

-441	Andry-Reilo Kahr	491	Andry-Reilo Kahr		
-442	Natalia Kuhi		3:0		
-443	Jora Clipii	492	Jora Clipii	533	Jora Clipii 69.
-444	Ülle Meritee		3:1		
				-533	Andry-Reilo Kahr 70.

-491	Natalia Kuhi	532	Natalia Kuhi	71.
-492	Ülle Meritee	3:0		
		-532	Ülle Meritee	72.

The diagram illustrates the iterative process of building a reference genome. It shows several stages of assembly:

- Initial Contigs:** Small DNA segments (contigs) are identified, such as 489, 490, 530, 487, and 488.
- Overlap Identification:** The process identifies overlapping regions between these contigs.
- Scaffolding:** Overlapping contigs are joined together to form larger scaffolds. For example, contigs 489 and 490 overlap, and their combined length is 75. Similarly, 487 and 488 overlap, with a combined length of 79.
- Iterative Process:** The process continues as more data is added, showing how smaller contigs (like 530 and 528) are integrated into the existing scaffolds to further expand the reference genome.
- Final Result:** The process culminates in a complete reference genome of 3,100,000,000 bp.

Diagram illustrating a sequence of operations on a stack:

- Initial stack: -527 , -485 , -486
- Operation 82: bye bye (removes -486)
- Operation 83: bye bye (removes -485)
- Operation 84: bye bye (removes -527)
- Stack after 84: Empty
- Operation 87: bye bye (removes -483)
- Operation 88: bye bye (removes -484)
- Stack after 88: Empty