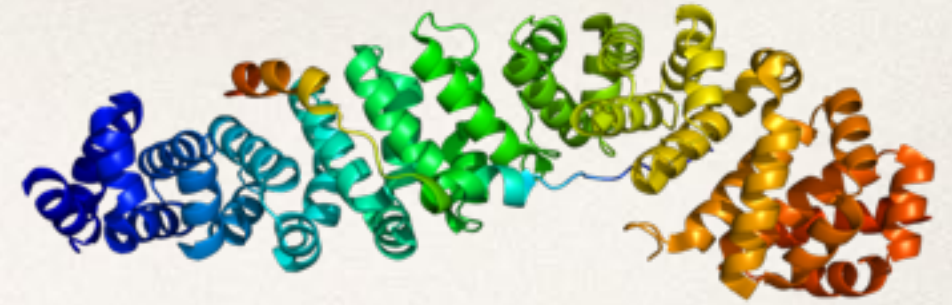


Alternative Splicing in the TCF/LEF Family of Transcription Factors

Elizabeth Lagesse - Professor Scott Roy

San Francisco State University - NSF REU Program

The TCF/LEF Family



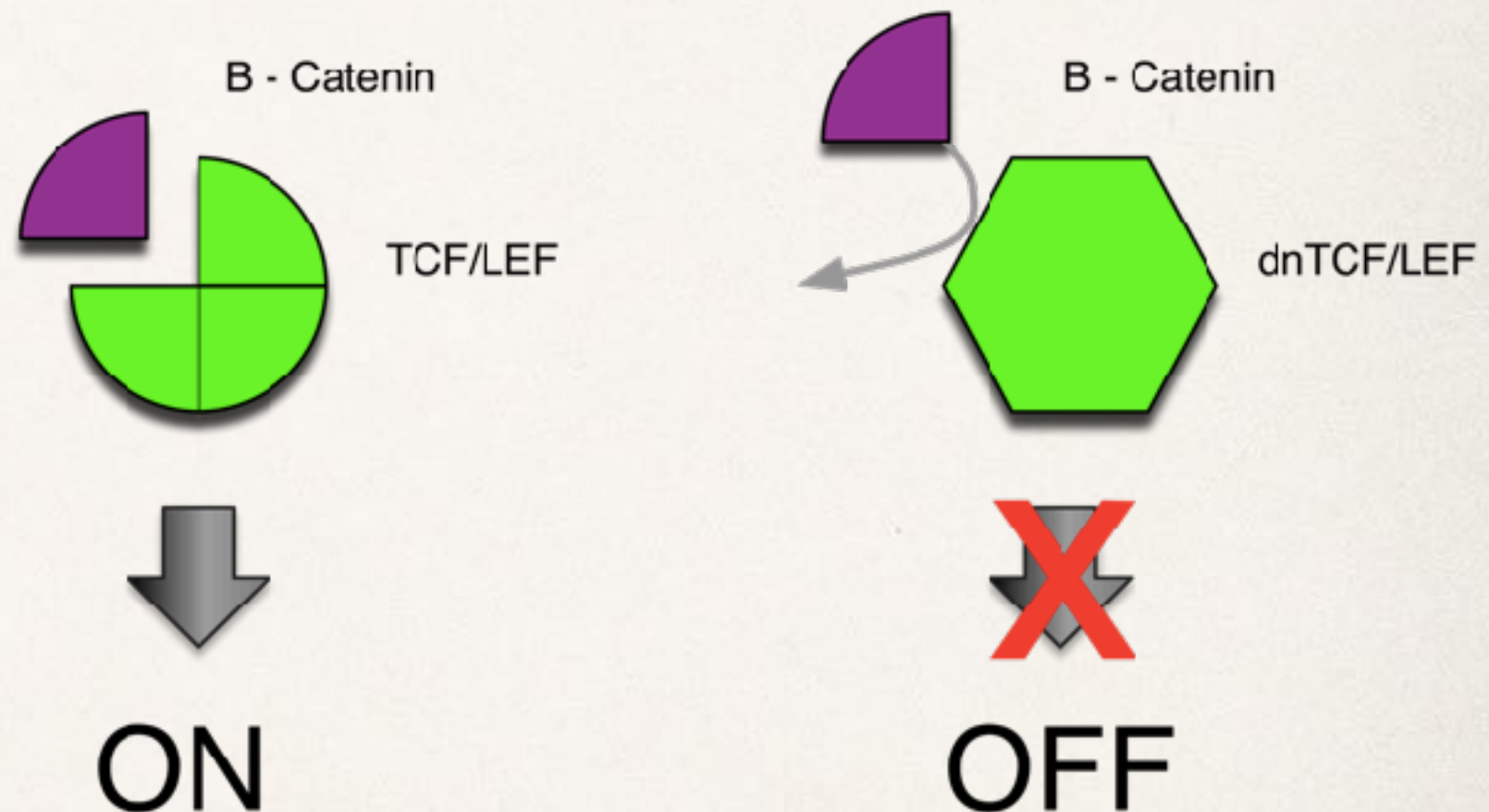
- Transcription factors
- Part of Wnt pathway
- 4 family members - TCF7, TCF7-11, TCF7-12, LEF1
- Transcripts expressed differently in different tissues / developmental stages



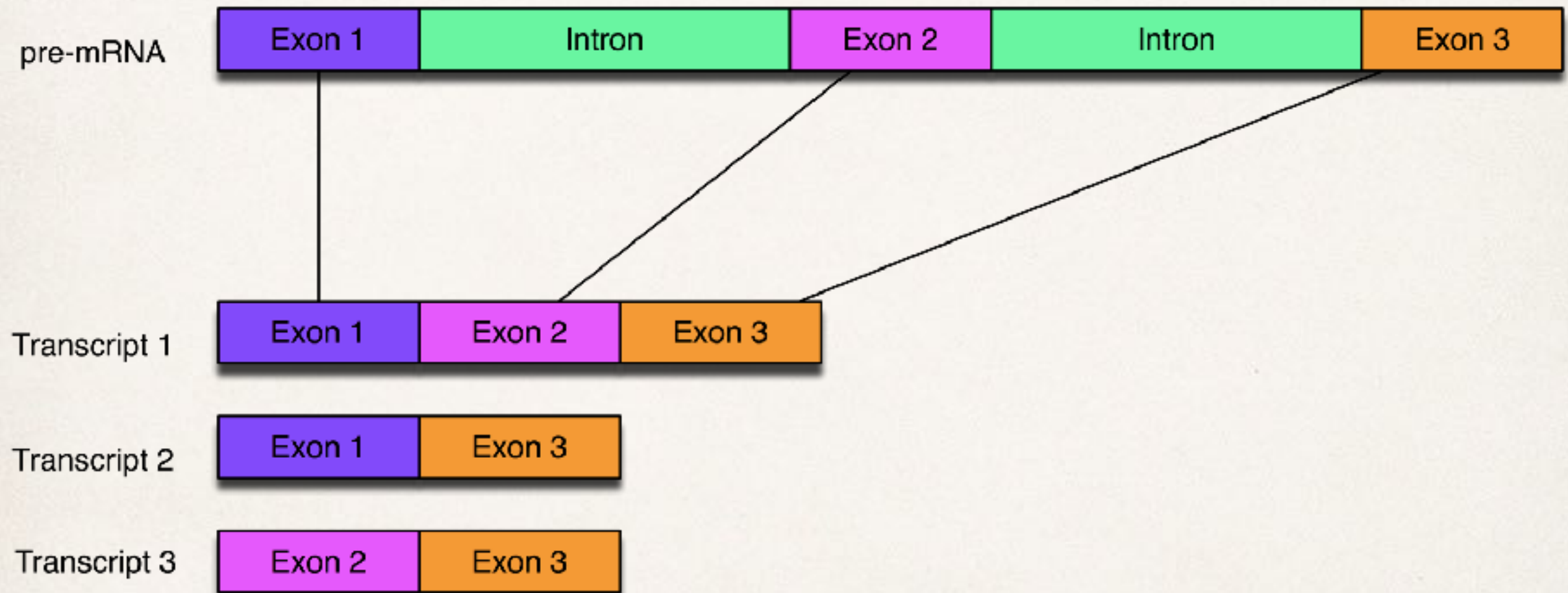
General TCF/LEF Structure

Dominant Negative Isoforms

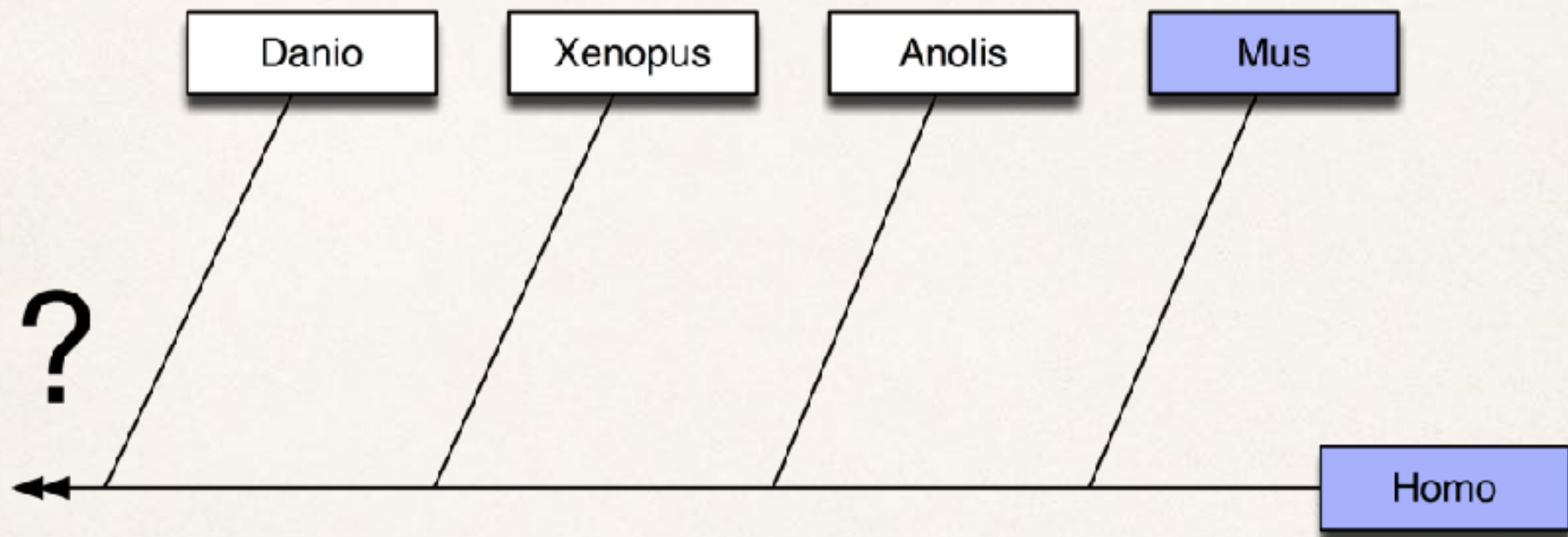
- Without a B-catenin binding site, the pathway remains off
- This serves as a regulatory mechanism
- Proteins lacking a binding site are created through alternative splicing



Introns, Exons, and Alternative Splicing



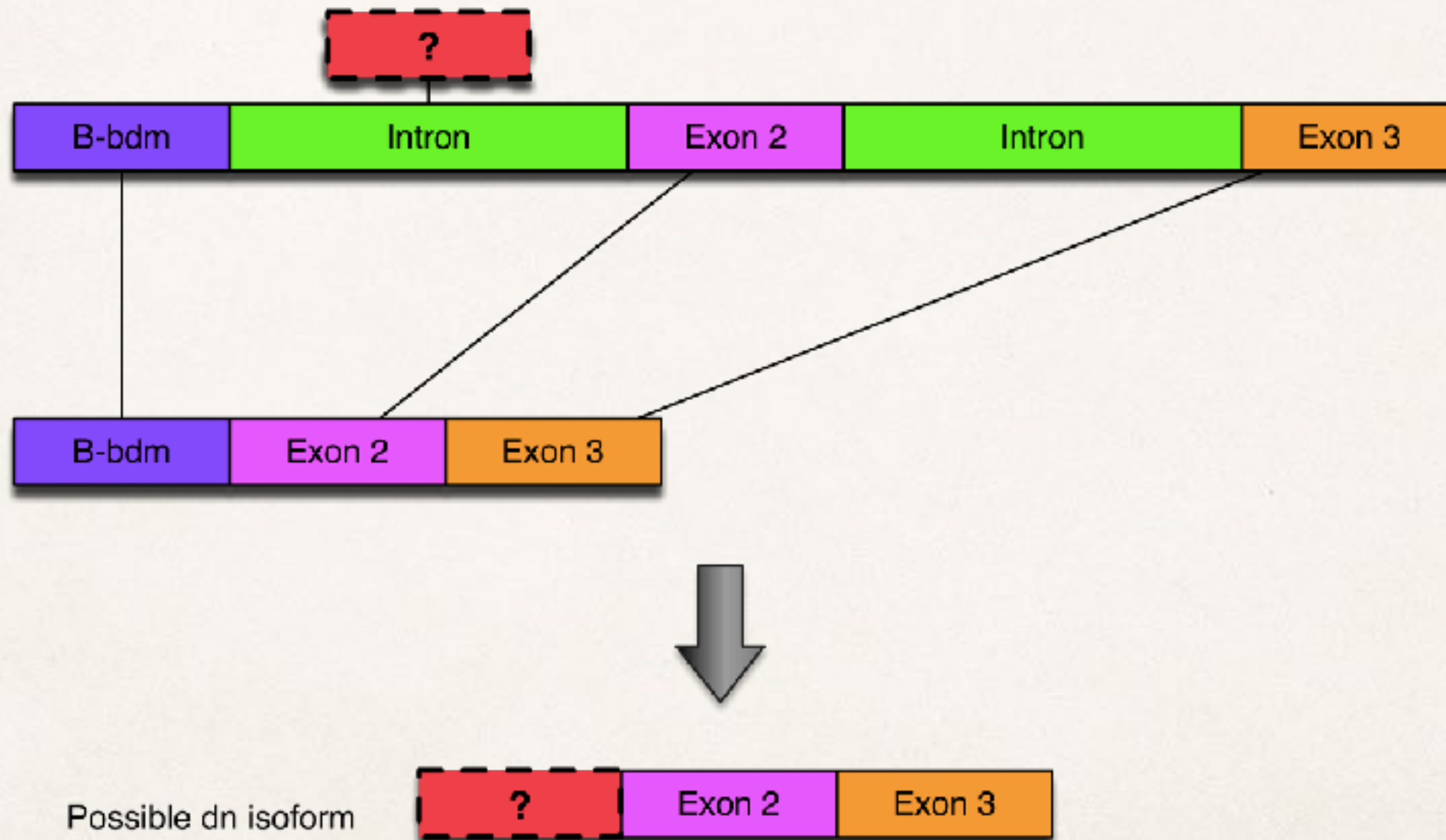
An Evolutionary Question



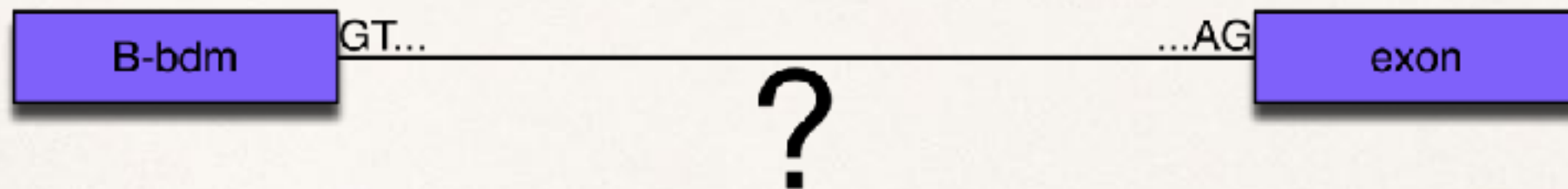
How far back do the dominant negative forms go?

How did they evolve?

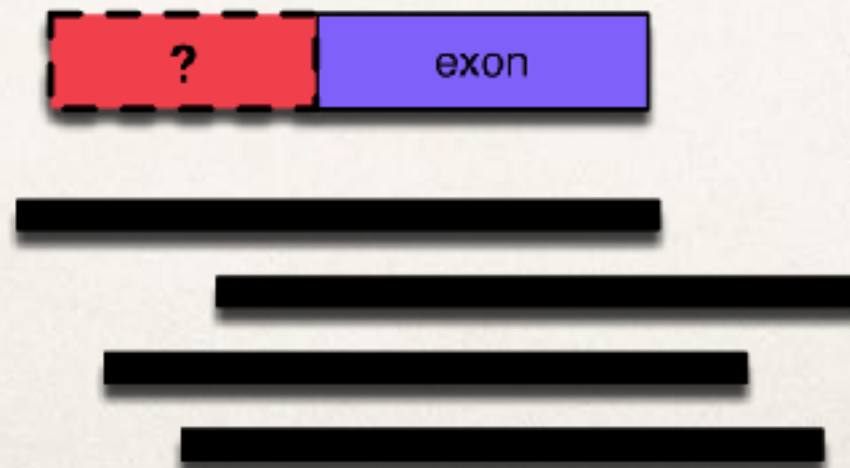
What we would expect to see



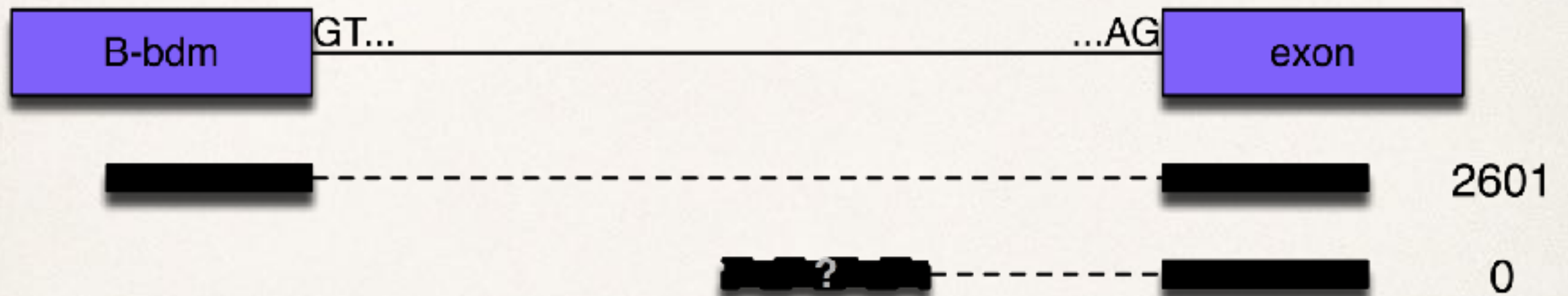
Methods



- Using sequence mapping to match intron sequence to cDNA data
- Looking for a mature RNA that contains sequence previously thought to be intron
- Data from *danio rerio* (fish), *xenopus tropicalus* (frog), *anolis carolinensis* (lizard)



Results



None of the data tested showed an alternative 1st exon
(for any of the species tested)

Interpretation

- Strong negative result
- *Implies* that TCF7l2 and LEF1 independently evolved dominant negative forms in mammals
- Inconclusive -- more data?

Moving Forward

- Get more cDNA data
- Learn more about the negative isoforms in mammals
- Look beyond vertebrates

Acknowledgements

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