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Fish genomes : a powerful tool to uncover new functional elements in vertebrates

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Stellingen behorende bij het proefschrift

“Fish genomes: a powerful tool to uncover new functional elements in vertebrates”

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door

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1. Vertebrate genomes contain large fractions of non-coding DNA which are not important for the basic function of a vertebrate.
[this Thesis, Chapter 2-3]
2. The portion of vertebrate genomes coding for proteins as well as a large bulk of regulatory sequences is highly conserved.
[this Thesis, Chapter 2-3]
3. Regulation of transcription initiation is far more complex than was previously thought.
[this Thesis, Chapter 4].
4. Assembly of large vertebrate genomes from next-generation sequencing data is achievable in a single laboratory environment on a reasonable budget.
[this Thesis, Chapter 5].
5. Despite the availability of next-generation sequencing technologies, comparative genomics is still a valuable methodology to study genome function.
6. In the medium-term genome sequencing will become a commodity, managing the data storage and analysis will become the bottleneck.
7. Sequencing will allow us to understand the molecular networks underlying physiological and pathological processes via a single methodology, be they genetic, epigenetic or transcriptional networks.
8. If we are to understand physiological mechanisms and the causes of disease we have to rapidly shift from single experiments to comprehensive and collaborative data-driven models.
9. The greatest bottleneck to scientific development of humankind is not technology but rather human barriers such as scientific culture, politics and bureaucracy.