



Sorting by TDRL and iTDRL

Bruno Schmidt, Tom Hartmann, Peter Stadler





Genome Rearrangements



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→ Depending on rearrangement types considered, sorting problem is NP-hard
- The **Tandem Duplication Random Loss/inverse Tandem Duplication Random Loss model** can mimic most “popular” rearrangements, and we developed a polynomial time algorithm for the sorting problem with TDRL/iTDRL





Genome Model



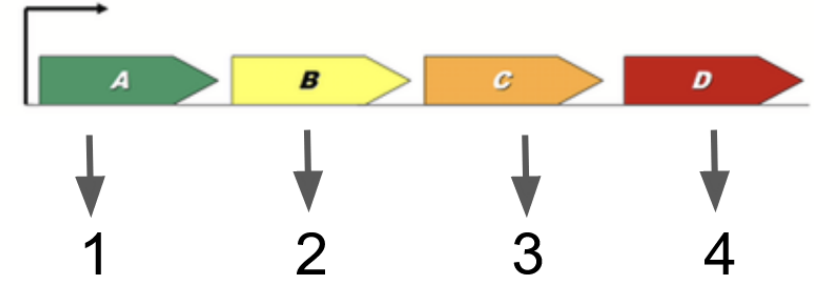
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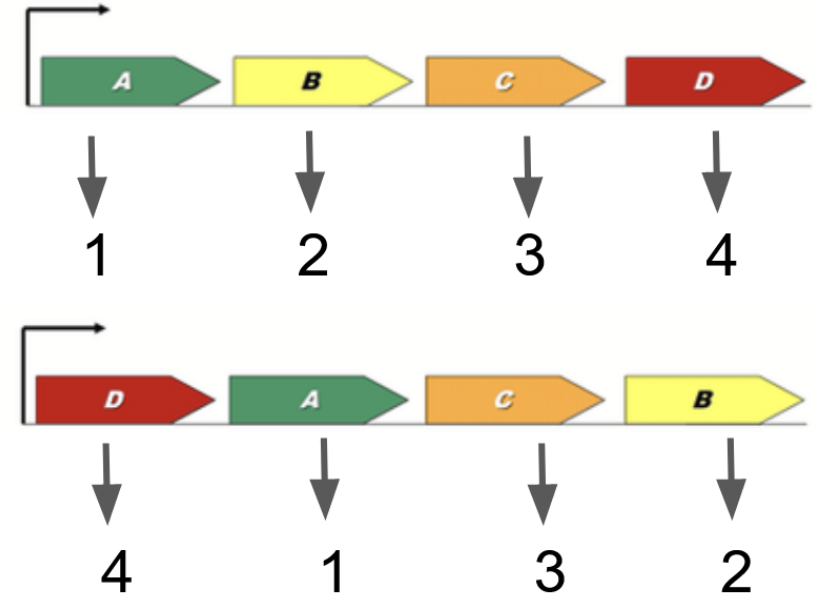
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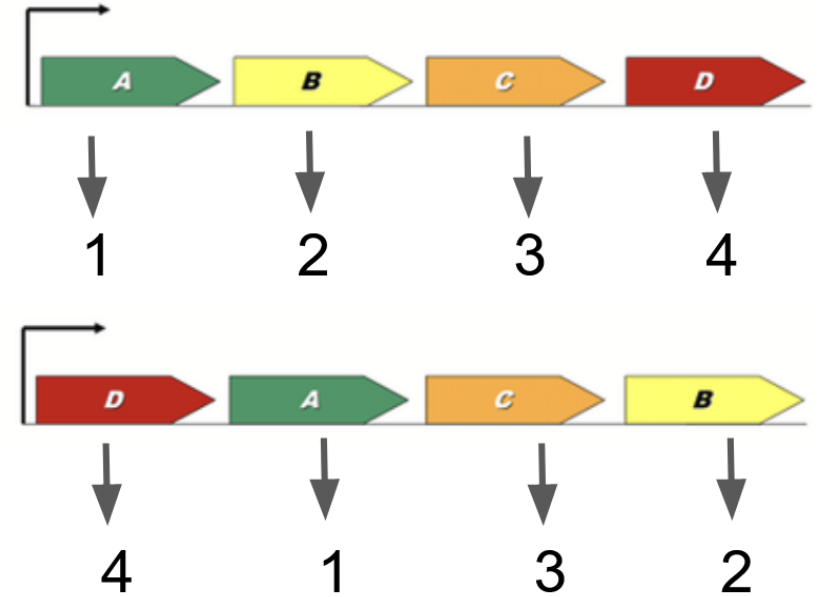
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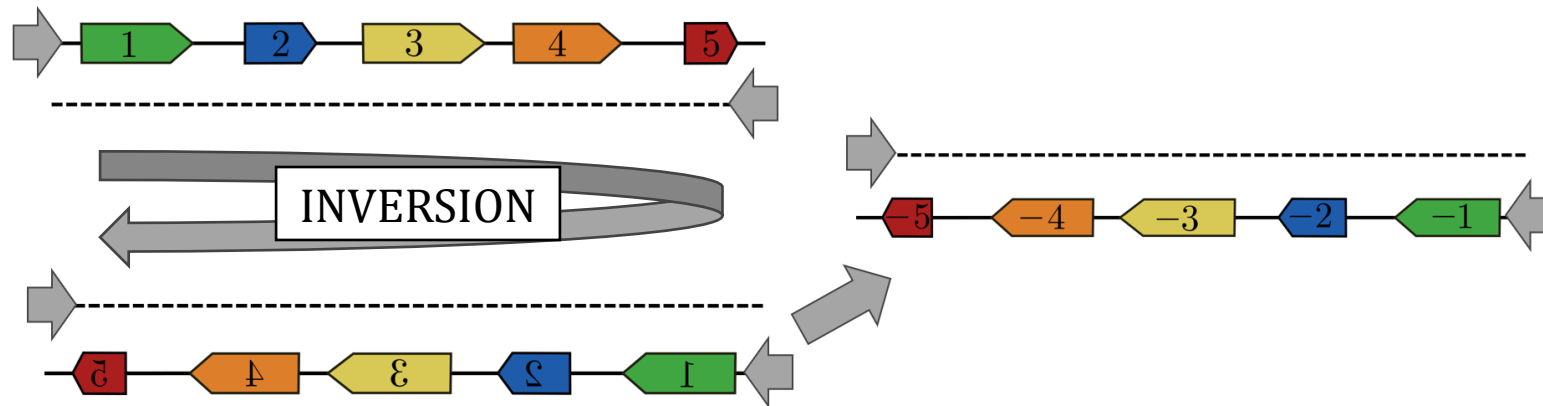
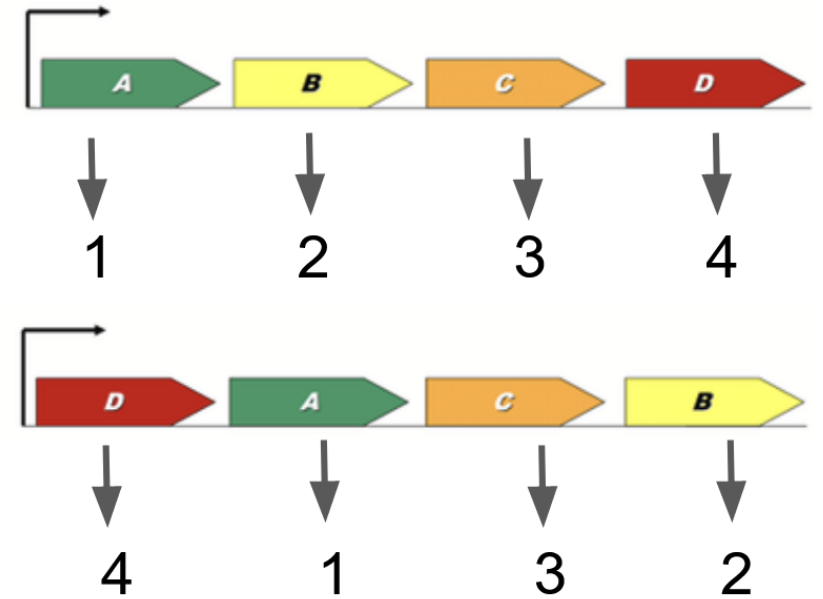
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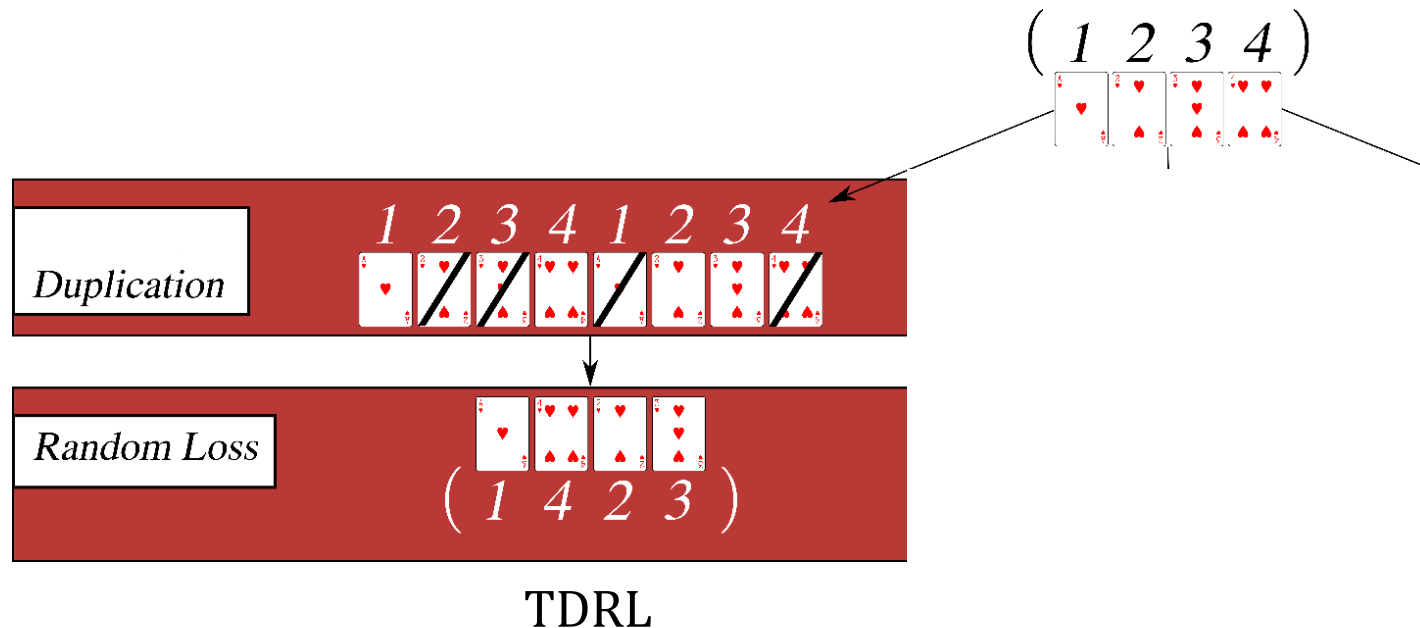
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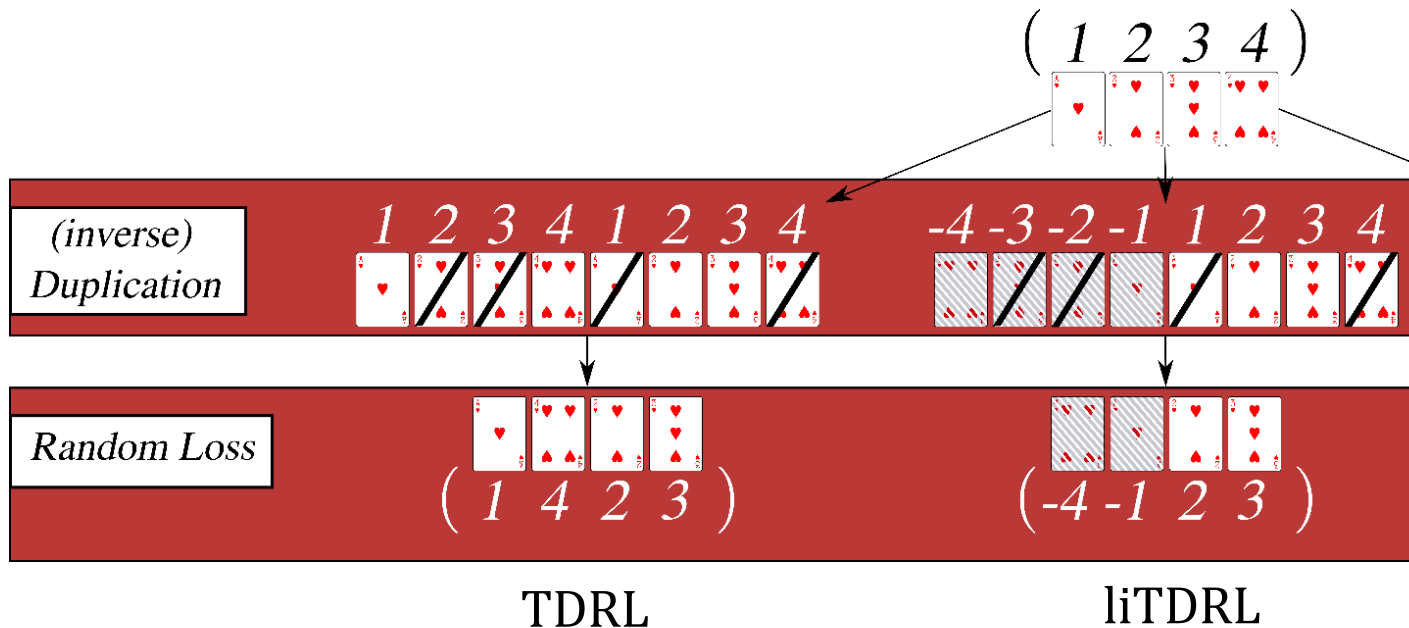
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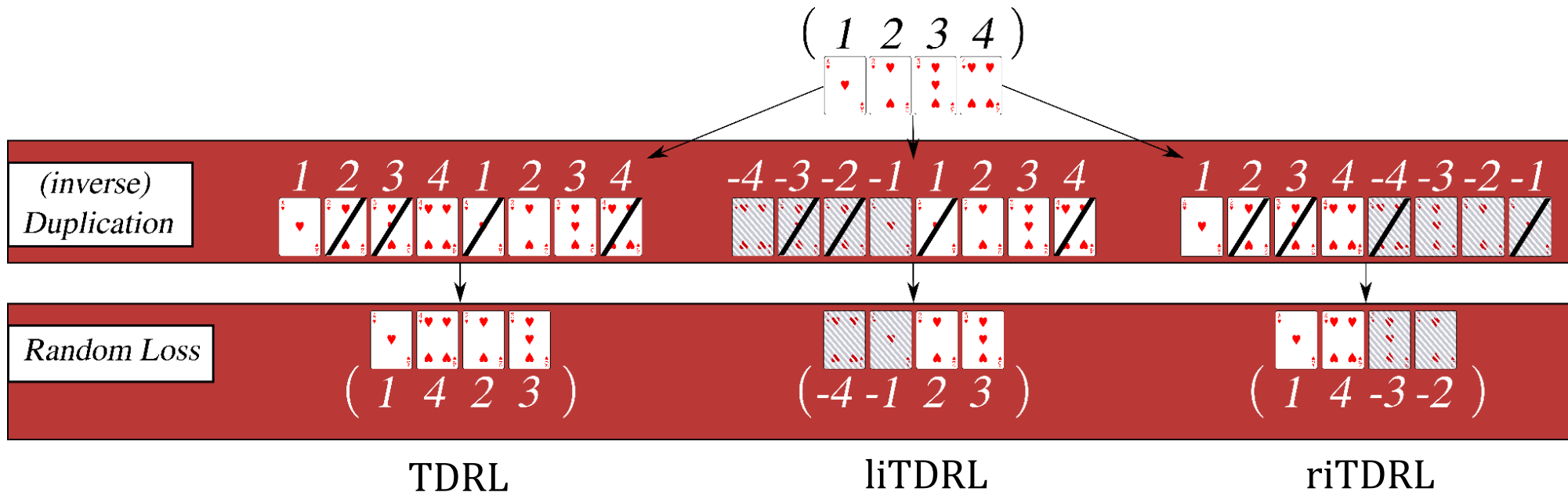
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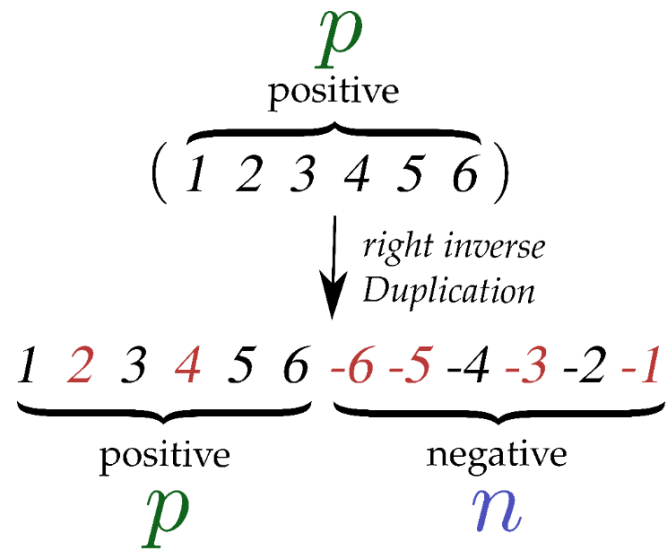
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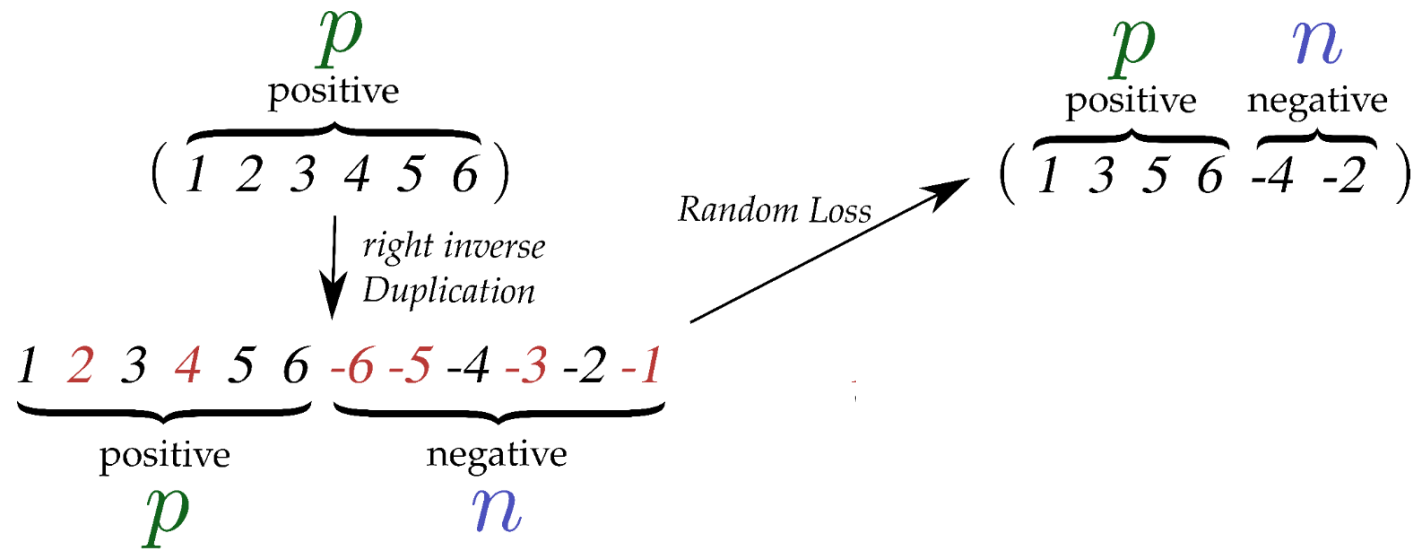


TDRL, iTDRL, and MISC-substrings



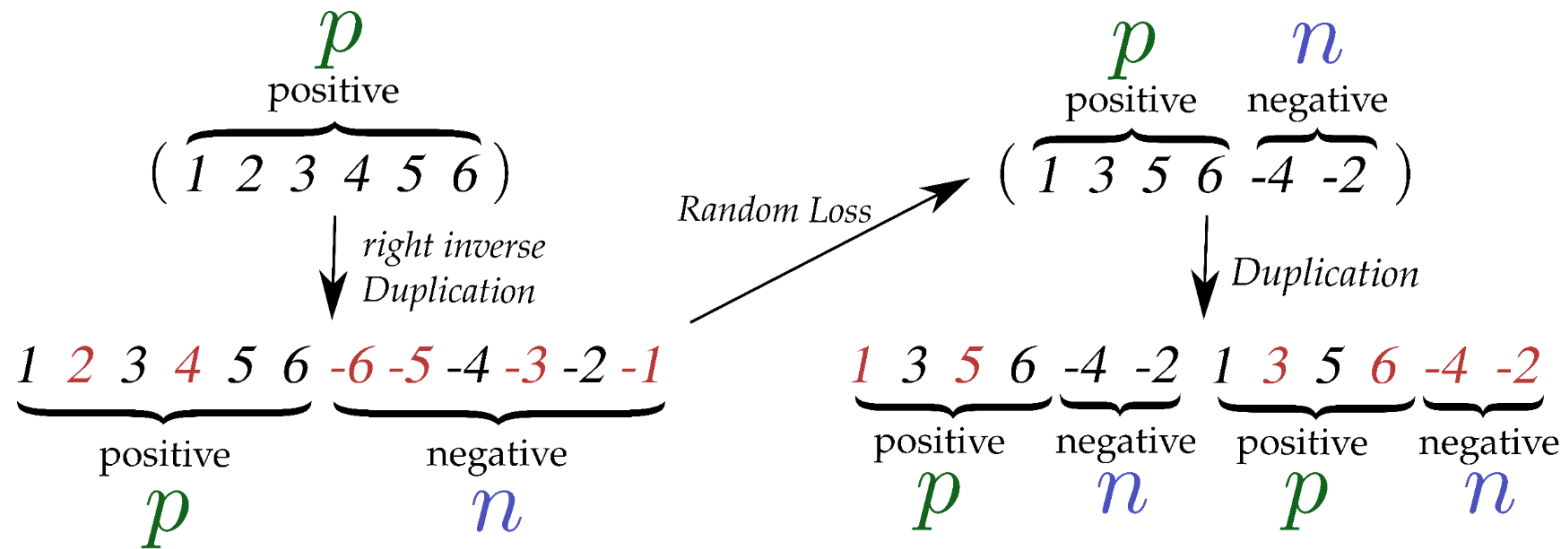


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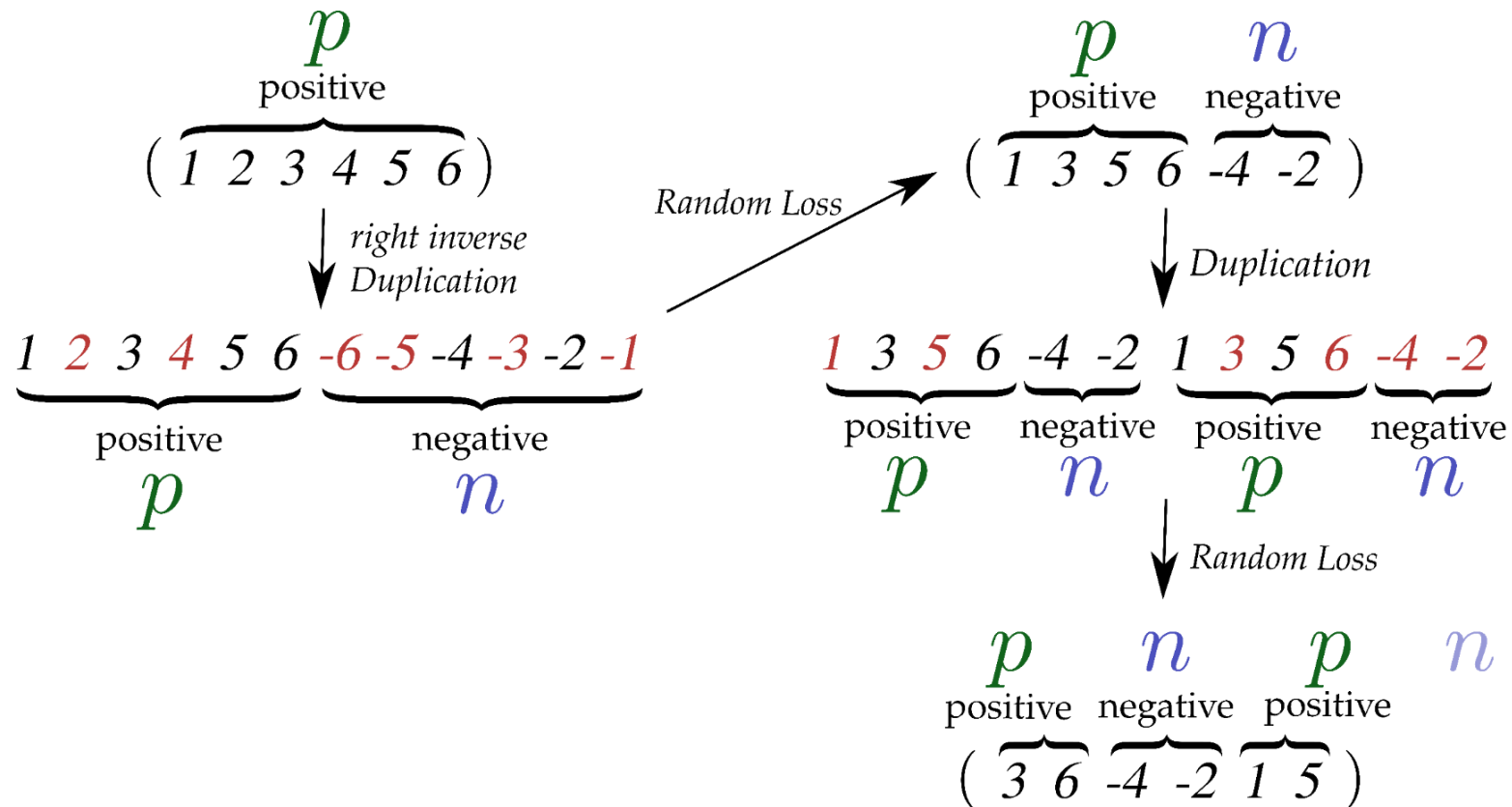


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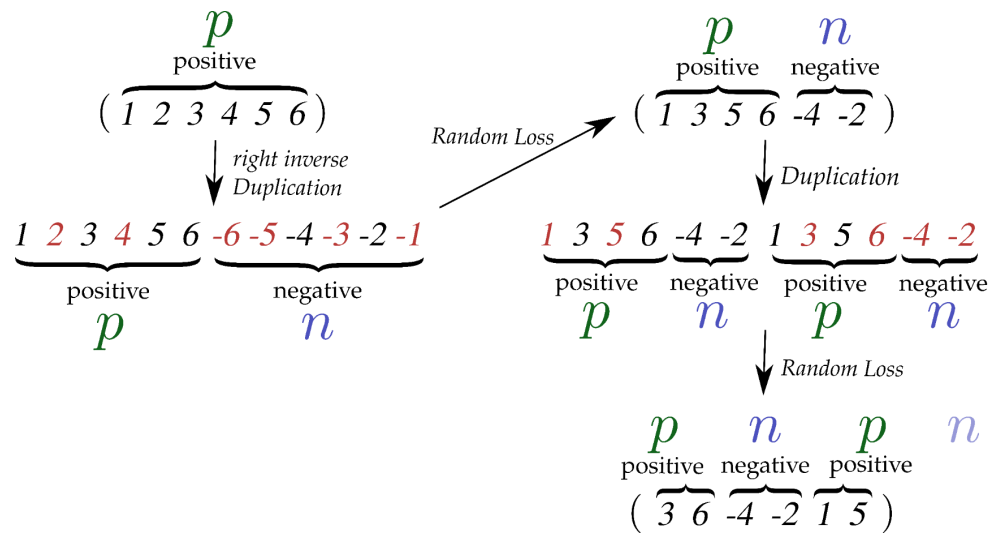


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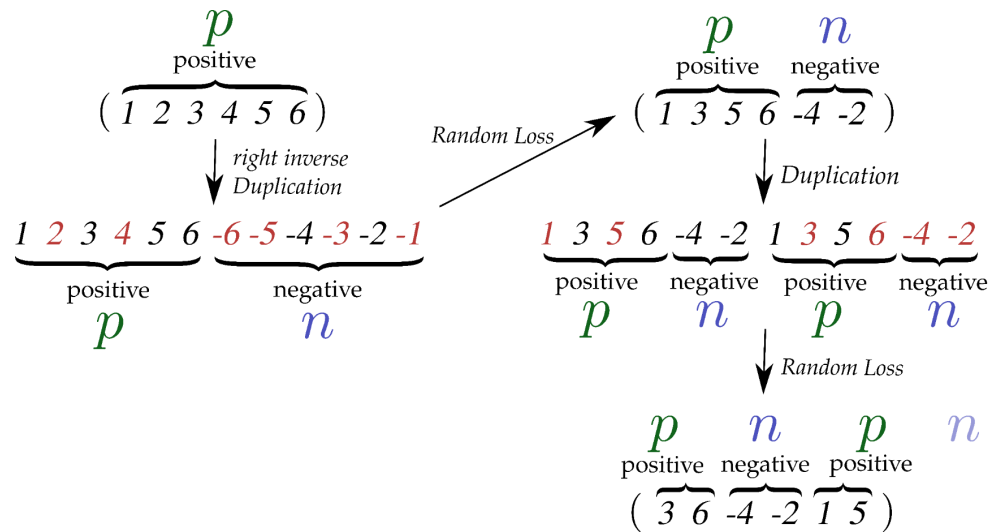


MISC-Substring Patterns





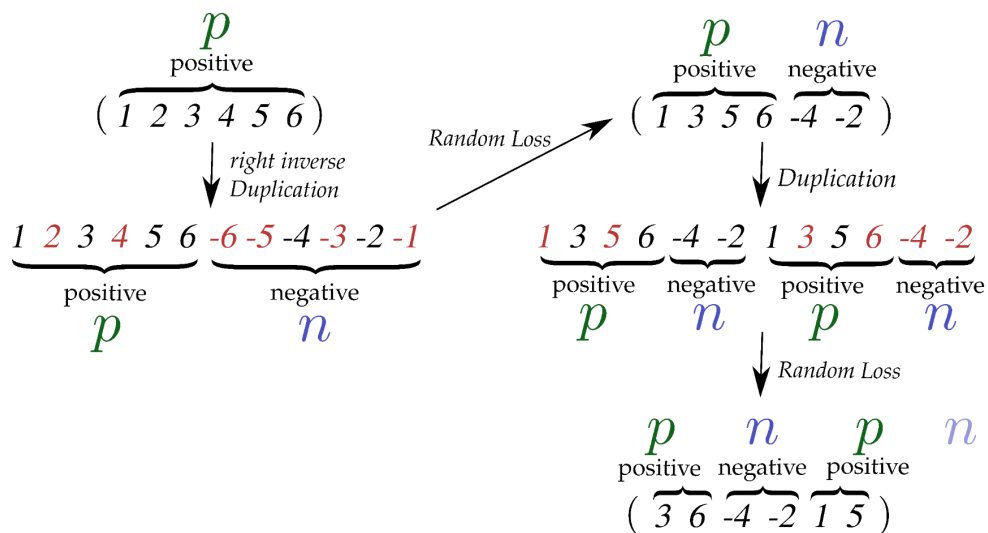
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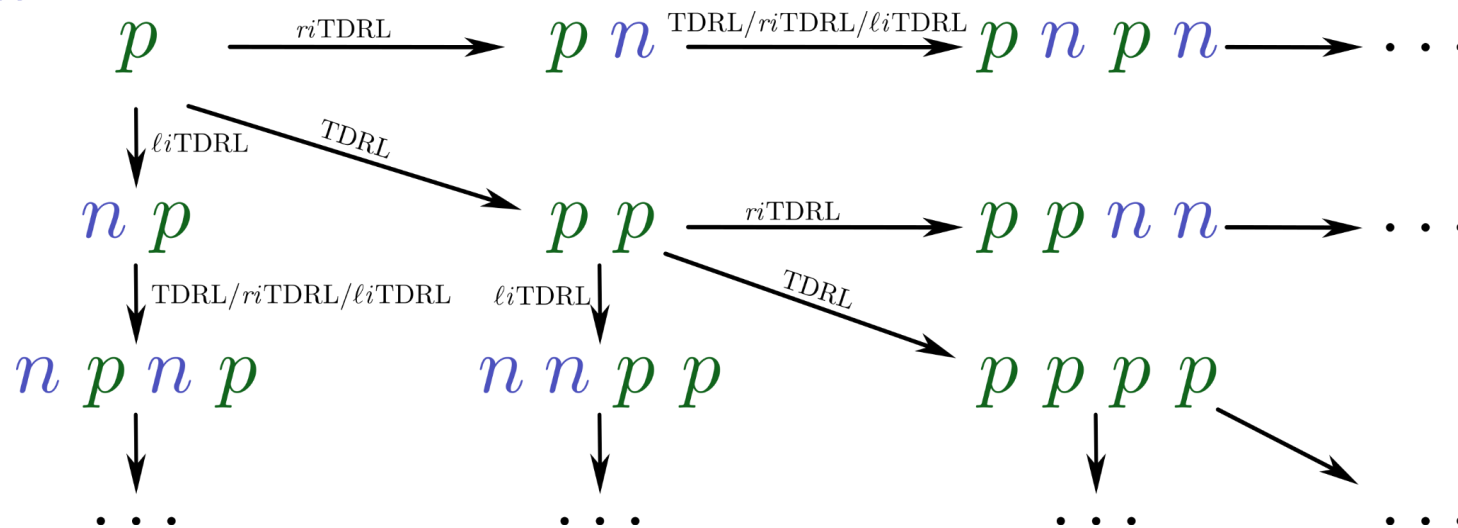
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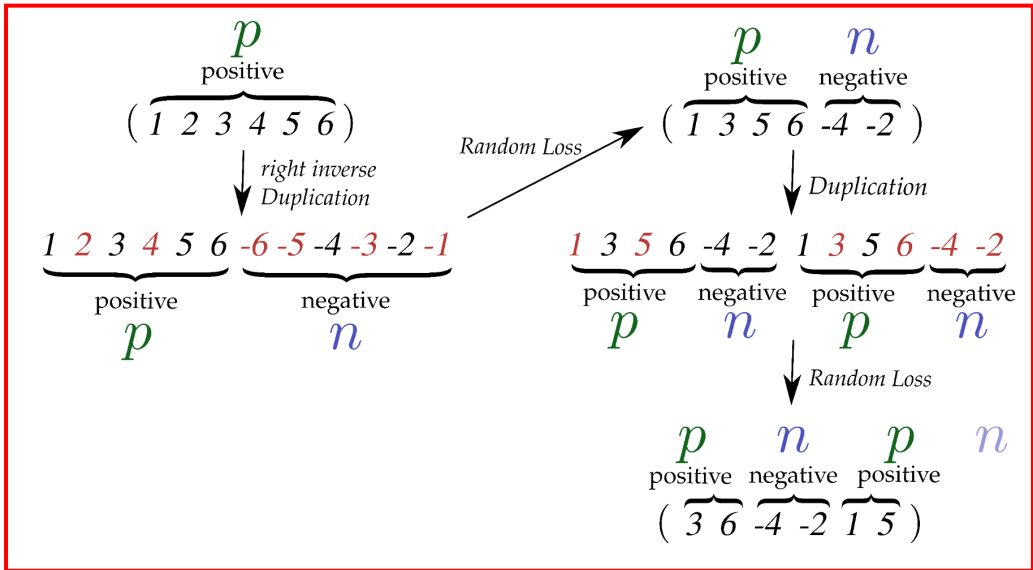


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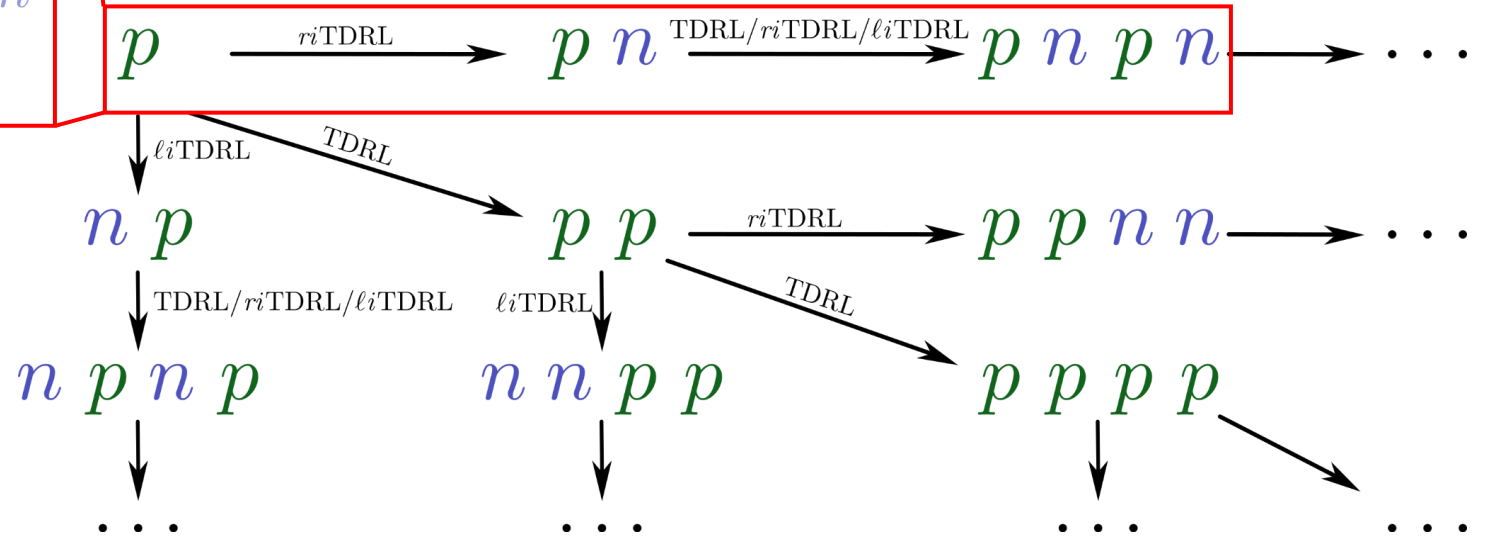




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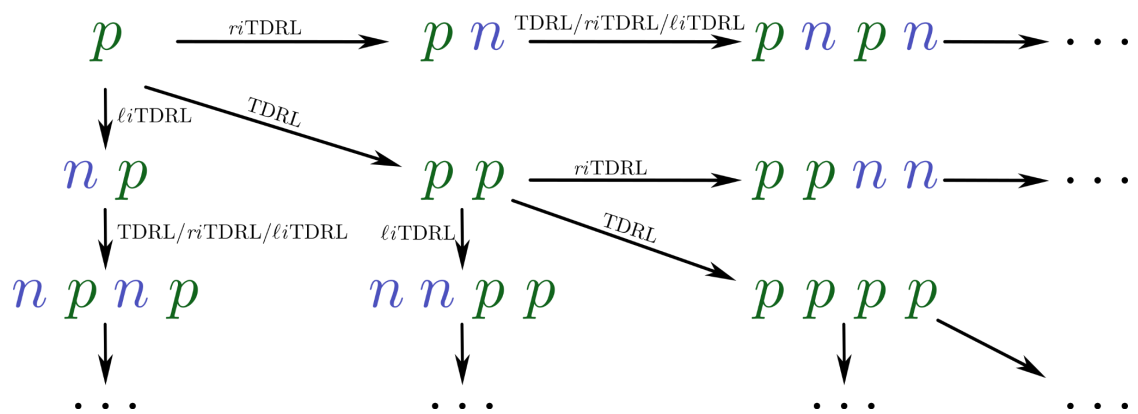
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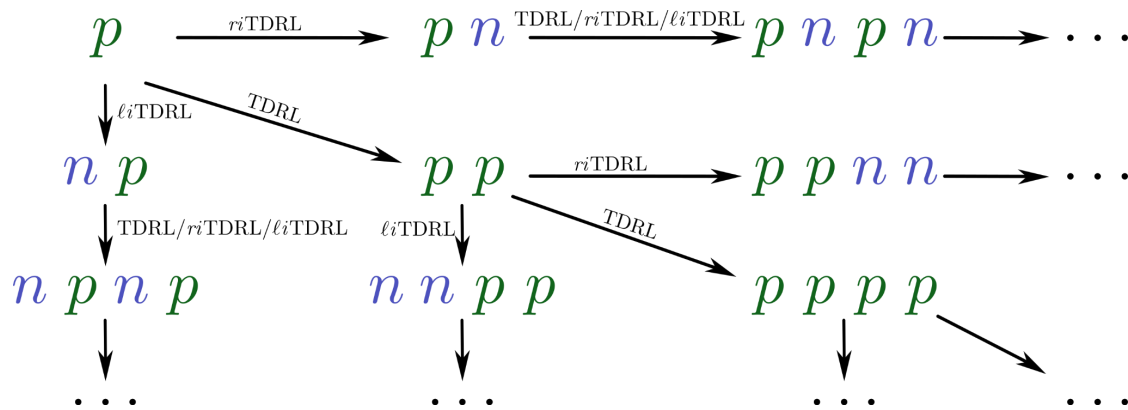




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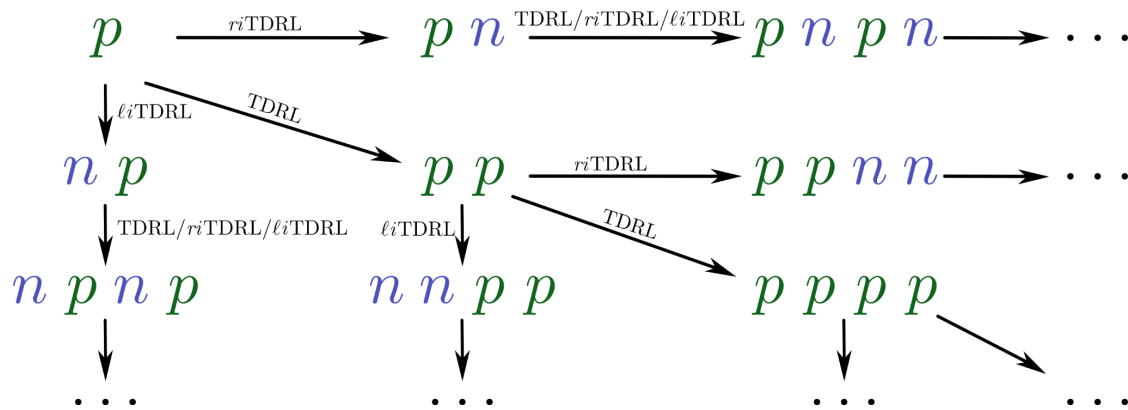




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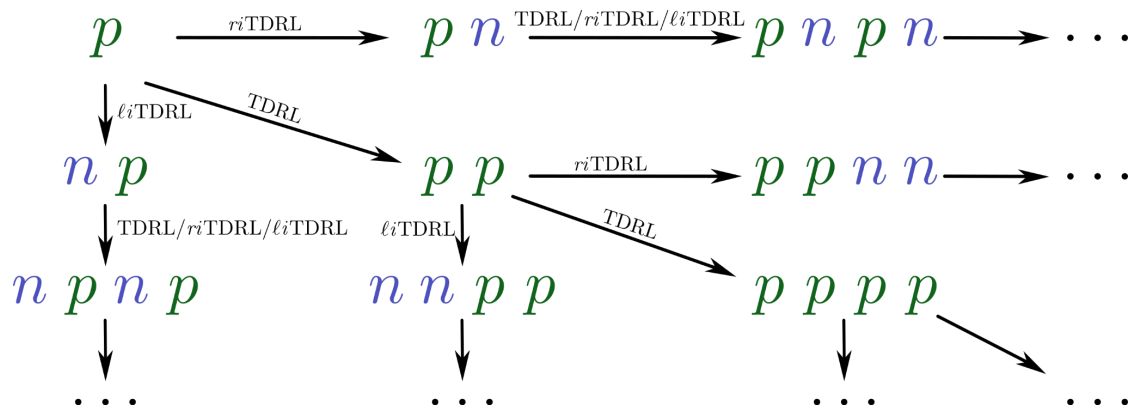




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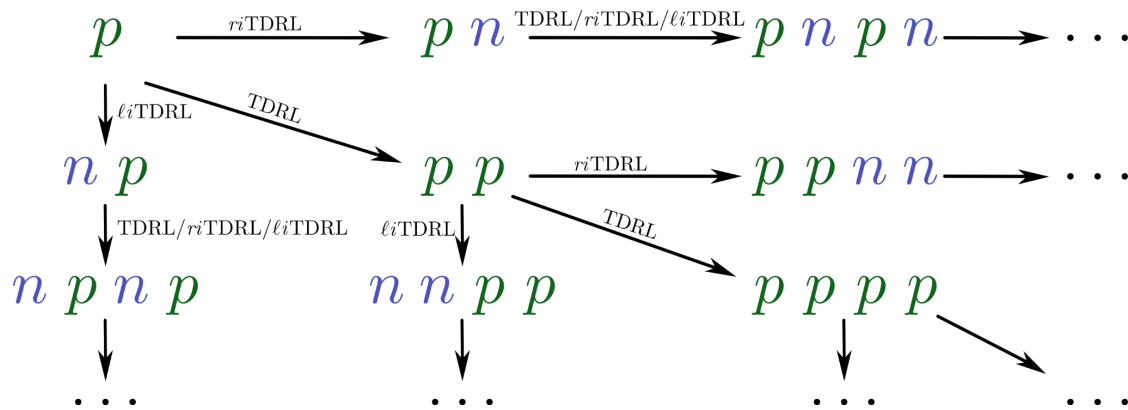




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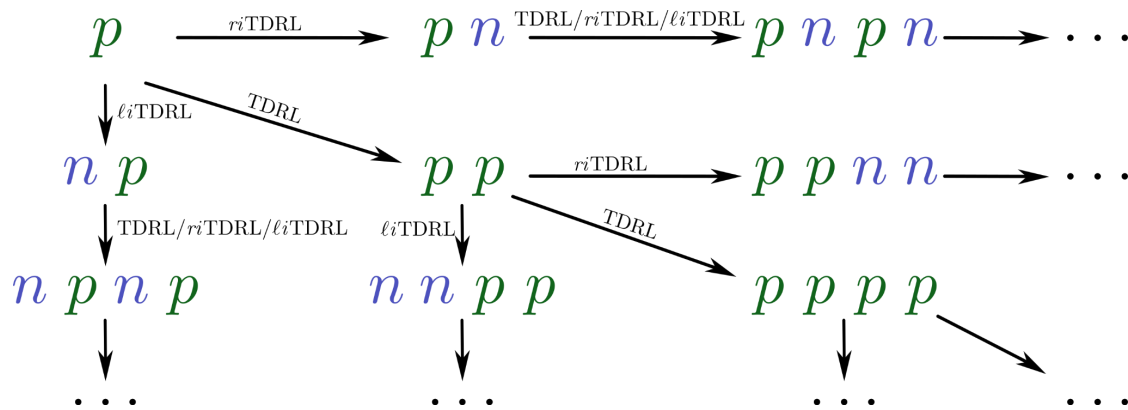




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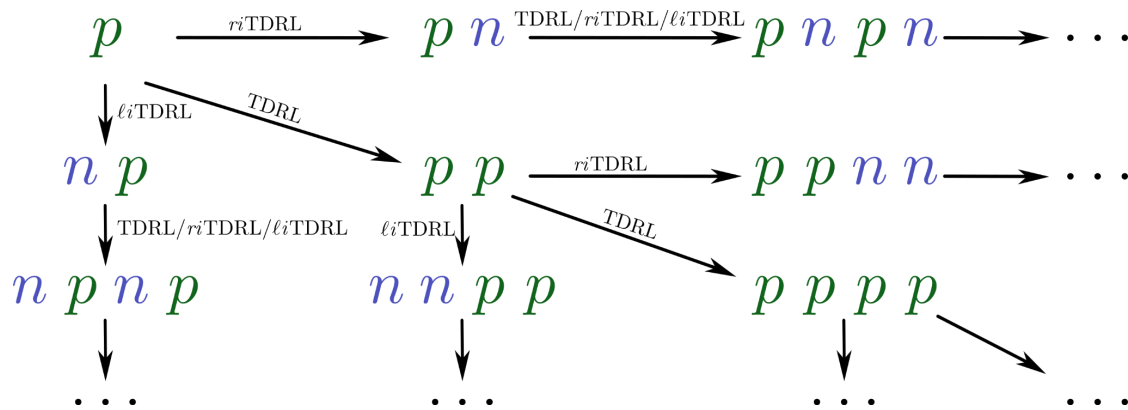


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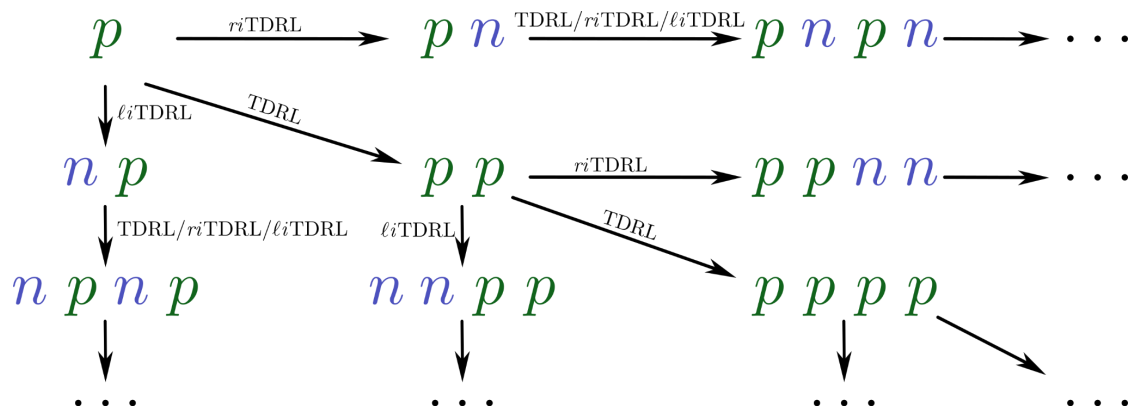
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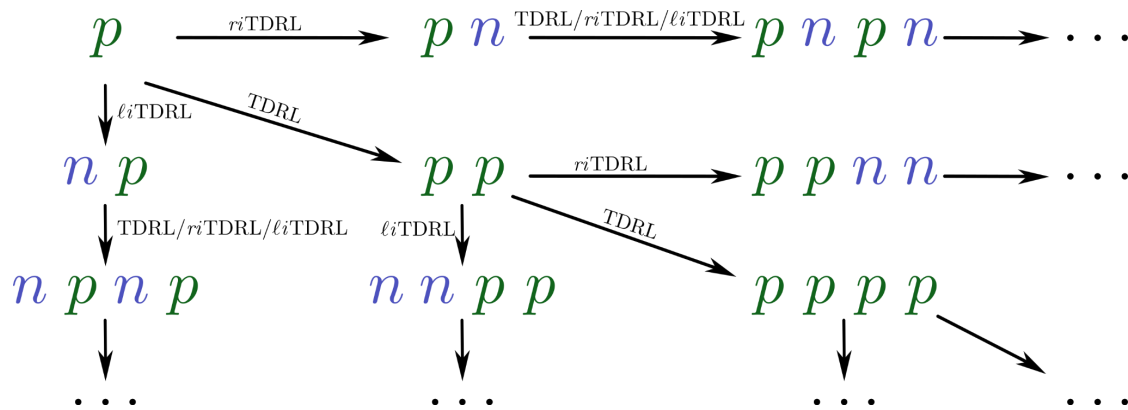
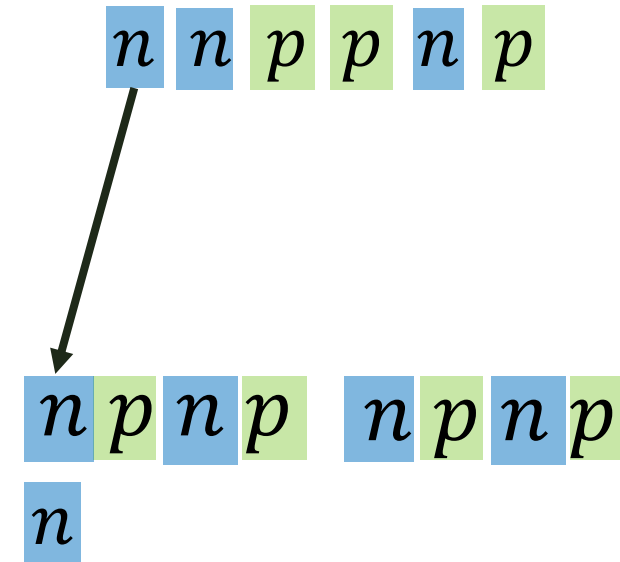




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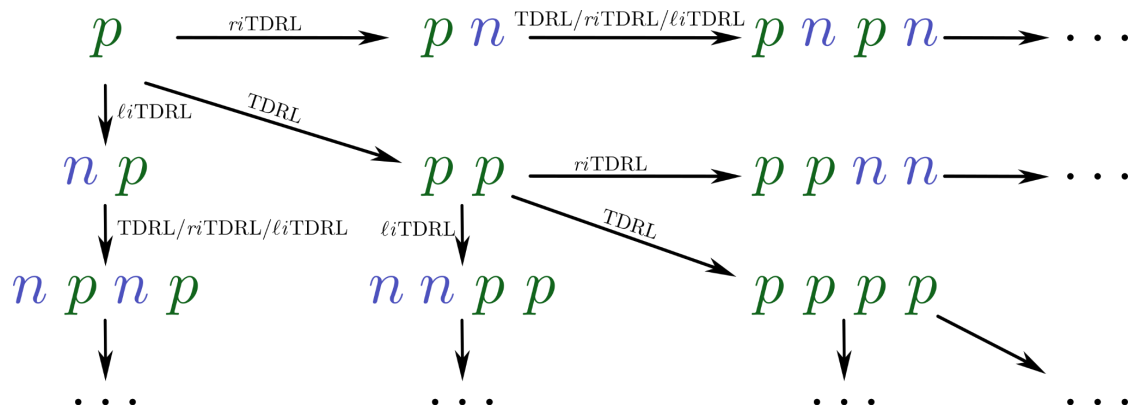
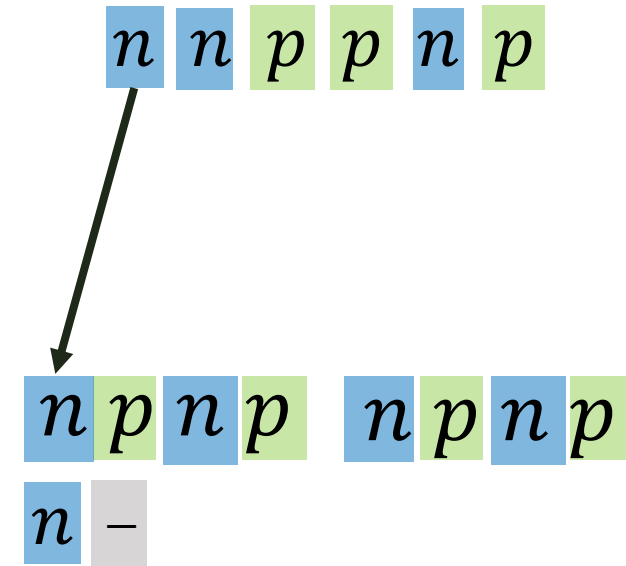




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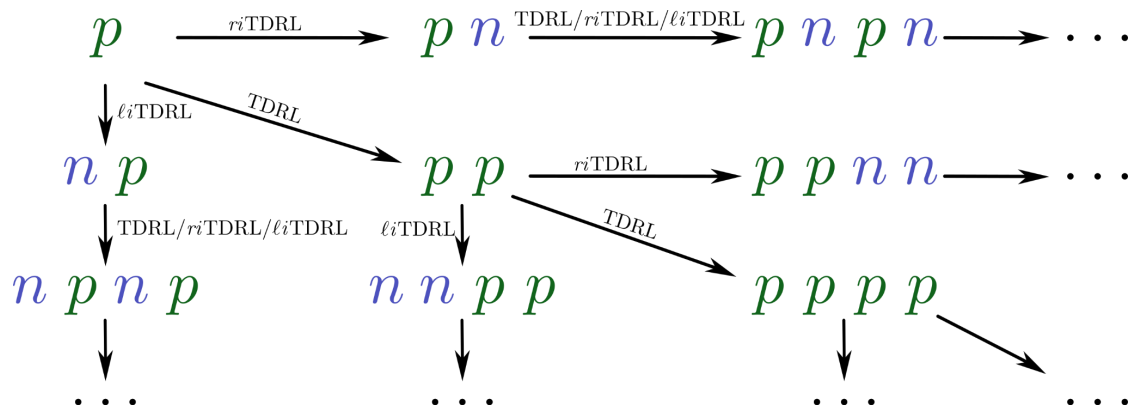
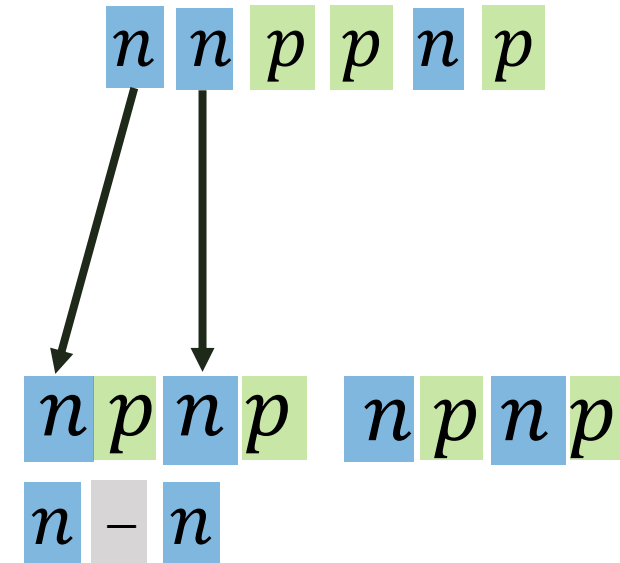




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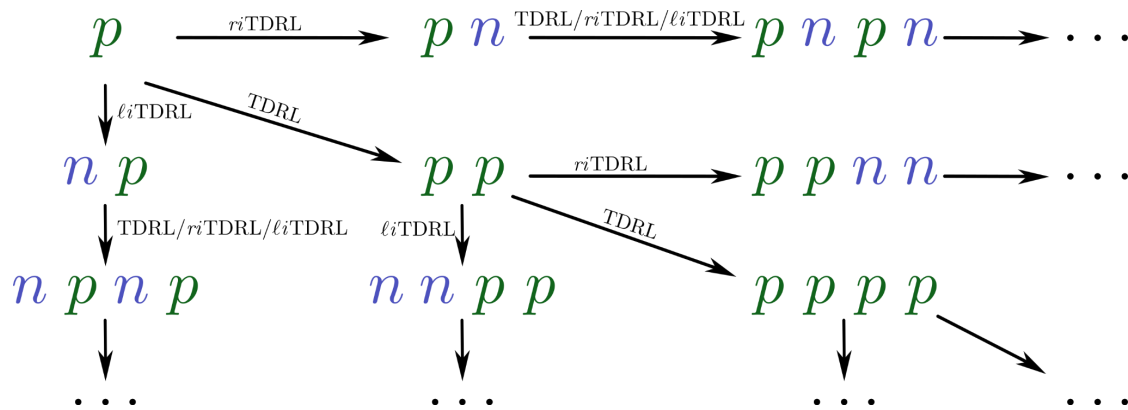
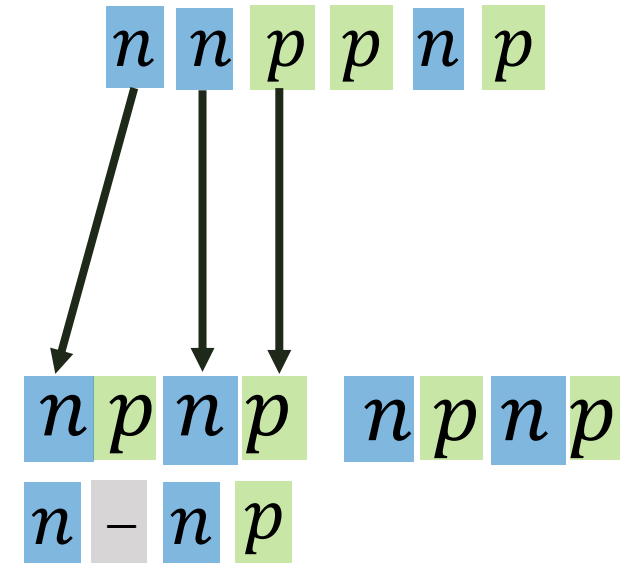




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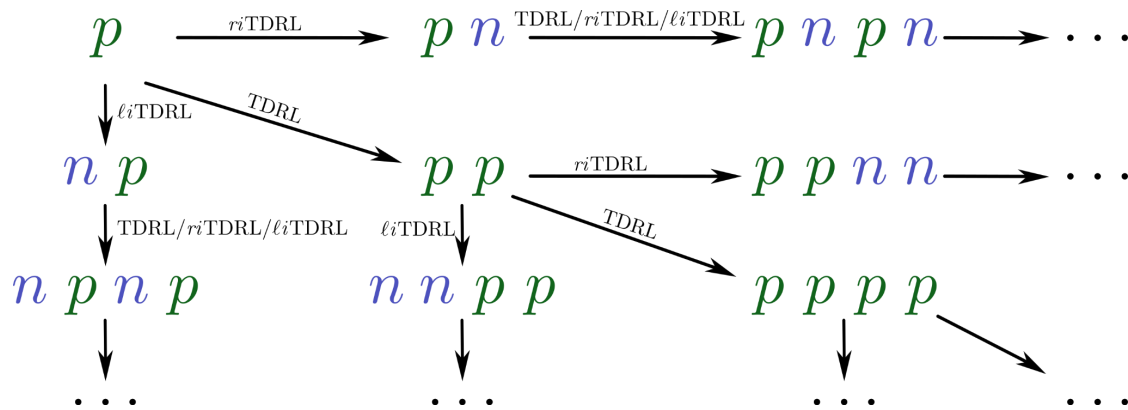
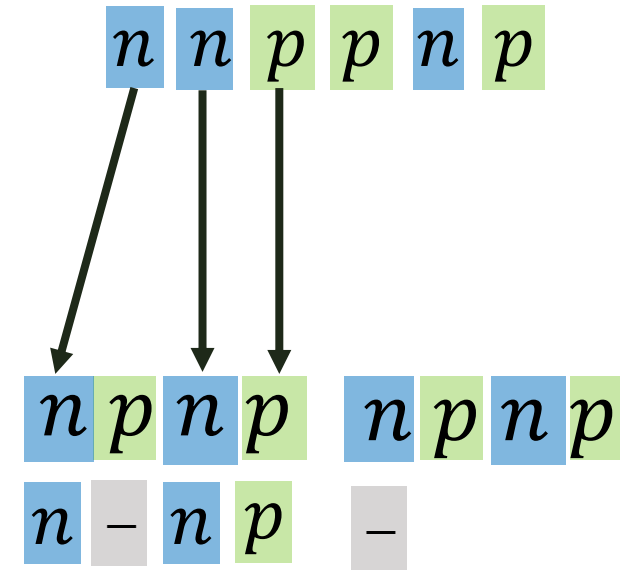




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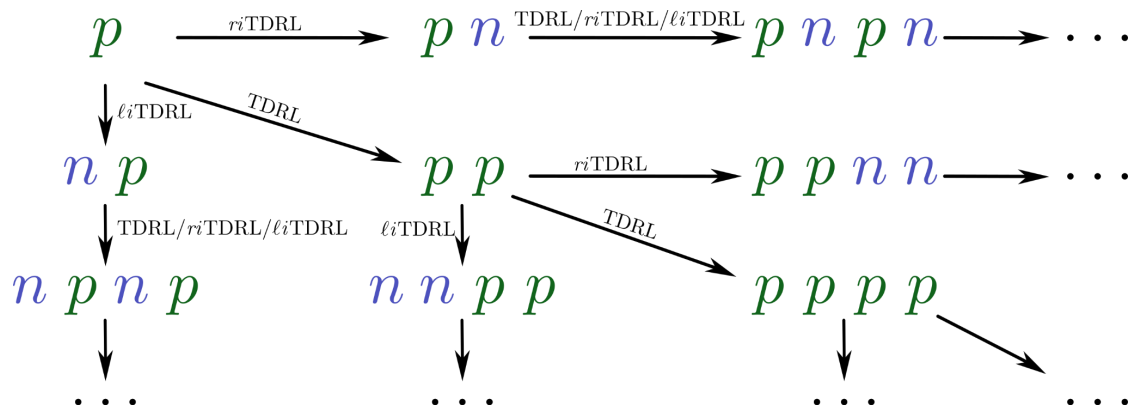
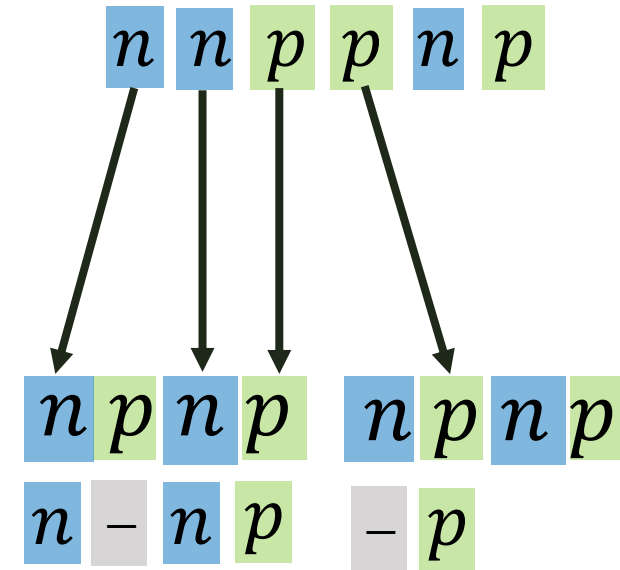




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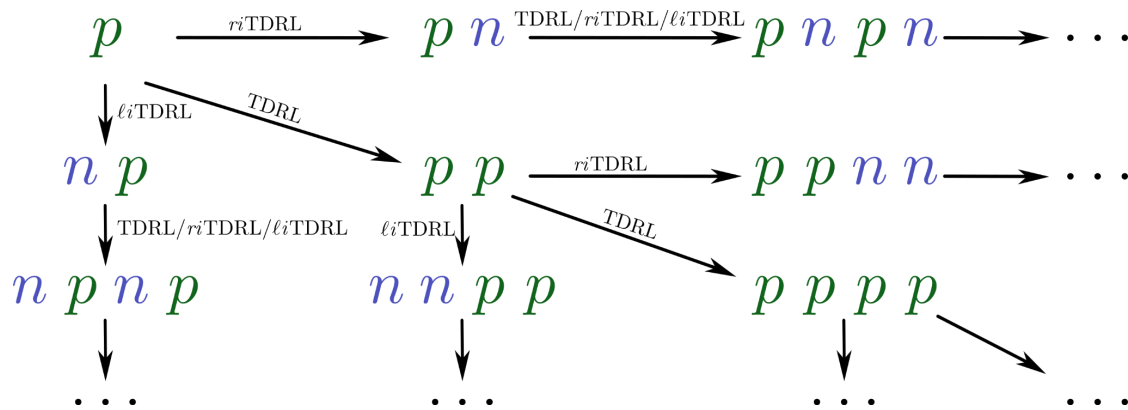
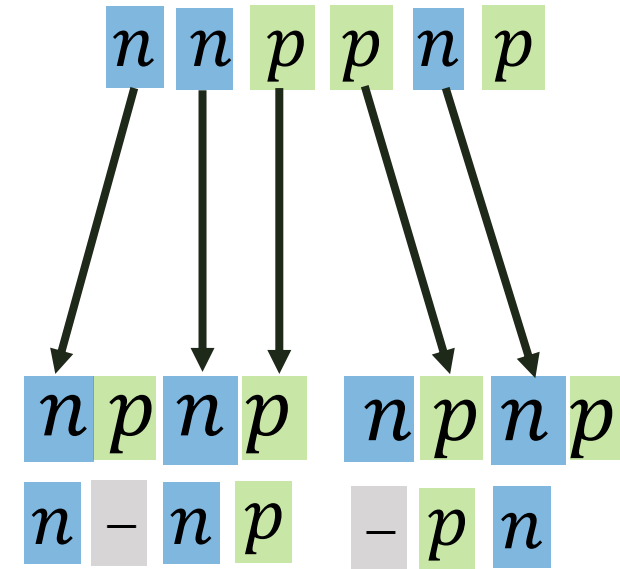




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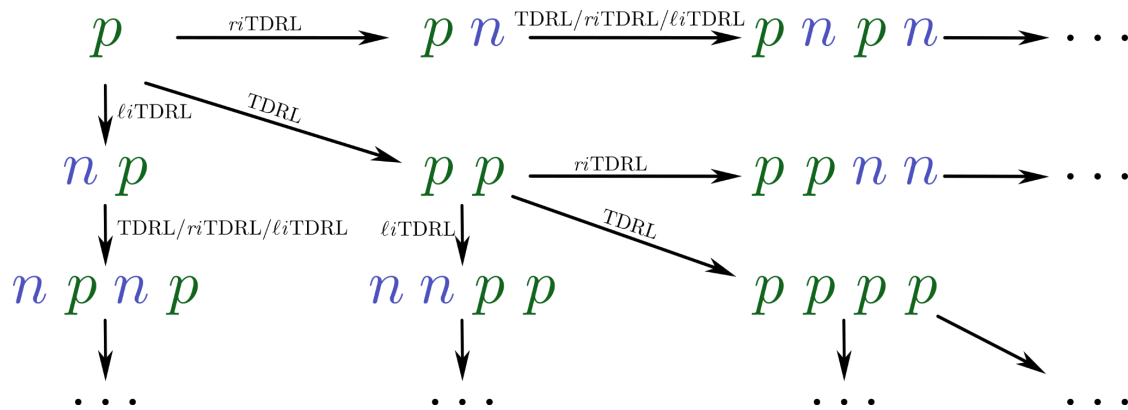
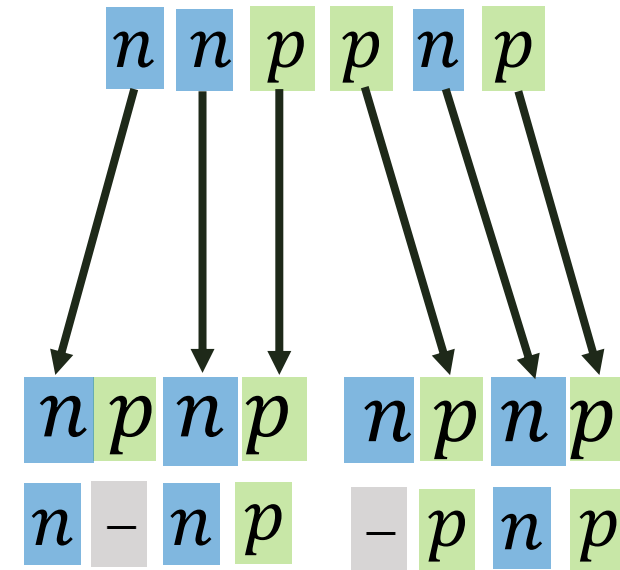




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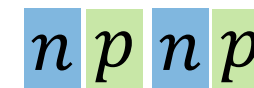
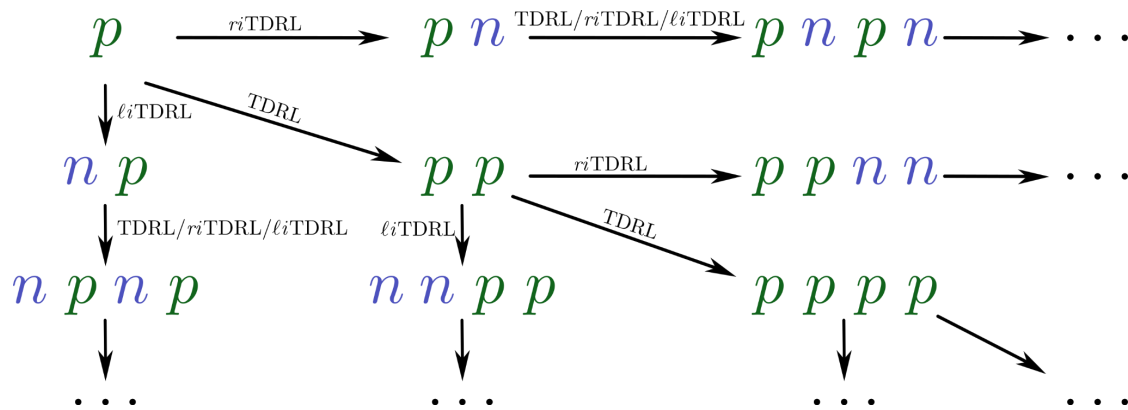
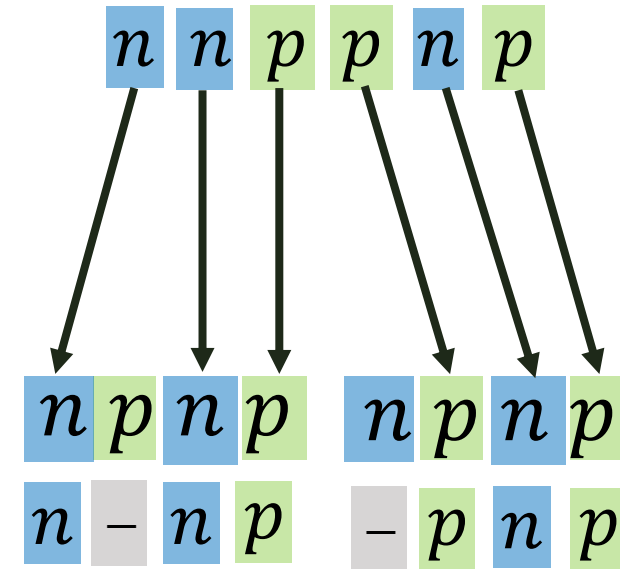




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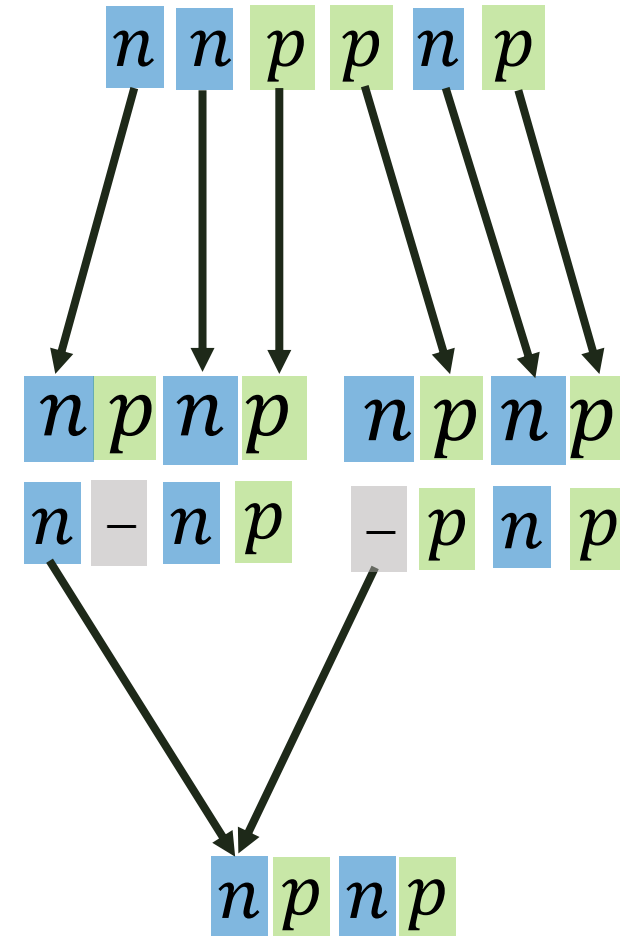
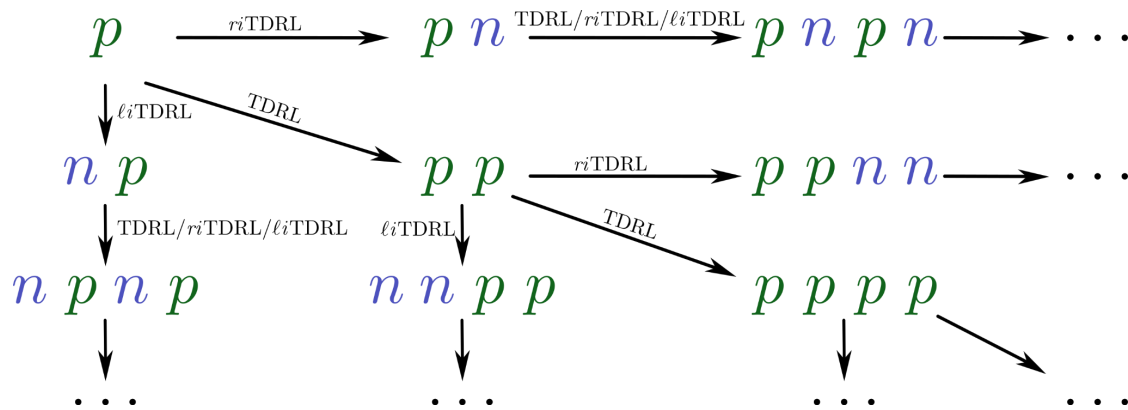




An Algorithm

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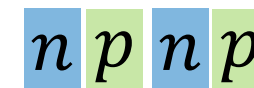
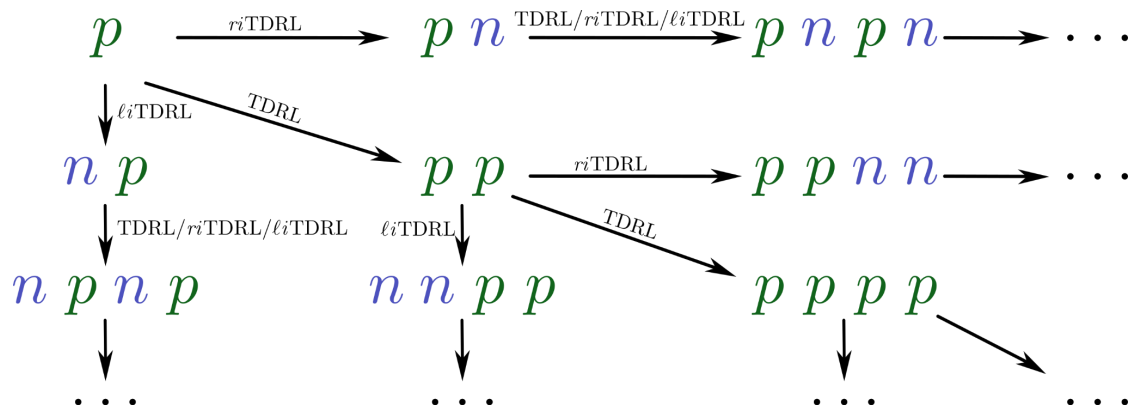
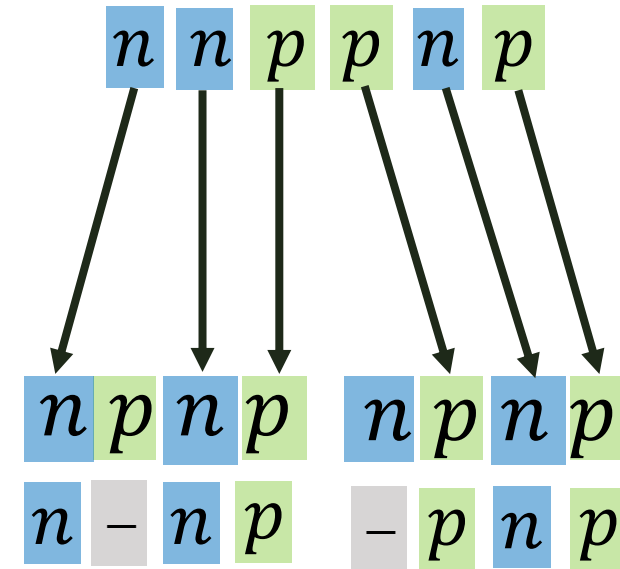




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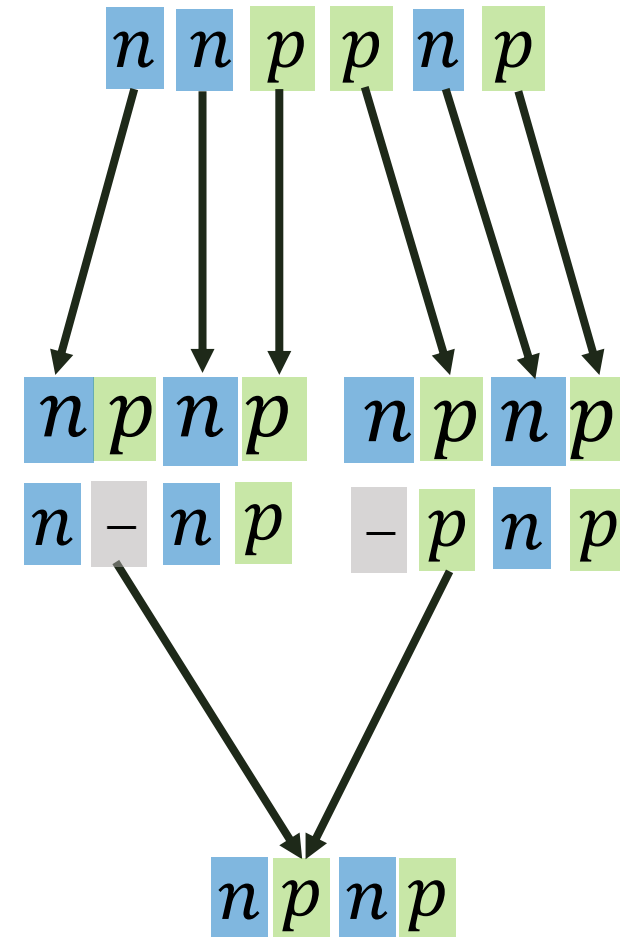
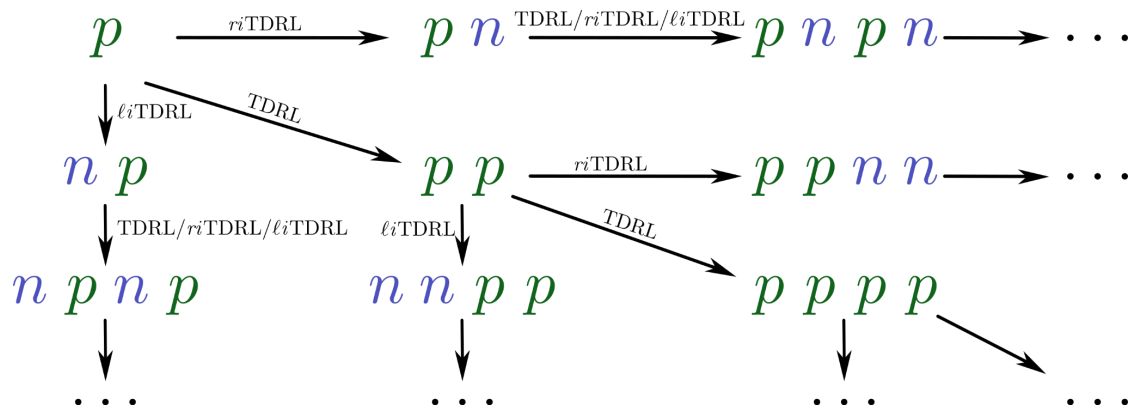




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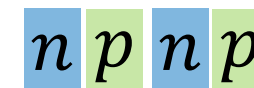
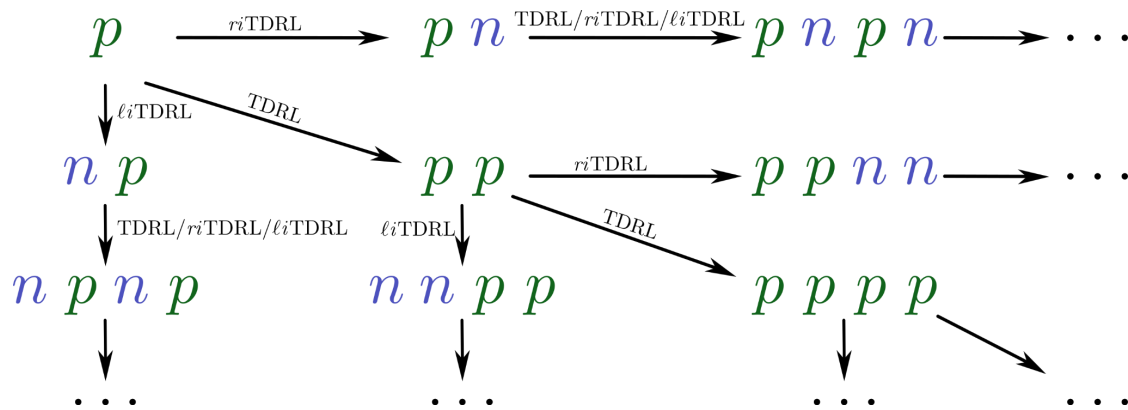
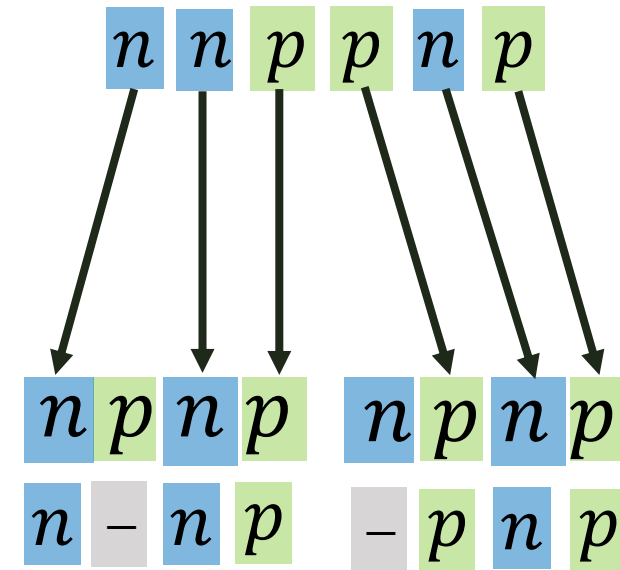




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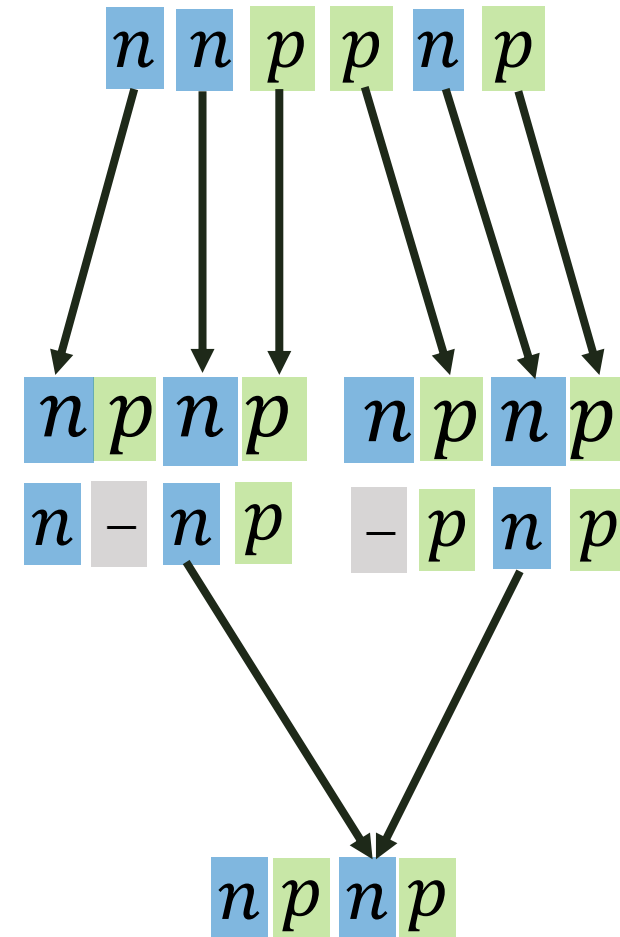
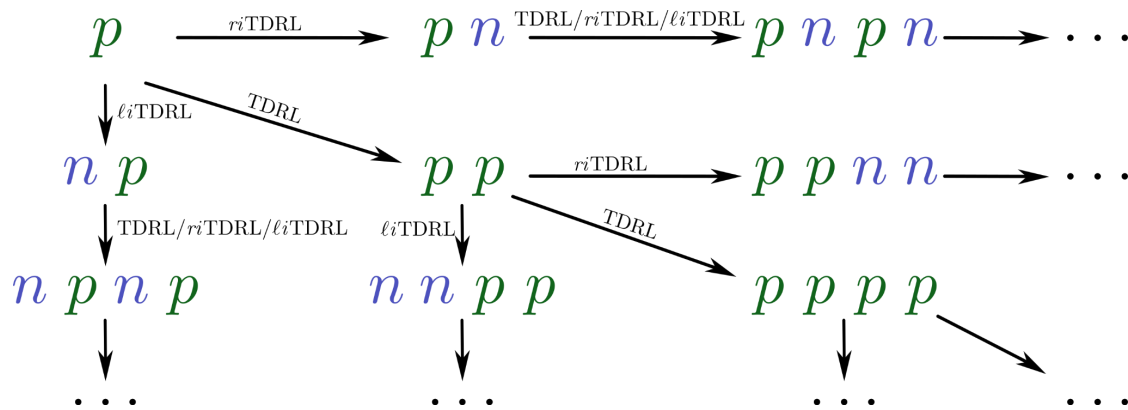




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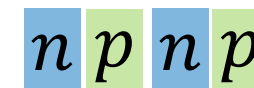
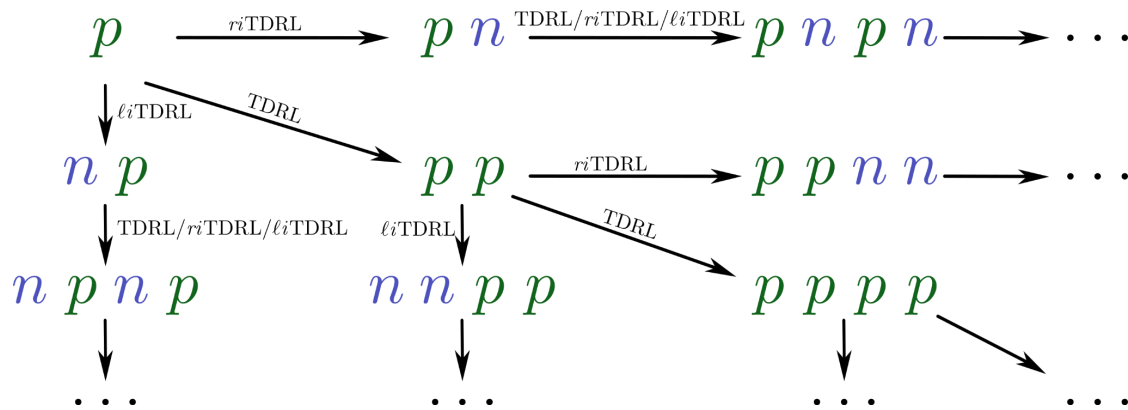
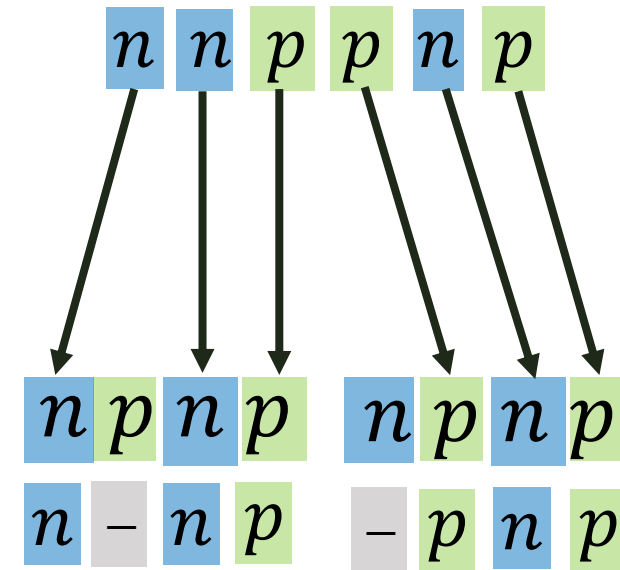




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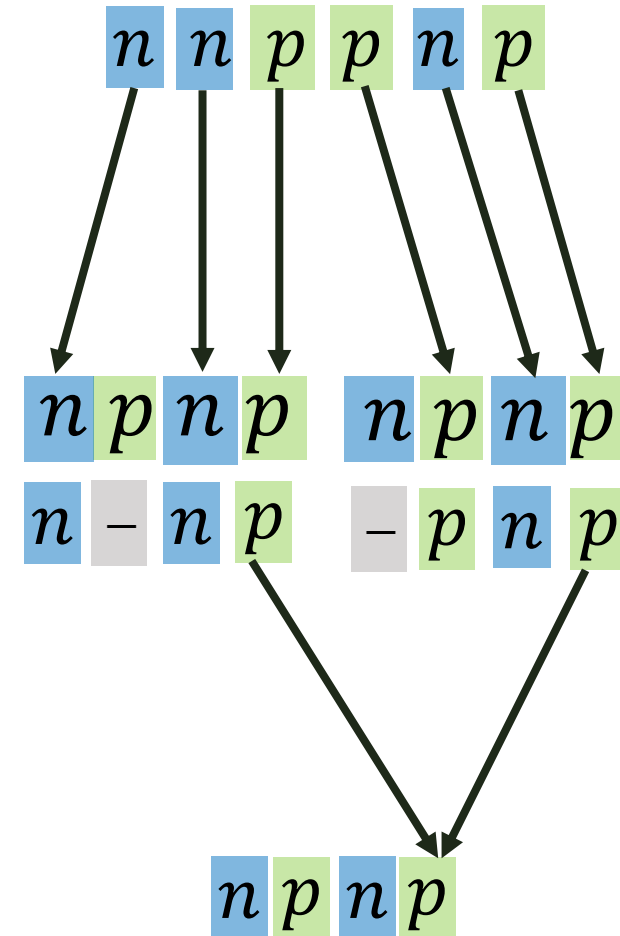
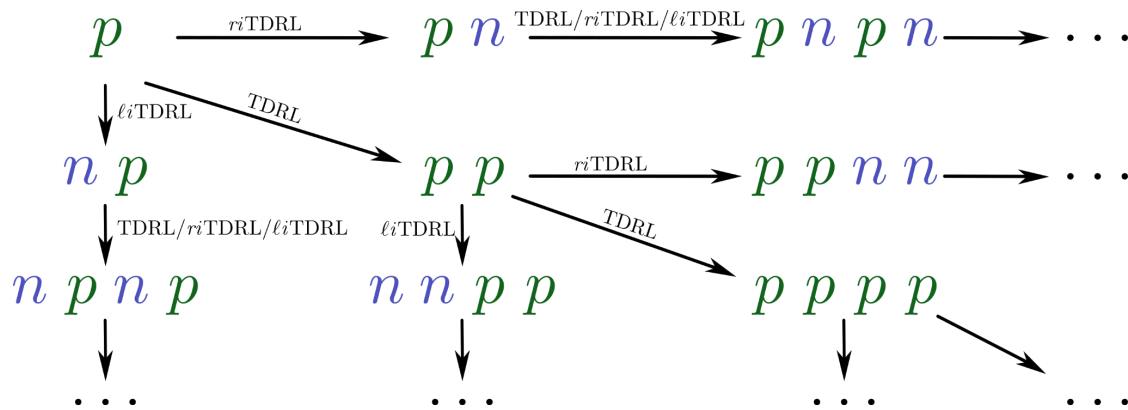




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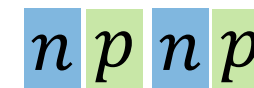
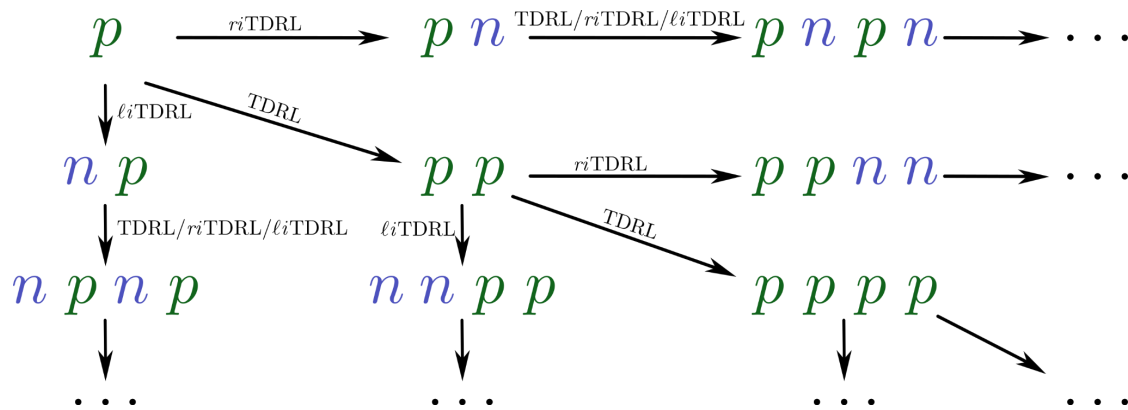
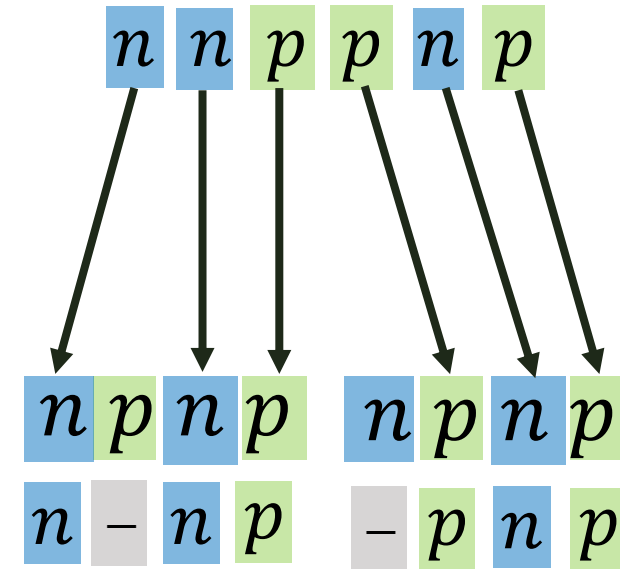




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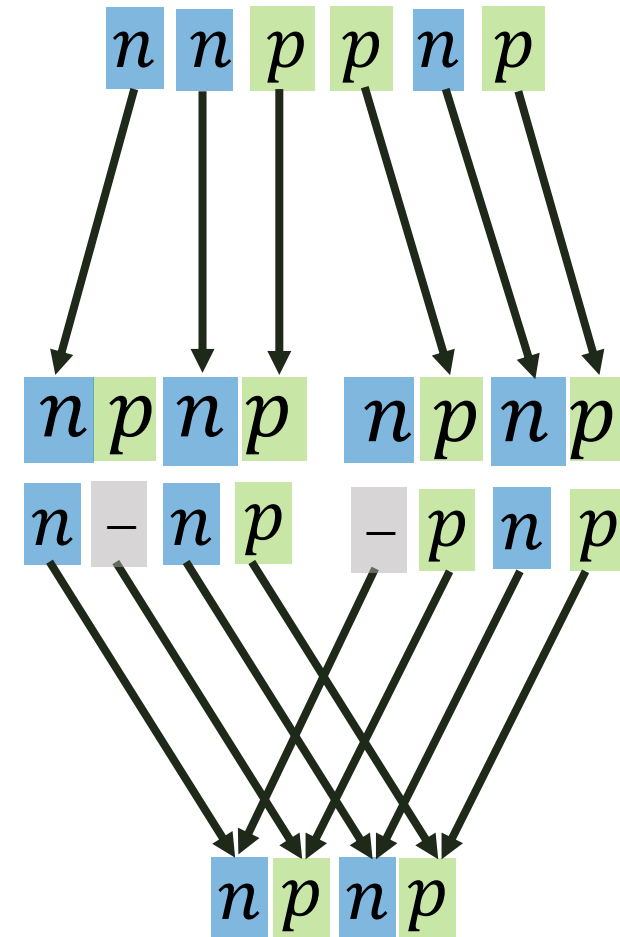
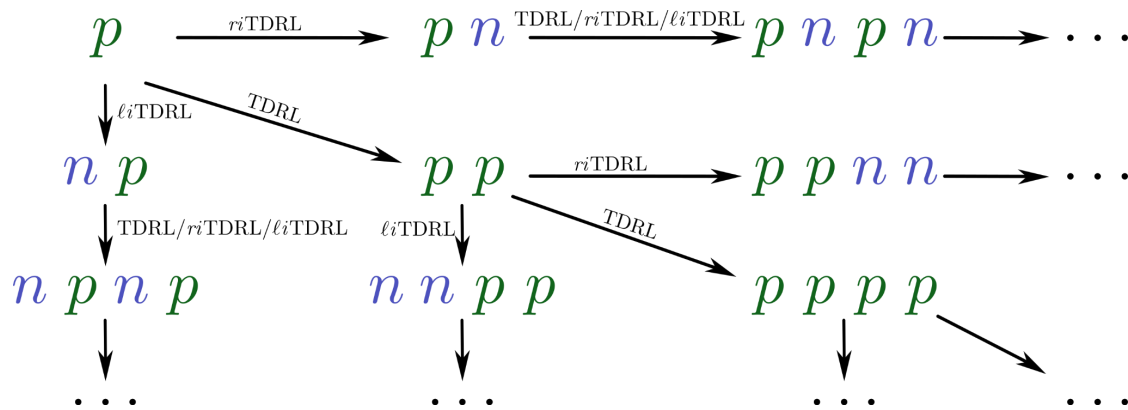




An Algorithm

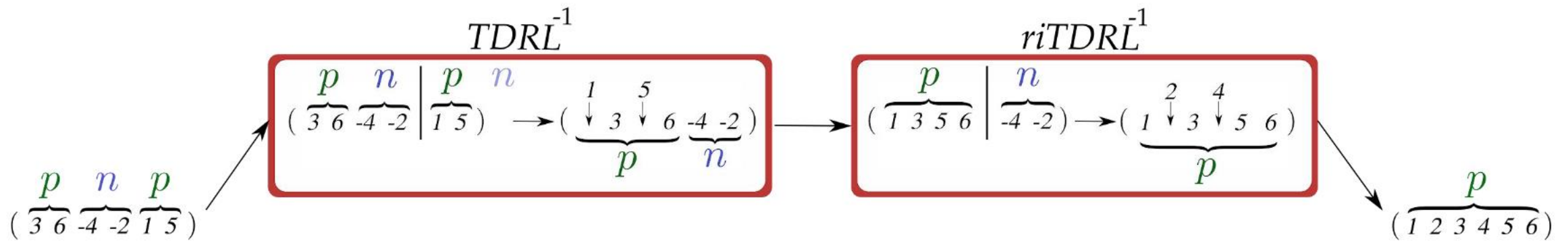
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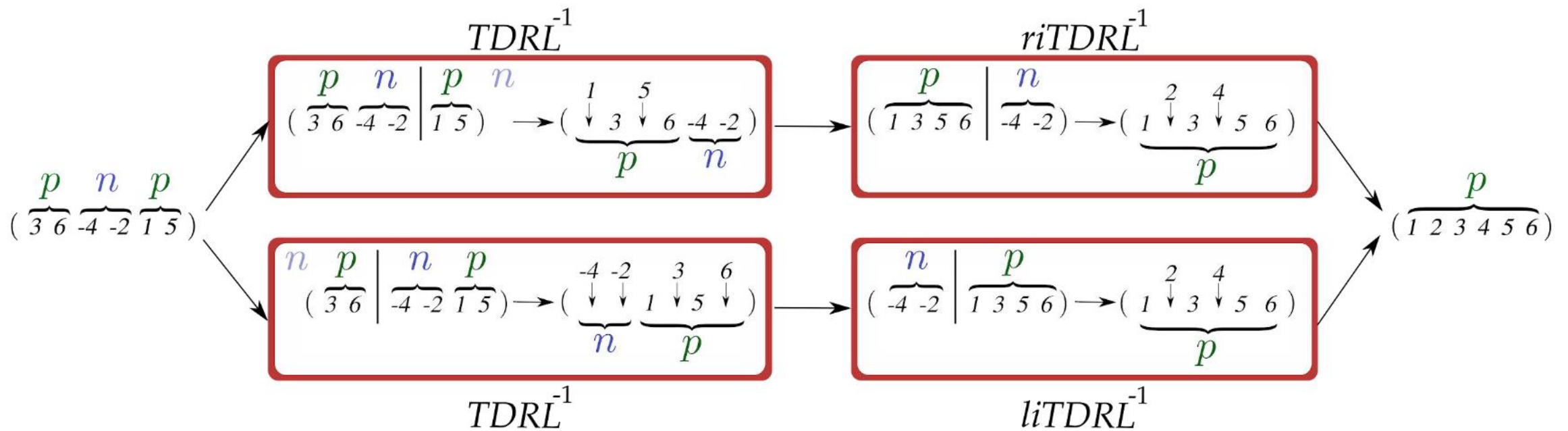


Sorting by TDRL and iTDRL



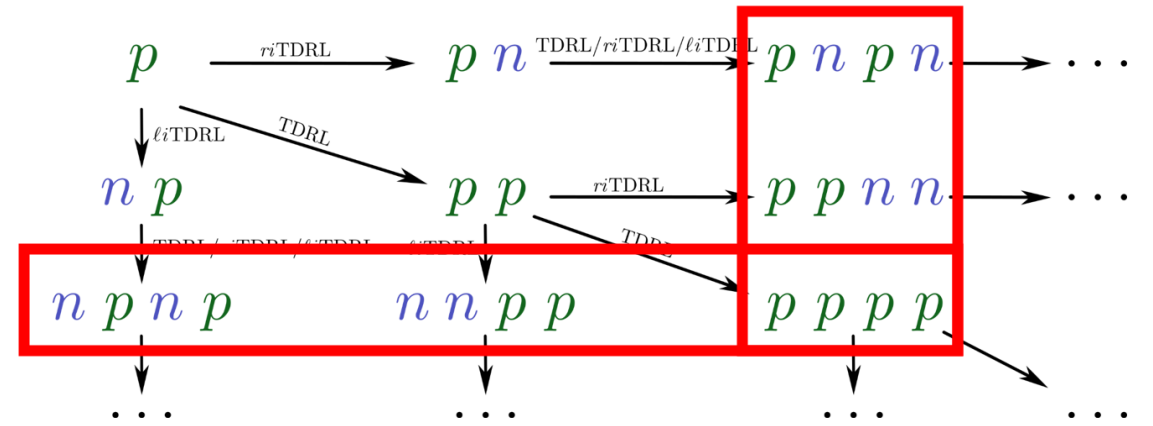


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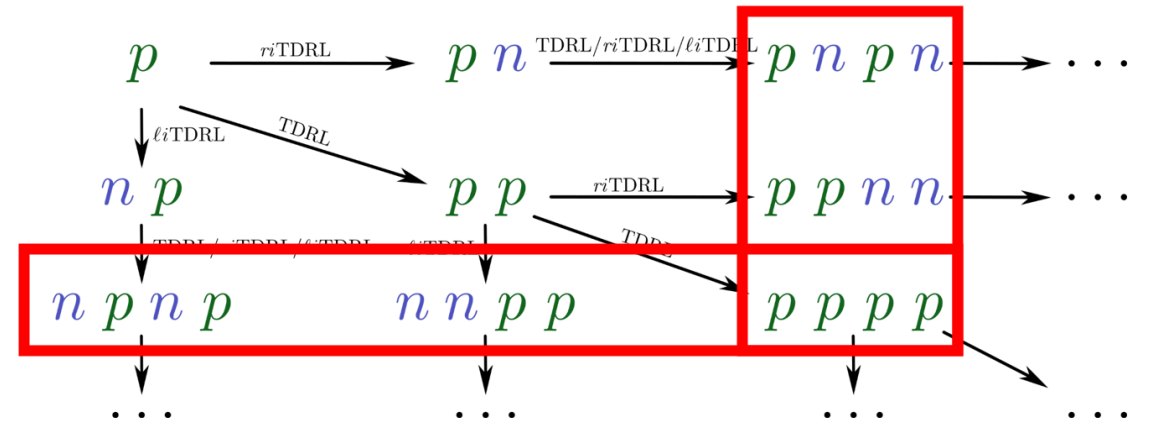
Complexity





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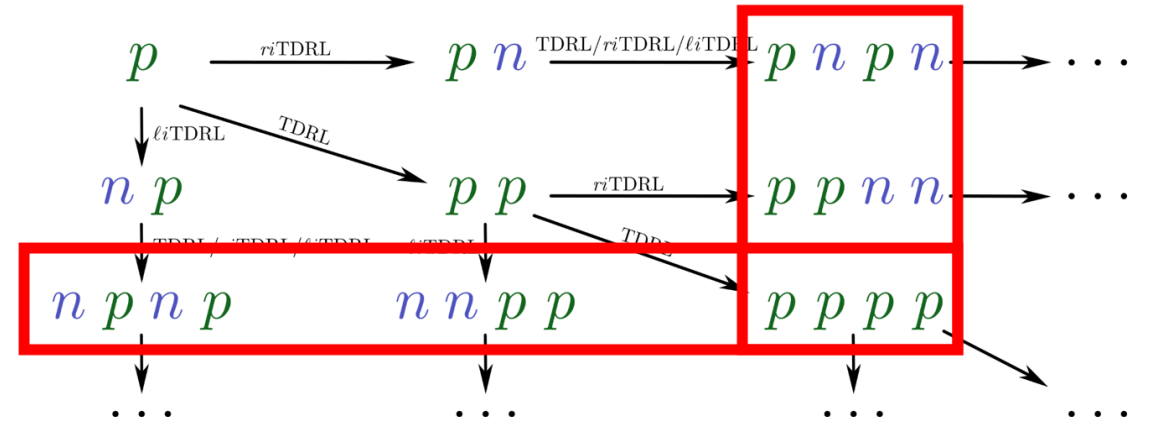
- Number of characters in MISC-encoding: $O(n)$





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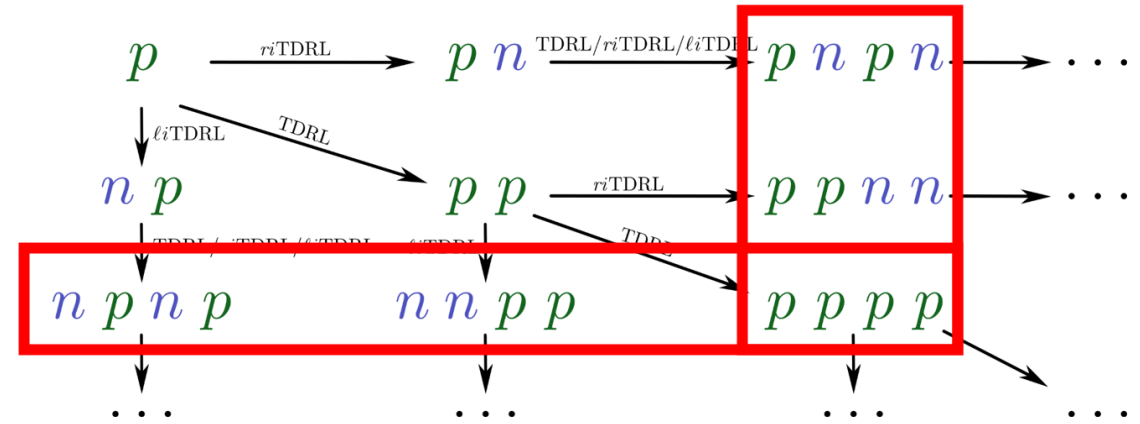
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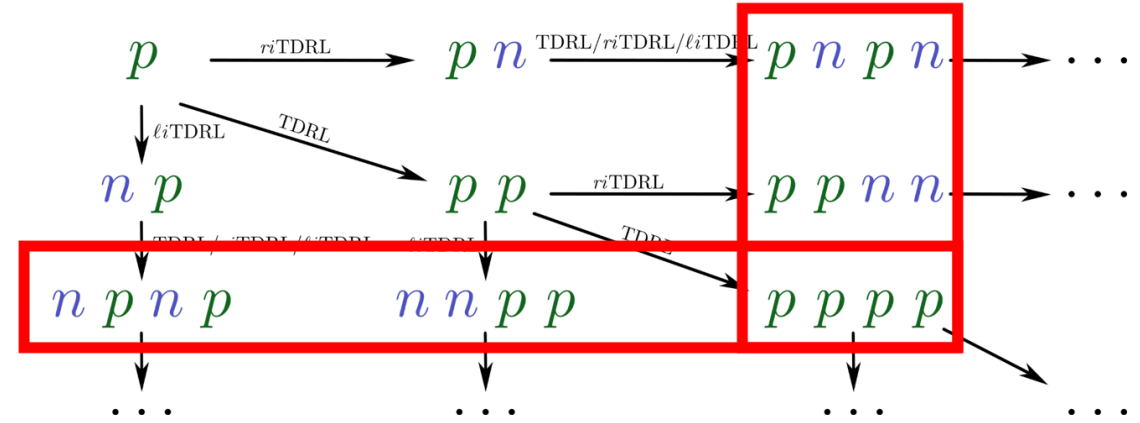
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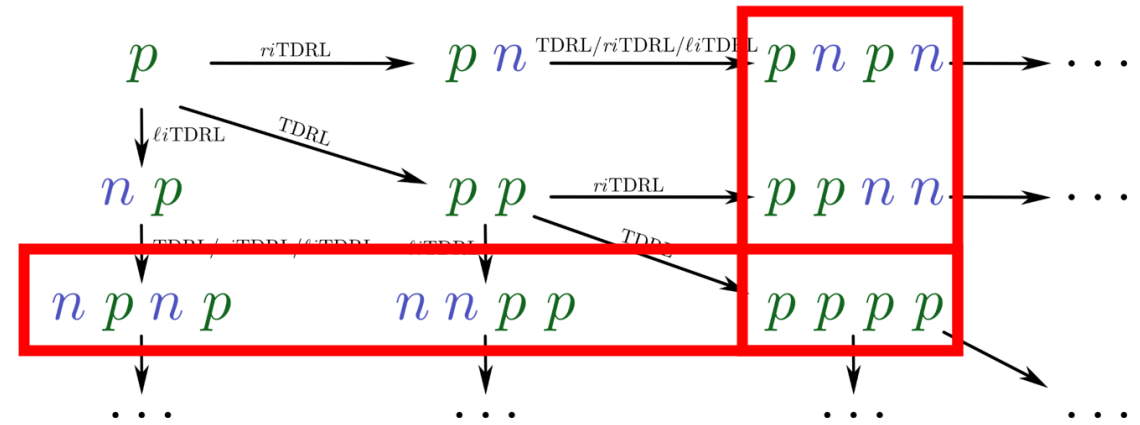
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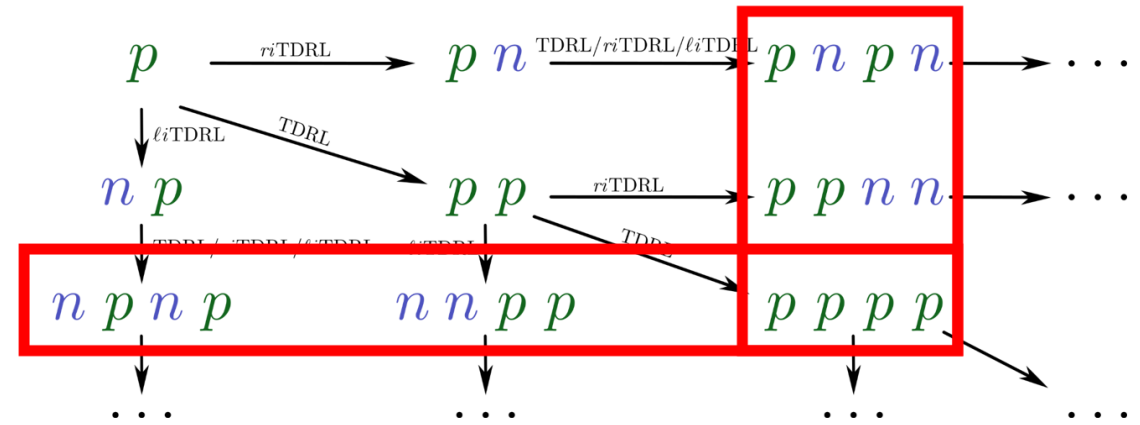
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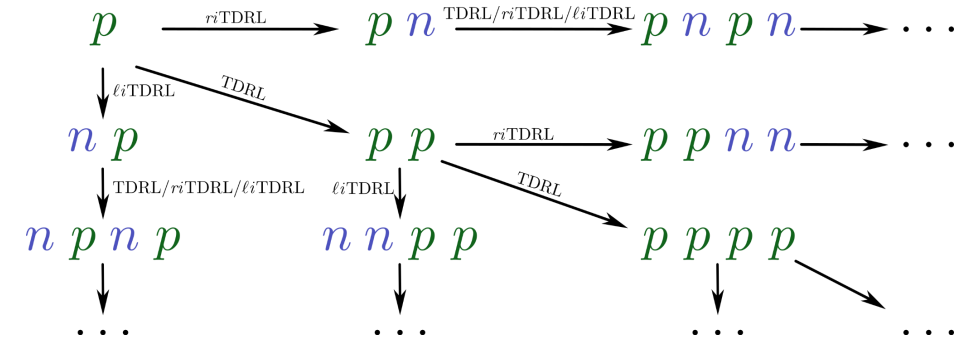
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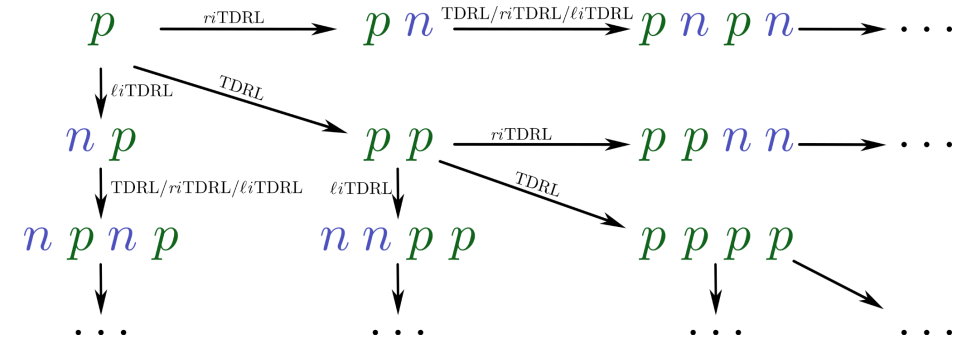
Conclusion





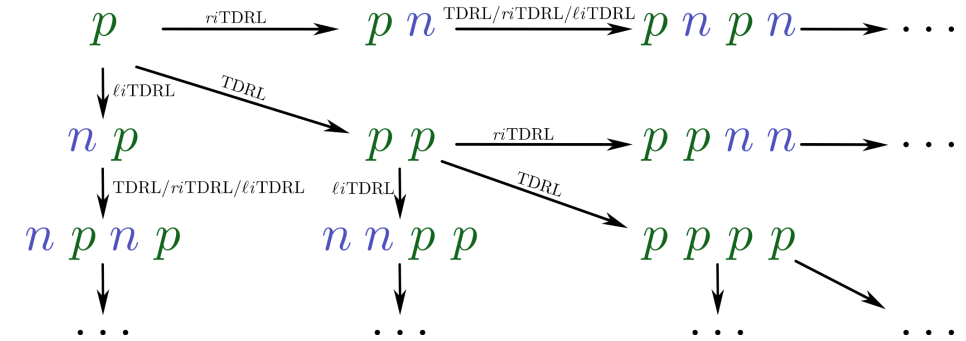
Conclusion

- TDRL/iTDRL distance between the identity, and any other permutation π is bounded by the number of characters in π 's MISC-encoding (logarithmic).
 → The sorting scenario can be computed in $\mathcal{O}(n \log n)$.





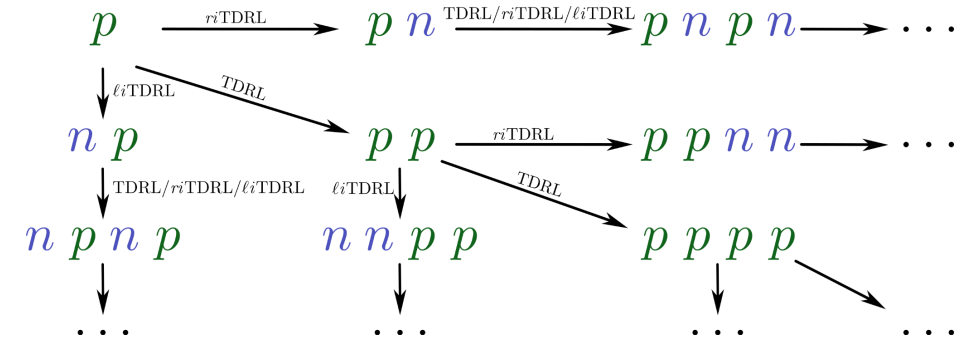
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- Powerful model as, for example for metazoan mitochondria, **at most 7 TDRLs/iTDRLs** are necessary to rearrange any of their gene orders into another.
- Biological constraints need to be considered
 → Keep common gene clusters at each sorting step
 → restrict number of genes on which a TDRL/iTDRL can act on