DNA Specifications and Codon: Expressing Combinatorial Designs at Scale

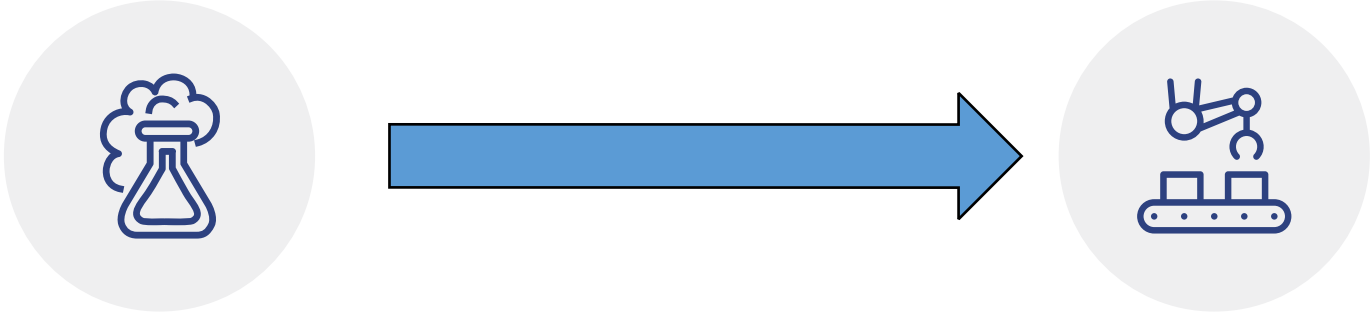
Zach Palchick

zymergen


zymergen

About Zymergen

zymergen



Designers/
Development Scientists

The Factory

What's the problem

1. **Can express large design spaces**
2. **Compact format**
3. **Transferable**
4. **Structure preserving**

DNA Specifications

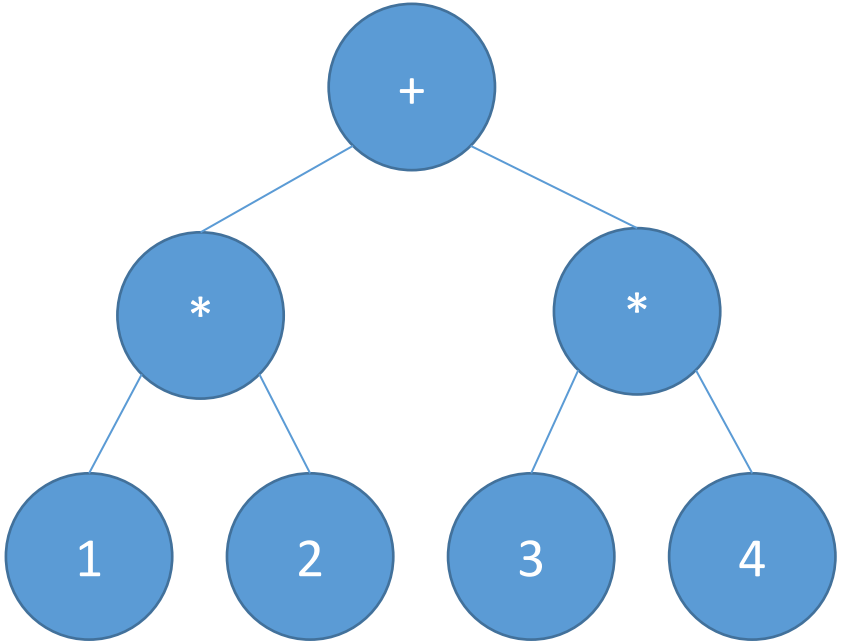
1. **Nested trees of functions**
2. **Leaves are collections of DNA sequences**
3. **Internals are string manipulating operations**
4. **Similar to an Abstract Syntax Tree**

Abstract syntax trees 101

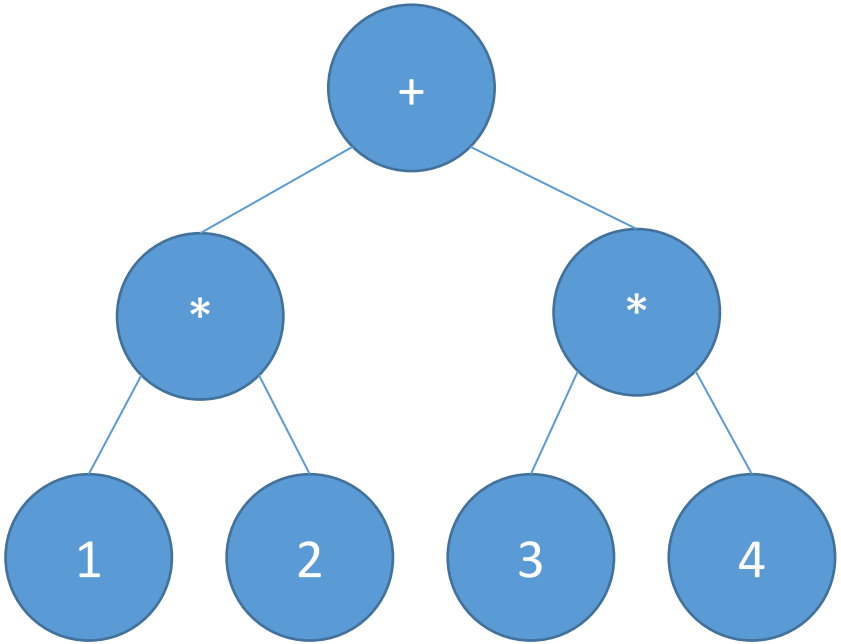
x = (1 * 2) + (3 * 4)
x = (2) + (3 * 4)
x = (2) + (12)
x = 2 + (12)
x = 2 + 12
x = 14

Algebra can be modeled as an AST

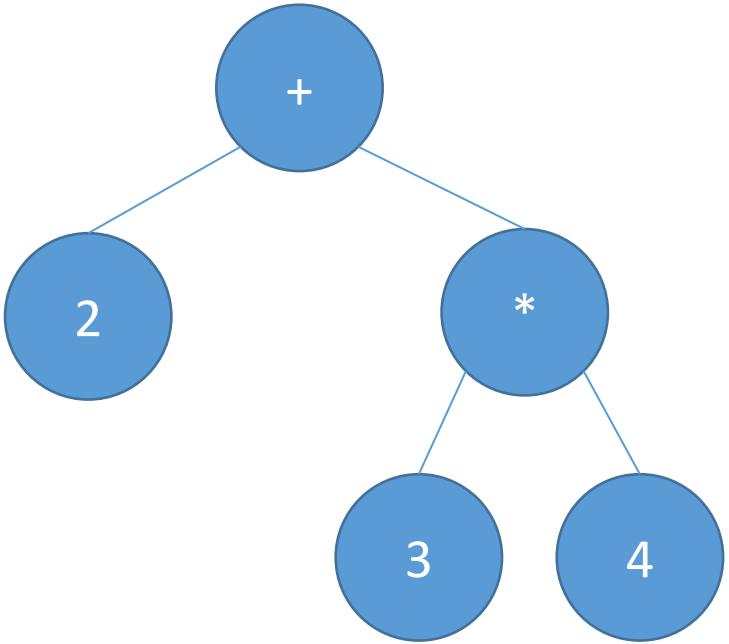
x = (1 * 2) + (3 * 4)



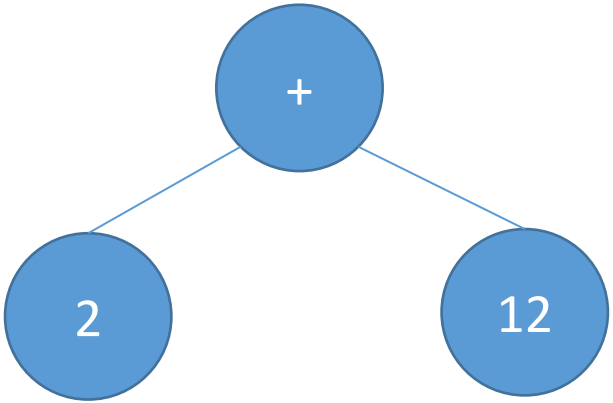
Evaluating ASTs



Evaluating ASTs

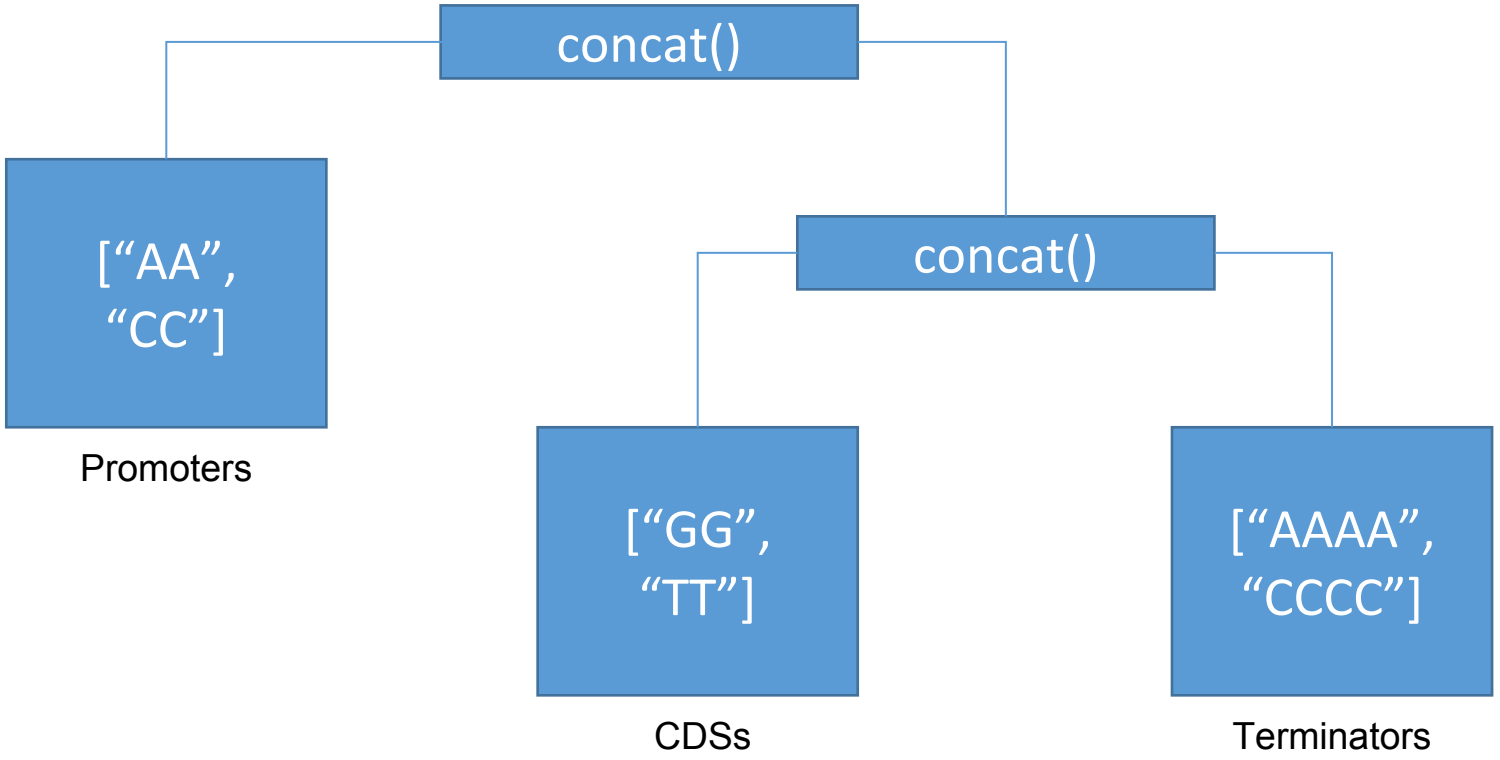


Evaluating ASTs



Evaluating ASTs

DNA Specifications are ASTs



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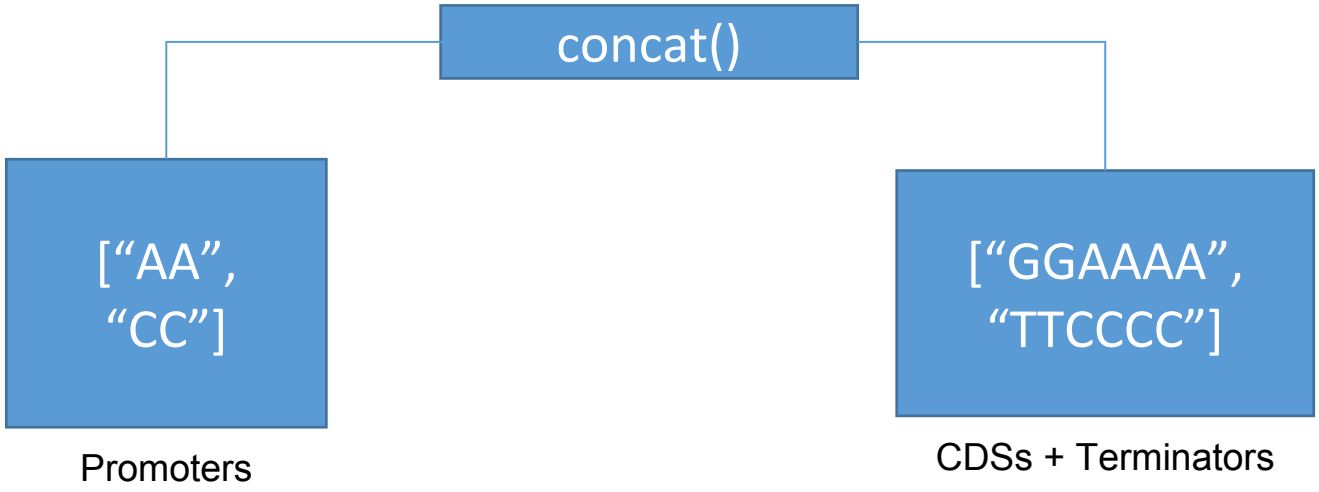
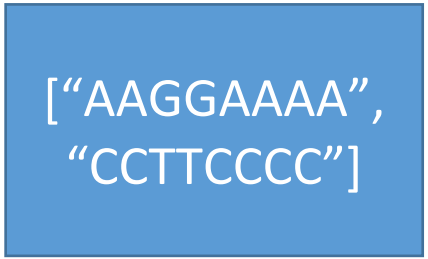
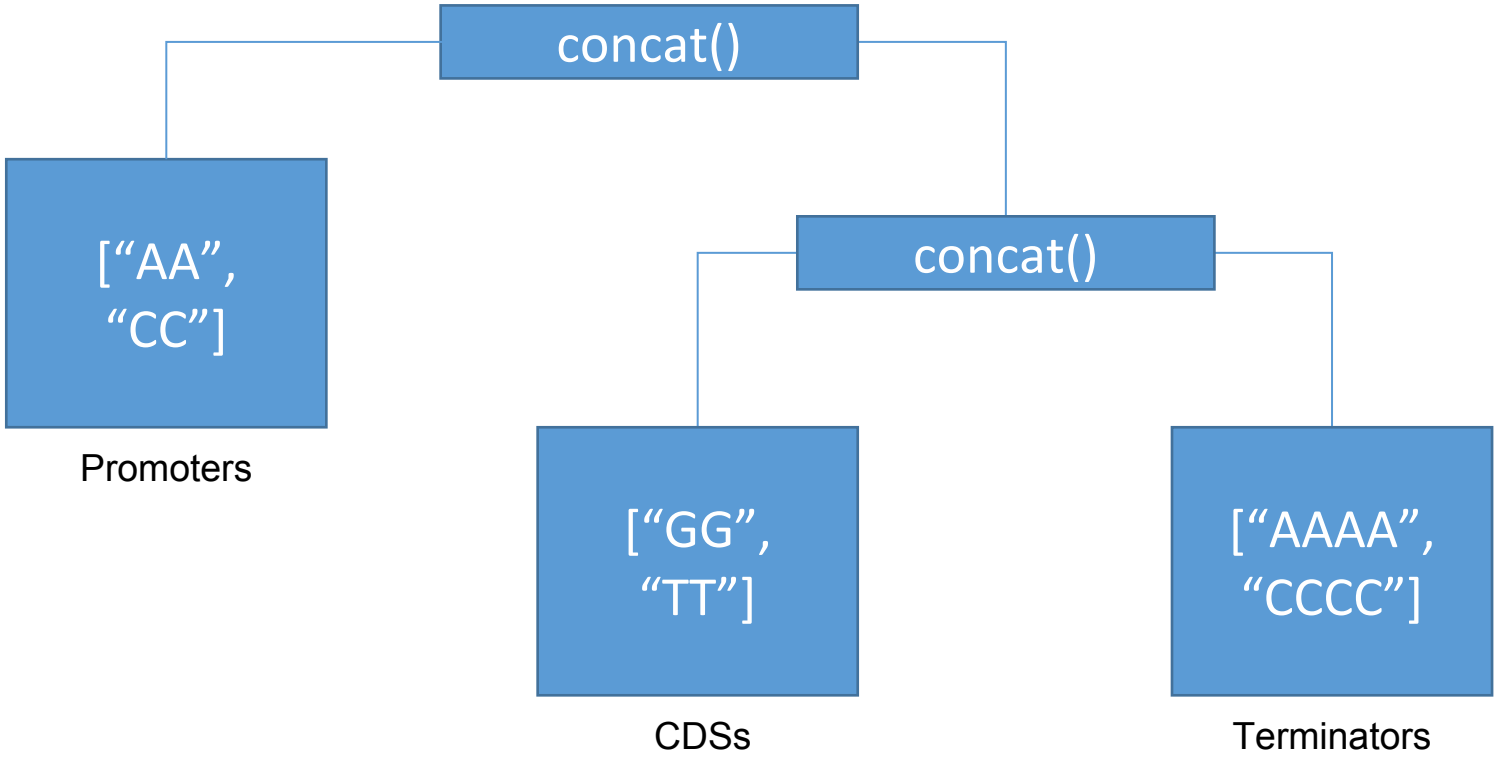


DNA Specifications are ASTs



Promoters + CDSs + Terminators

ASTs let us preprocess structure



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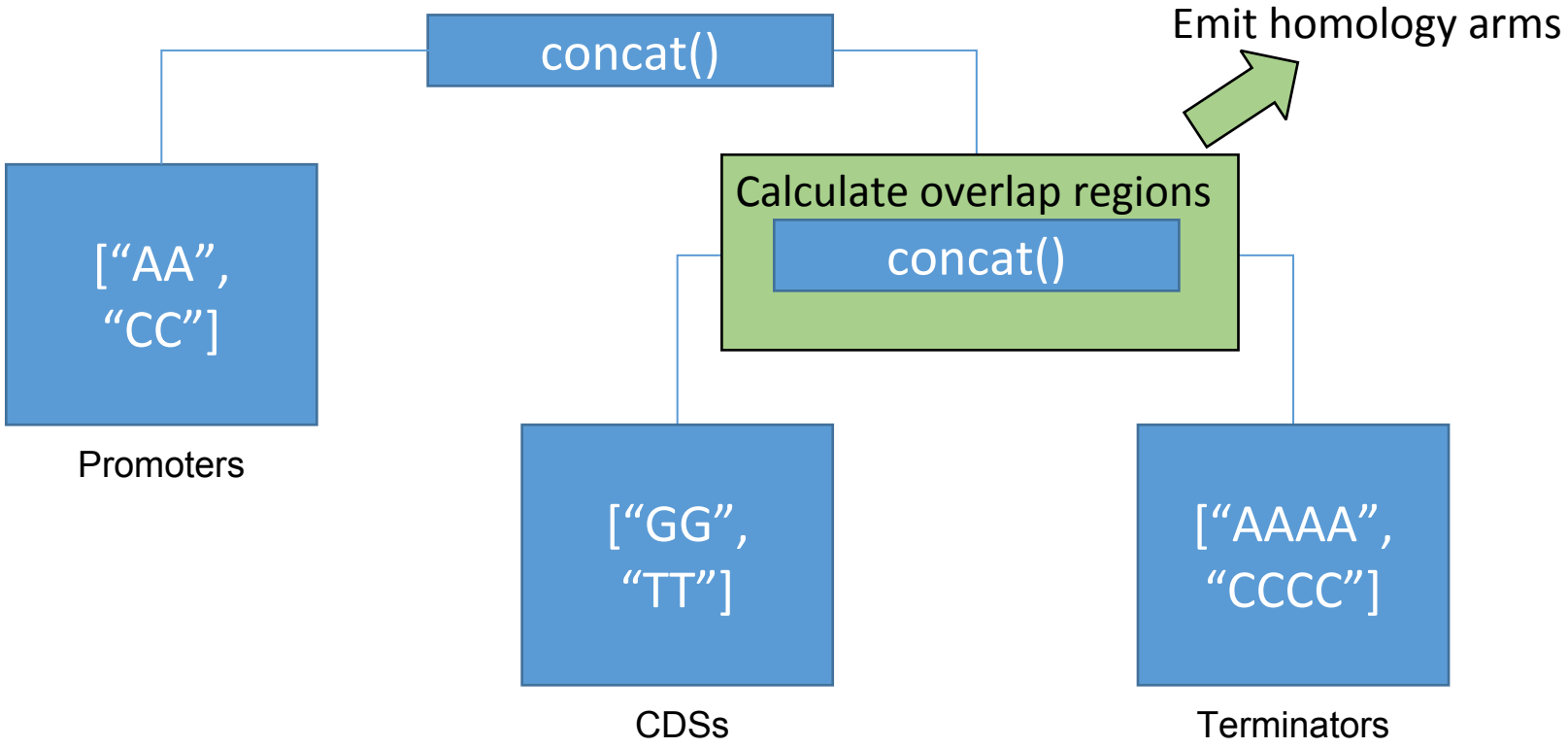

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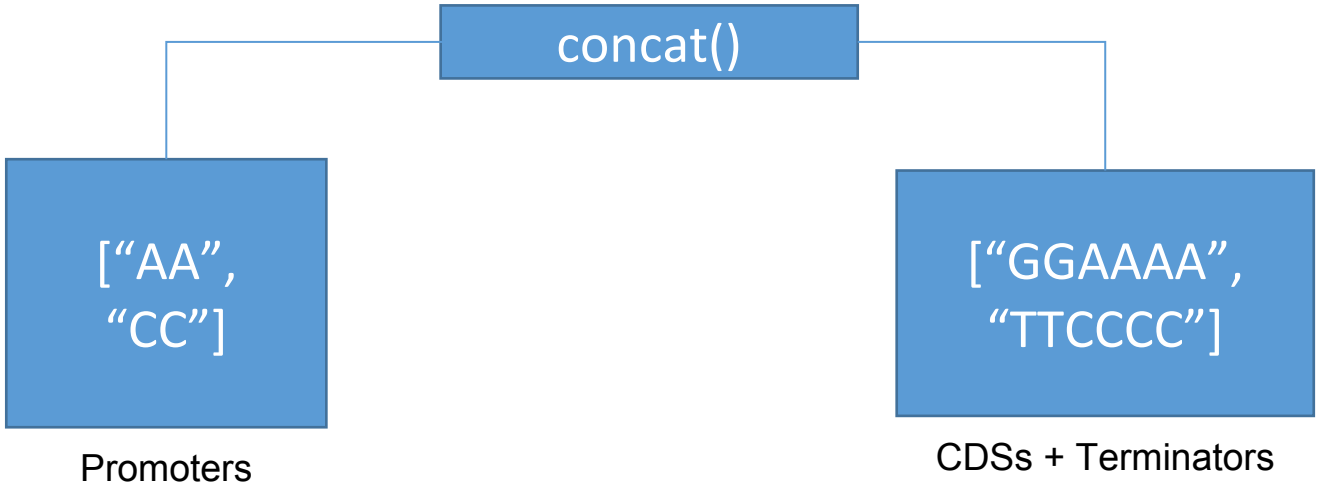

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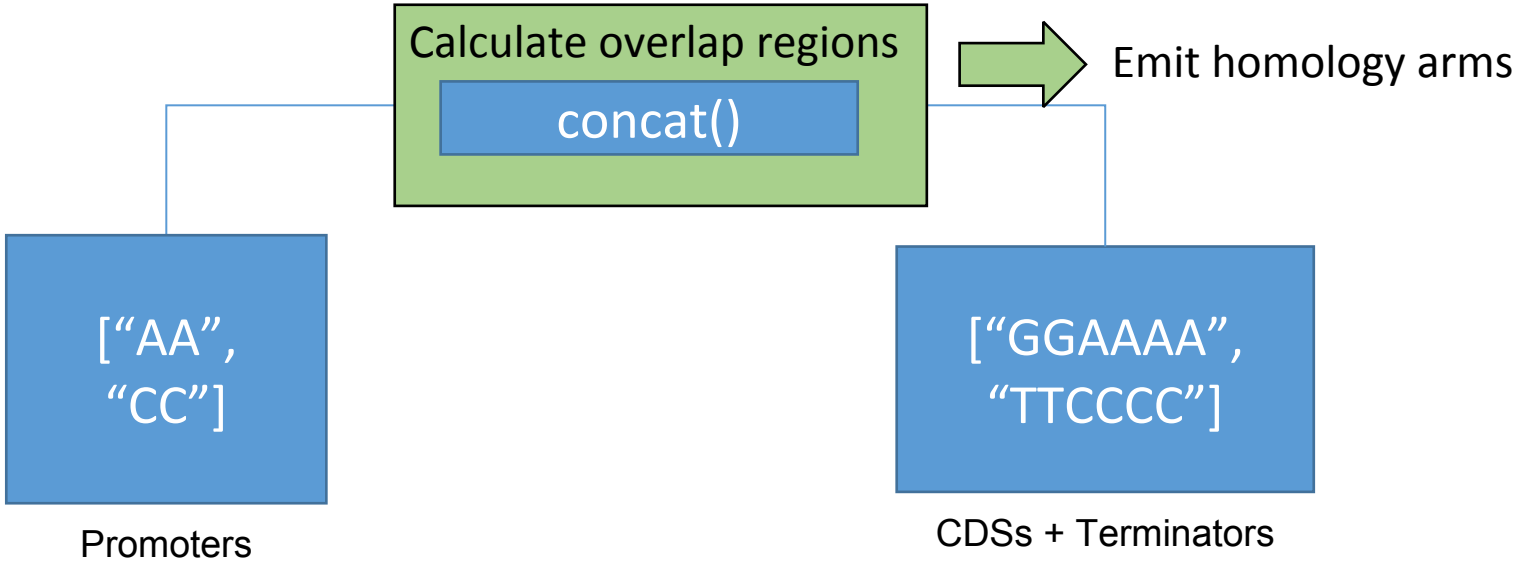

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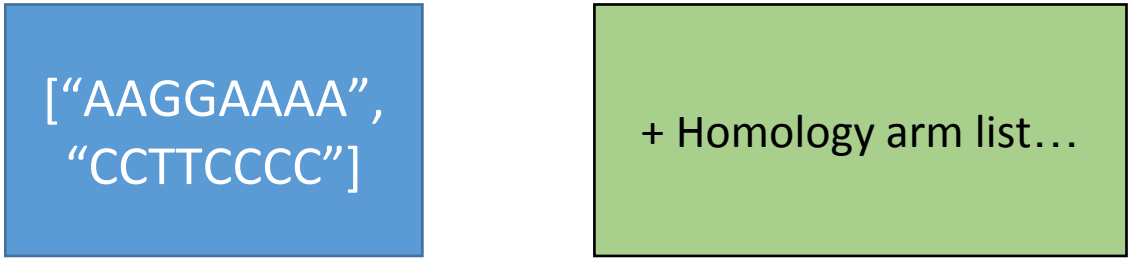
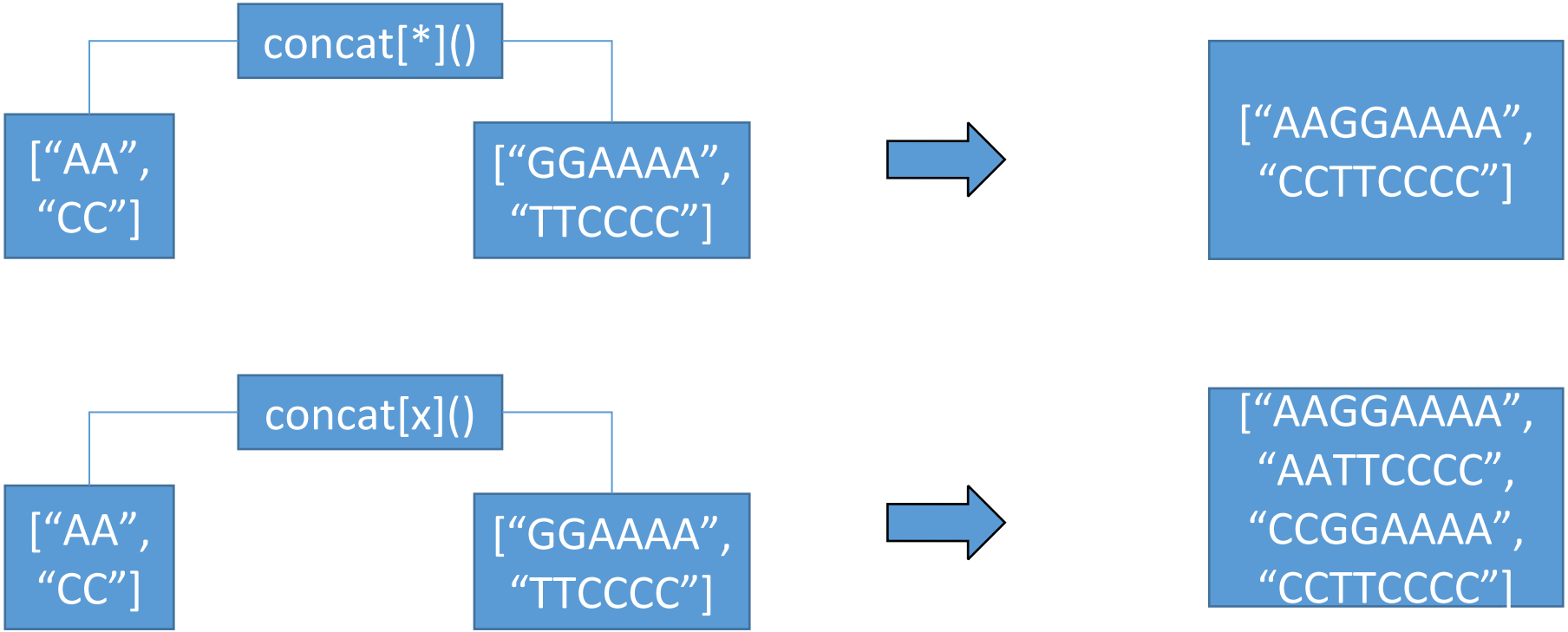


Functions can be parametric



Codon: Promoter Swapping

```
replacePromoter[x](locateGenes(hostStrain, "YFG*"), promoters)
```

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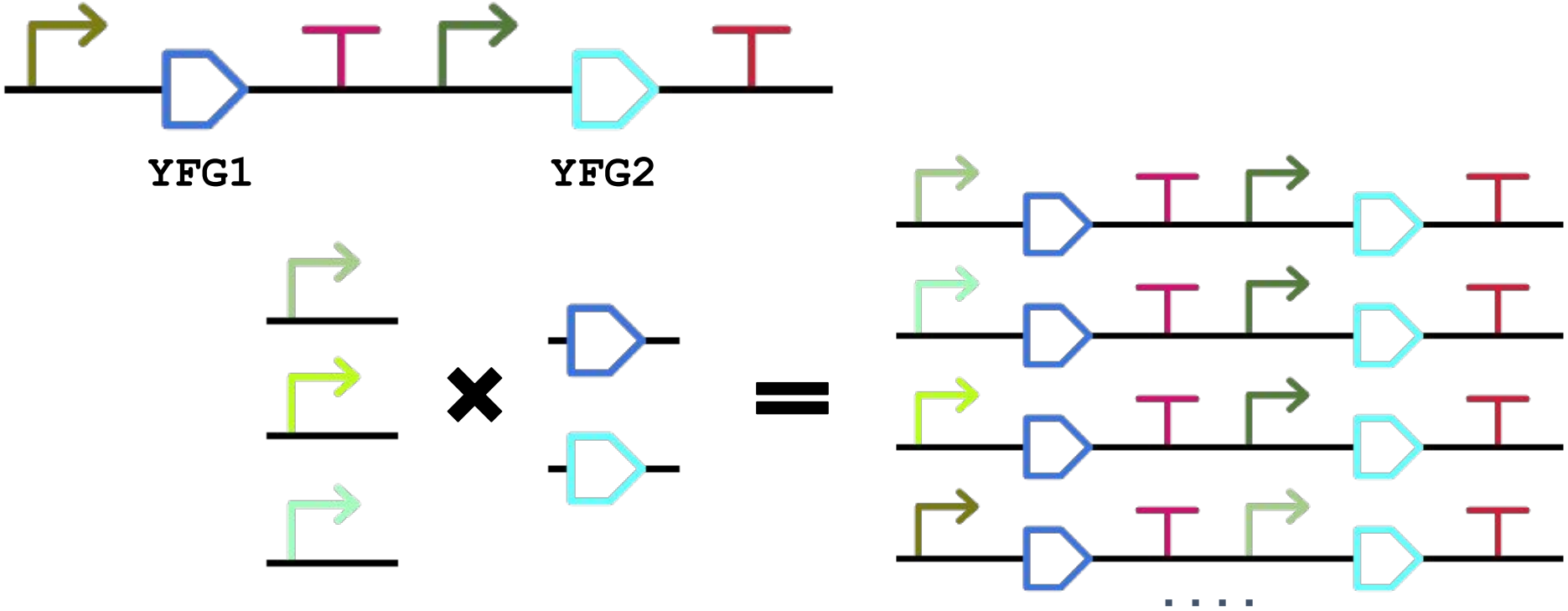


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replacePromoter[x](locateGenes(hostStrain, "YFG*"), promoters)
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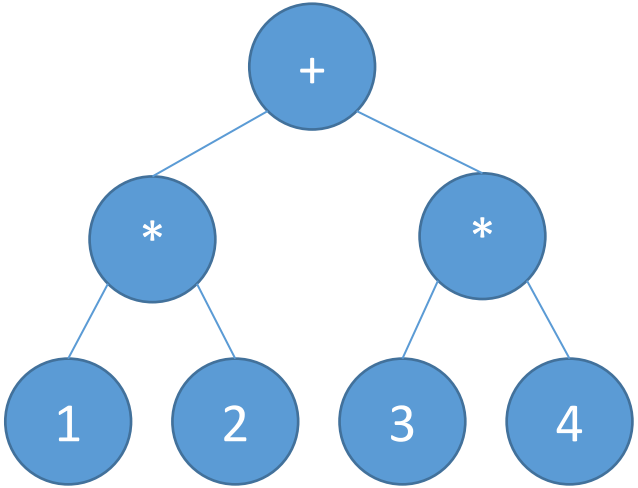
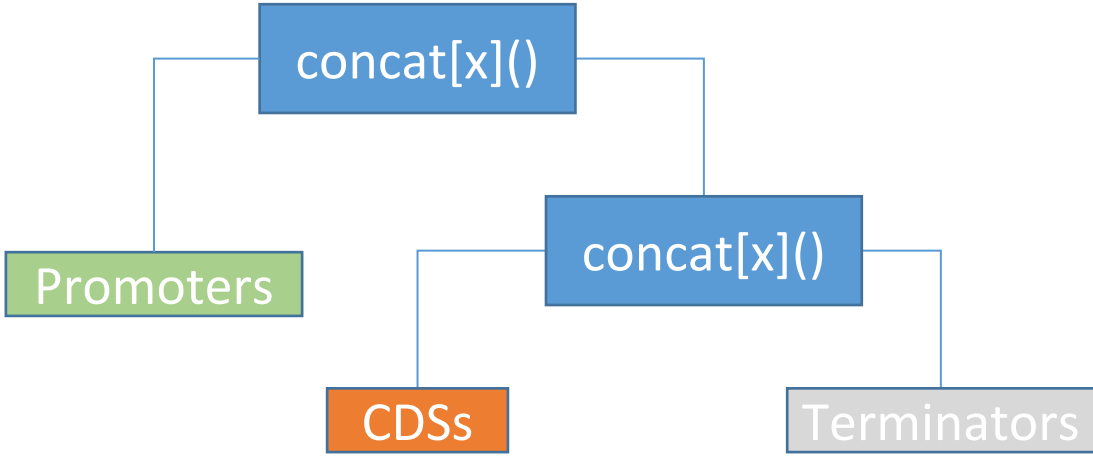
How well do DNA Specifications work?

Demonstration of mapping

x = (1 * 2) + (3 * 4)



Promoters x CDSs x Terminators



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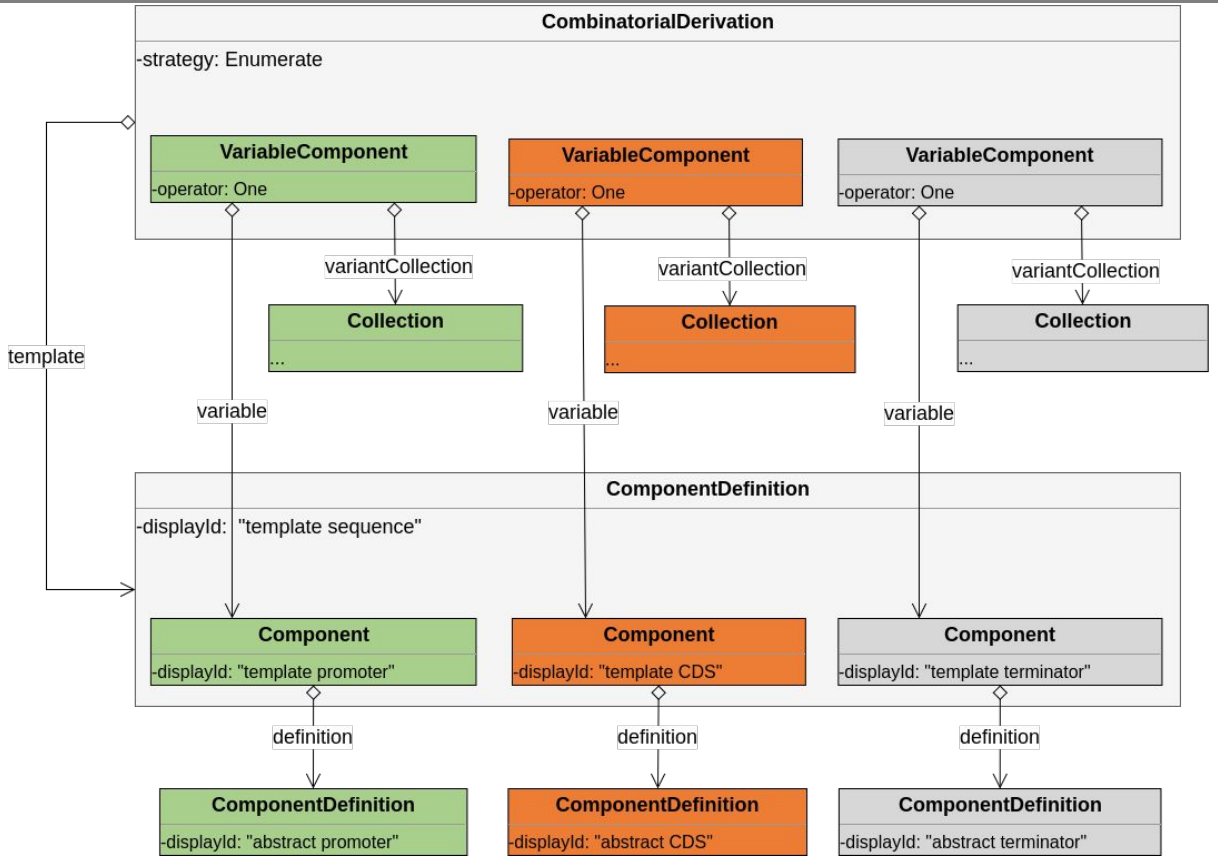
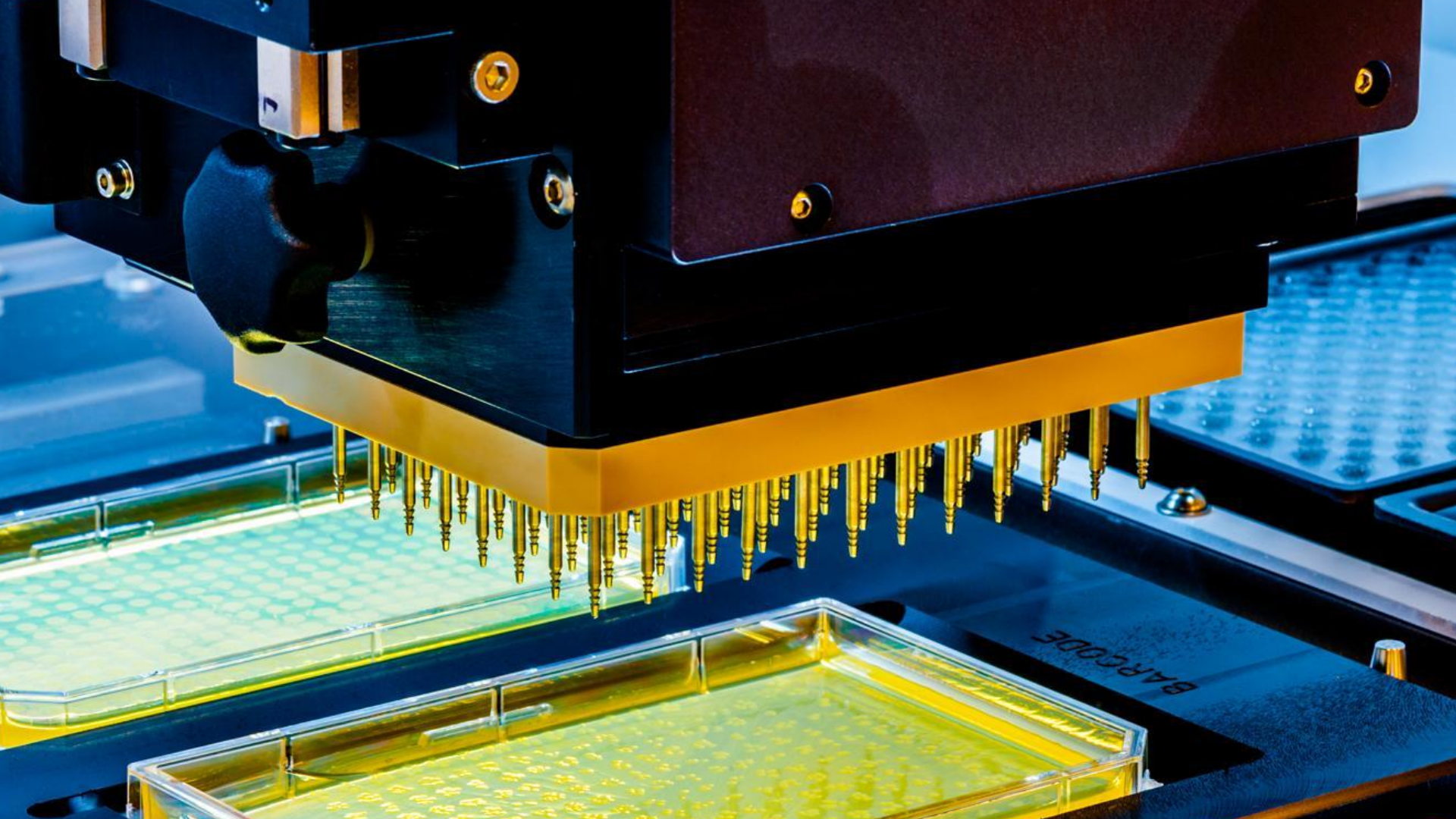


Thank You

Zach Palchick - palchicz@zymergen.com


BARCODE