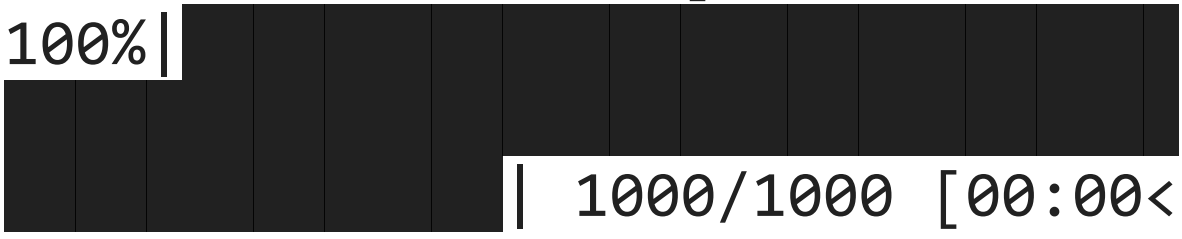

100%| | 50/50 [00:00<00:00, 1162.54it/s]


100%| | 1000/1000 [00:00<00:00, 22216.65it/s]

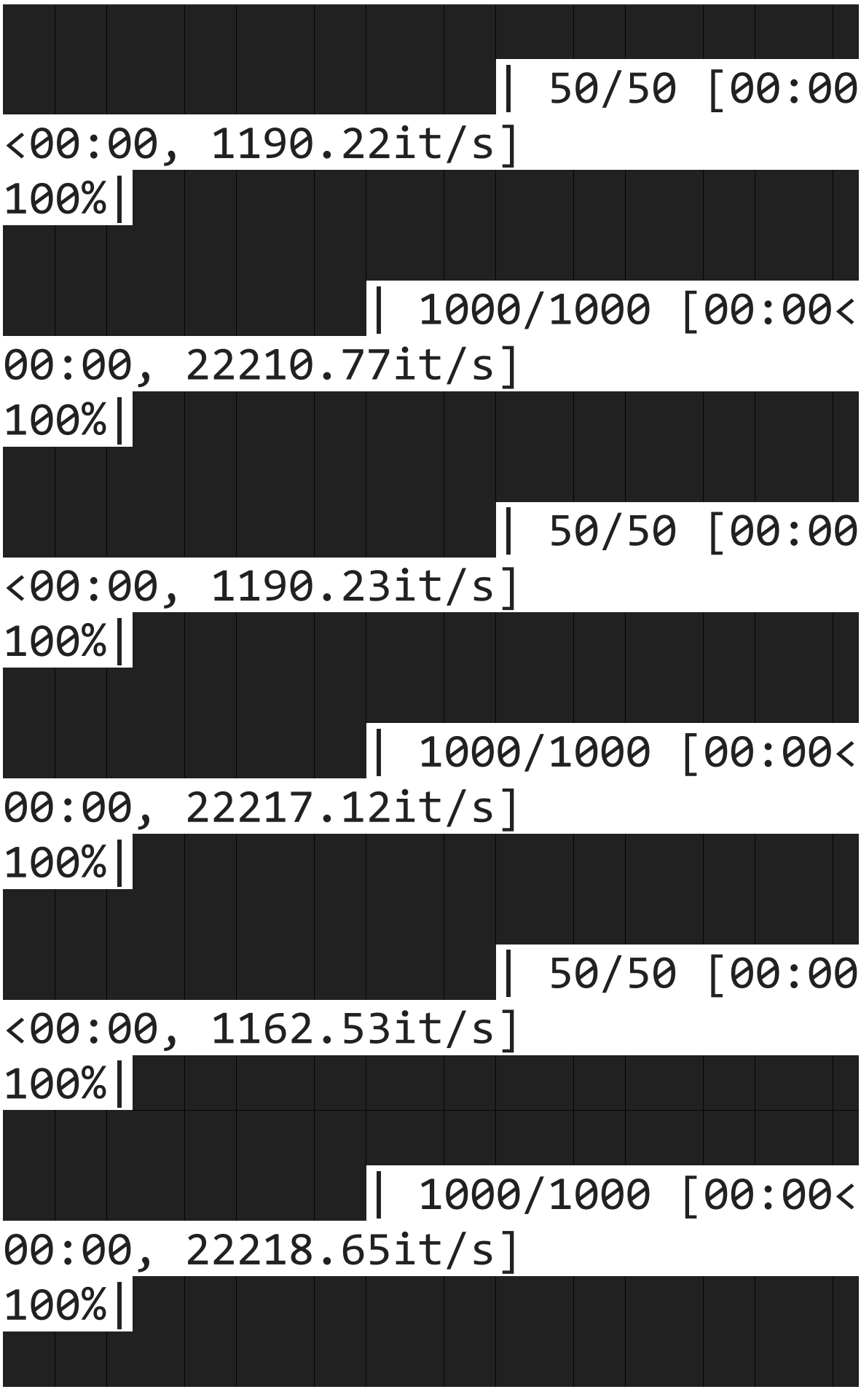

100%| | 50/50 [00:00<00:00, 1190.22it/s]

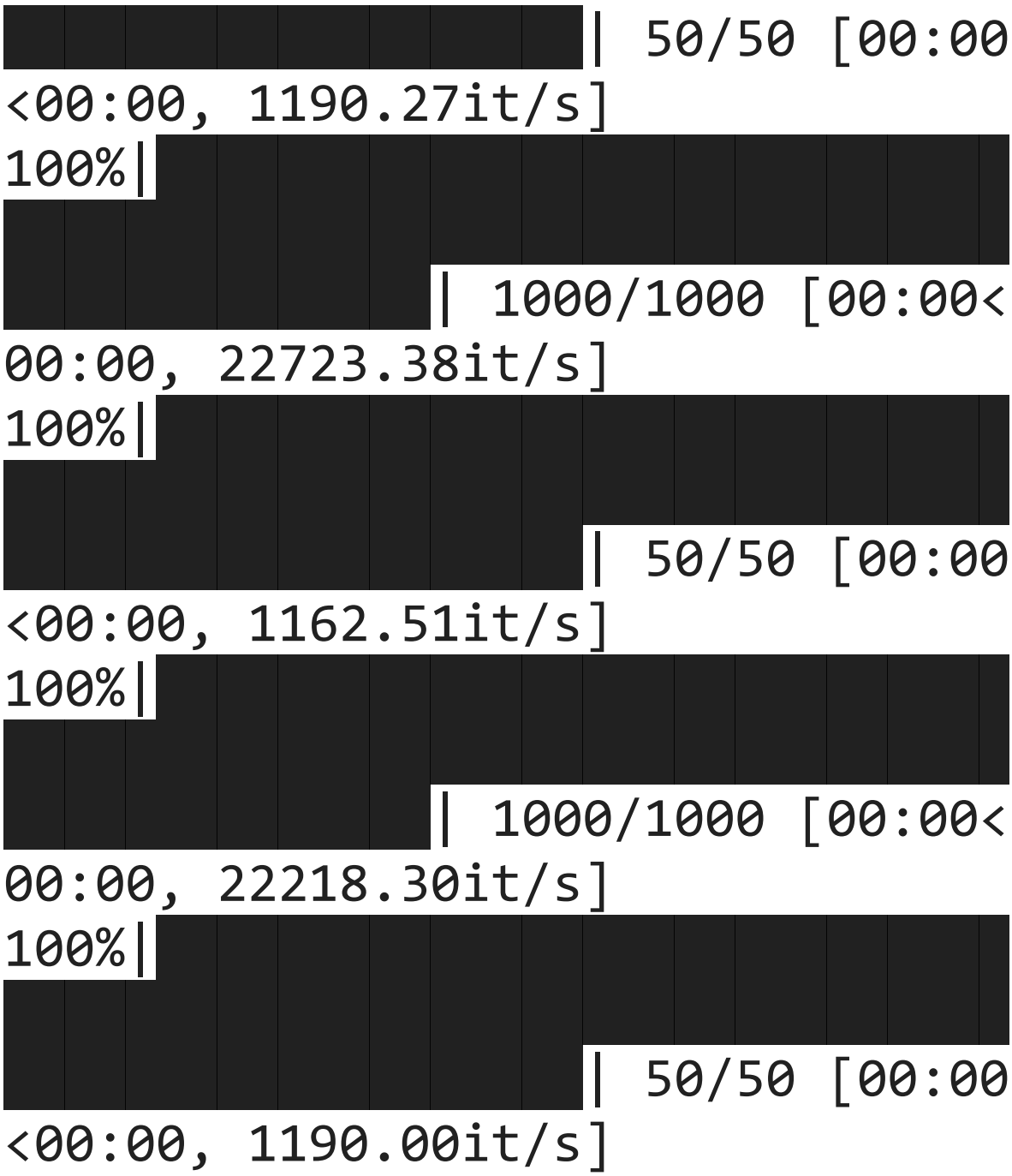

100%| | 1000/1000 [00:00<00:00, 22217.48it/s]


100%| | 50/50 [00:00<00:00, 1190.22it/s]


100%| | 1000/1000 [00:00<00:00, 22724.98it/s]


100%|


| 50/50 [00:00<00:00, 1190.22it/s]
100%|
| 1000/1000 [00:00<00:00, 22210.77it/s]
100%|
| 50/50 [00:00<00:00, 1190.23it/s]
100%|
| 1000/1000 [00:00<00:00, 22217.12it/s]
100%|
| 50/50 [00:00<00:00, 1162.53it/s]
100%|
| 1000/1000 [00:00<00:00, 22218.65it/s]
100%|


| 50/50 [00:00<00:00, 1190.27it/s]
100%| | 1000/1000 [00:00<00:00, 22723.38it/s]
100%| | 50/50 [00:00<00:00, 1162.51it/s]
100%| | 1000/1000 [00:00<00:00, 22218.30it/s]
100%| | 50/50 [00:00<00:00, 1190.00it/s]

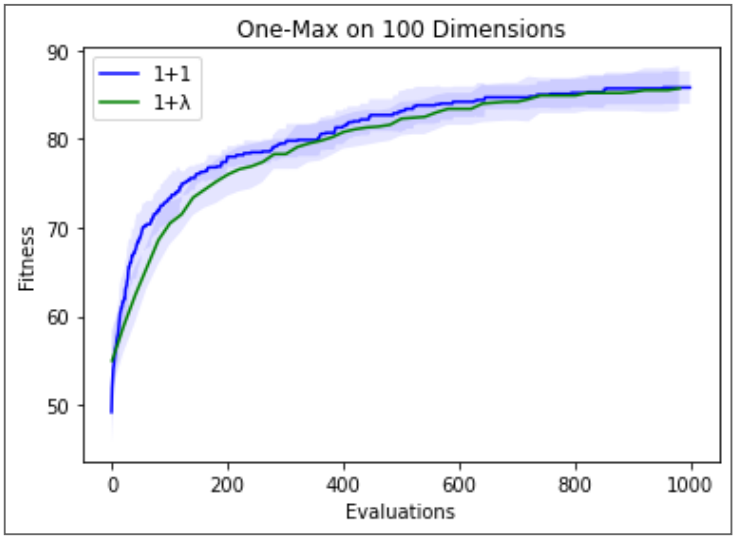
In [31]:

```
μ_1 = np.mean(fits_1, axis=1)
σ_1 = np.std(fits_1, axis=1)
μ_λ = np.mean(fits_λ, axis=1)
σ_λ = np.std(fits_λ, axis=1)
print(np.shape(μ_1), np.shape(σ_1))
print(np.shape(μ_λ), np.shape(σ_λ))
```

```
(1000,) (1000,)
(50,) (50,)
```

In [32]:

```
plt.plot(μ_1, label="1+1", color='b')
plt.fill_between(np.arange(0, n_gens), μ_1+σ_1, μ_1-σ_1, facecolor='b', alpha=0.1)
plt.plot(np.arange(1,n_gens,λ), μ_λ, label="1+λ", color='g')
plt.fill_between(np.arange(0, n_gens, λ), μ_λ+σ_λ, μ_λ-σ_λ, facecolor='b', alpha=0.1)
plt.xlabel("Evaluations")
plt.ylabel("Fitness")
plt.title(f"One-Max on {n} Dimensions")
plt.legend();
```



Question: Compare the (1+1)-EA and (1+λ)-EA on the Leading Ones problem.

Algorithm control parameters

- In practice, the choice of mutation rate p and population size λ greatly influence experimental results.
- We can also use **self-adjusting parameters**, which is similar to what simulated annealing uses.

https://link.springer.com/article/10.1007/s00453-018-0502-x

Question:

- Investigave the effect of population size λ and mutation rate p on (1+1)-EA and (1+λ)-EA.
- Try implementing a dynamic mutation rate (e.g., a mutation rate that decreases over time) and compared it with the fixed mutation rate $p = \frac{1}{n}$.