

# IICR of structured populations with size change: strong and weak migration

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## Classic coalescent processes

We first review two classical coalescent models in population dynamics. They can be seen as generalizations of the Kingman's coalescent where either the population is panmictic (its size changes in time and there is no structure) and the structured population models (with constant population size).

### Panmictic models

The size of a population  $N(t)$  changes according to a function  $\lambda$ :

$$\frac{N(\lceil Nt \rceil)}{N(0)} \rightarrow \lambda(t), \quad (1)$$

$T_2$  is the coalescence time of two genes sampled in the population. Then,

$$\mathbb{P}[T_2 > t] = \exp \left\{ - \int_0^t \frac{1}{\lambda(s)} ds \right\}.$$

From this formula, the Inverse Instantaneous Coalescent Rate (IICR) [4] is defined as:

$$\text{IICR}(t) = \mathbb{P}[T_2 > t] / f_{T_2}(t).$$

Under panmixia the IICR function is exactly the population size change function  $\lambda$ .

### Structured models (with constant pop. size)

- the population is split in islands,
- individuals can migrate among the islands and they coalesce when they are in the same island.

- the time until the coalescence is given by the absorbing time of an homogeneous continuous-time Markov chain.

### A particular case: $n$ -island model

The population is divided in  $n$  symmetric islands with  $\rho N$  individuals each. With the same rate  $M$ , the individuals migrate among the islands. The coalescence time  $T_2$ , is the absorption time of the Markov chain with  $Q$ -matrix

$$Q = \begin{pmatrix} -(M+1/\rho) & M & 1/\rho \\ \frac{M}{n-1} & -\frac{M}{n-1} & 0 \\ 0 & 0 & 0 \end{pmatrix}. \quad (2)$$

In a model with population structure, the IICR can be unrelated to the population size, see e.g. [2].

## Main goal

We want to define simple-enough models integrating structured population and size change, to explore the relation between their IICR functions and the real population size change.

## References

- [1] Arredondo, A. et al. *Inferring number of populations ... under the  $n$ -island model.*, Heredity (2021)
- [2] Chikhi, L. et al. *The IICR as a summary of genomic diversity...*, Heredity (2018)
- [3] Mazet, O. et al. *Demographic inference using genetic data from a single individual...*, Theoretical Population Biology (2015)
- [4] Mazet, O. et al. *On the importance of being structured...*, Heredity (2016)
- [5] Rodríguez, W. et al. *The IICR and the non-stationary structured coalescent...*, Heredity (2018)
- [6] Teixeira, H. et al. *Impact of model assumptions on demographic inferences...* BMC Ecol Evo (2021)

## Strong and weak migration

The population is split in islands and its size changes according to a function  $\lambda$  as in (1).

**Strong migration:** a fixed number  $M > 0$  of individuals (independent on  $\lambda$ ) migrate each generation. The infinitesimal migration rate at time  $t$  is  $M/\lambda(t)$ .

**Weak migration:** a variable quantity  $M\lambda(t) > 0$  of individuals (depending on  $\lambda$ ) migrate each generation. The infinitesimal migration rate at time  $t$  is  $M$ .

$T_2$  is now the absorption time of an in-homogeneous Markov chain, with rate matrix  $(Q_t)_{t \geq 0}$ .

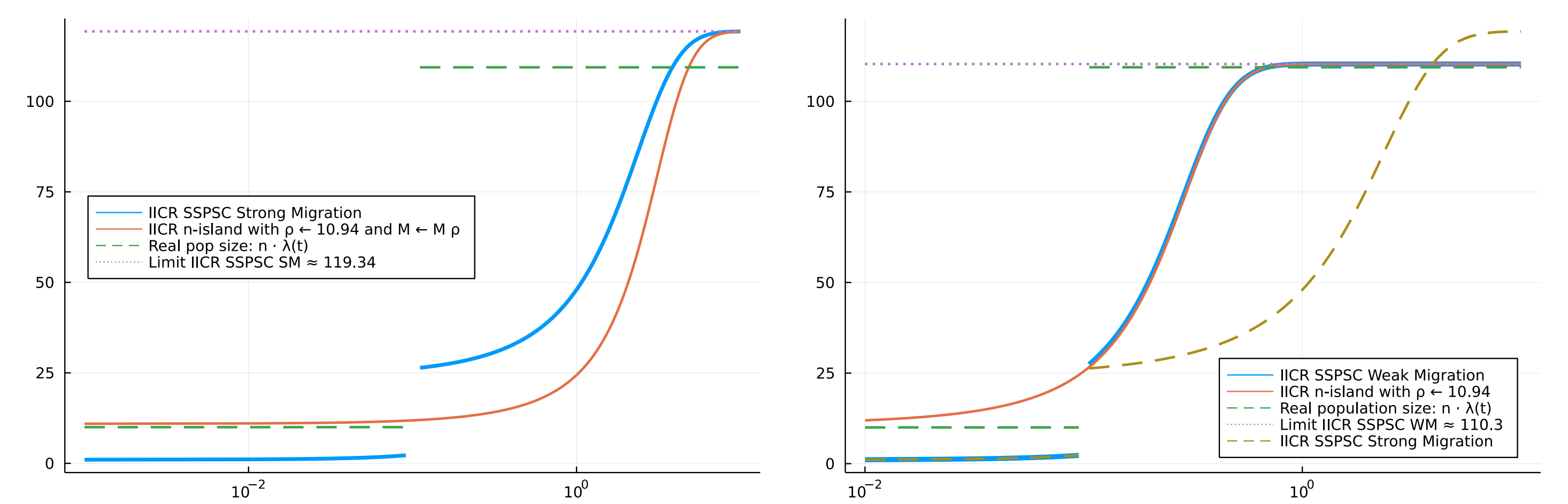
	Strong Migration (SM)	Weak Migration (WM)
Pop. size	$\lambda(t)N$	$\lambda(t)N$
Nb. of migrants	$M$	$\lambda(t)M$
Prop. of migrants	$M/(\lambda(t)N)$	$M/N$
$(n\text{-island}) Q_t =$	$\frac{1}{\lambda(t)} \begin{pmatrix} -(M+1) & M & 1 \\ \frac{M}{n-1} & -\frac{M}{n-1} & 0 \\ 0 & 0 & 0 \end{pmatrix}$	$\begin{pmatrix} -(M + \frac{1}{\lambda(t)}) & M & \frac{1}{\lambda(t)} \\ \frac{M}{n-1} & -\frac{M}{n-1} & 0 \\ 0 & 0 & 0 \end{pmatrix}$

In general, the distribution of  $T_2$  is computed using the Kolmogorov forward equation:  $\frac{d}{dt} P_t = P_t Q_t$ . For the strong migration case, the IICR function simplifies to  $\text{IICR}_{\text{SM}}(t) = \lambda(t) \cdot \text{IICR}_Q \left( \int_0^t \frac{du}{\lambda(u)} \right)$ .

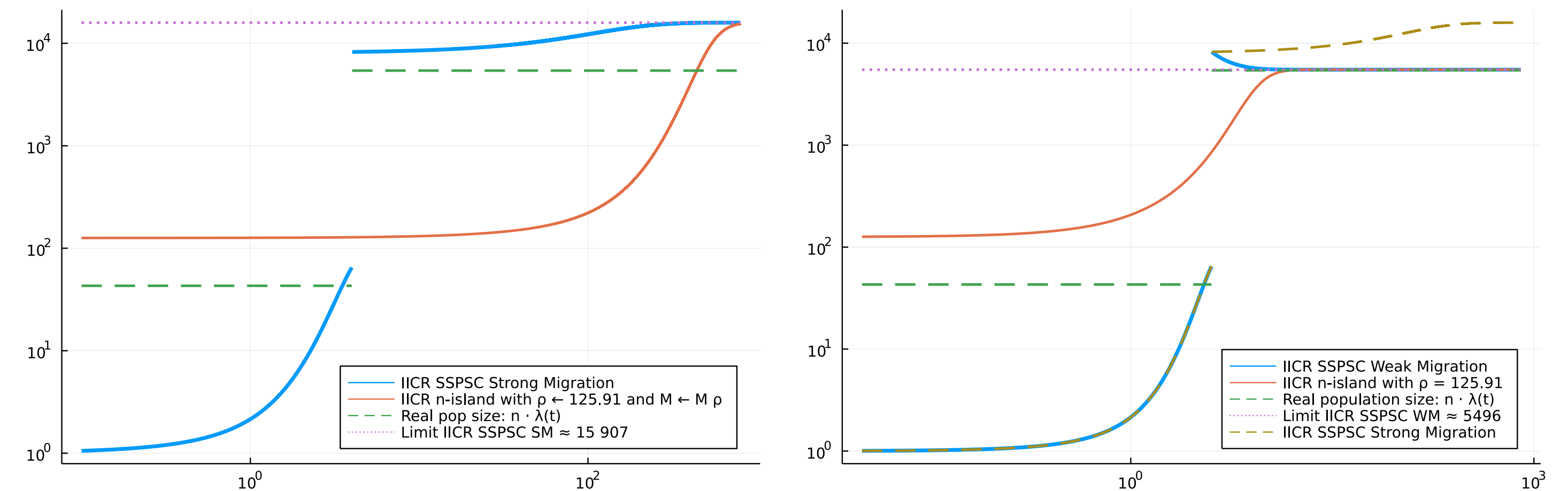
## Numerical examples

**Single step population size change:**  $\lambda(t) = \mathbf{1}_{[0,T)}(t) + \alpha \mathbf{1}_{[T,\infty)}(t)$

The migration rate is  $M = 9$  and the number of islands is  $n = 10$ . Also,  $\alpha = 10.94$  and  $T = 0.1$ . See [3].

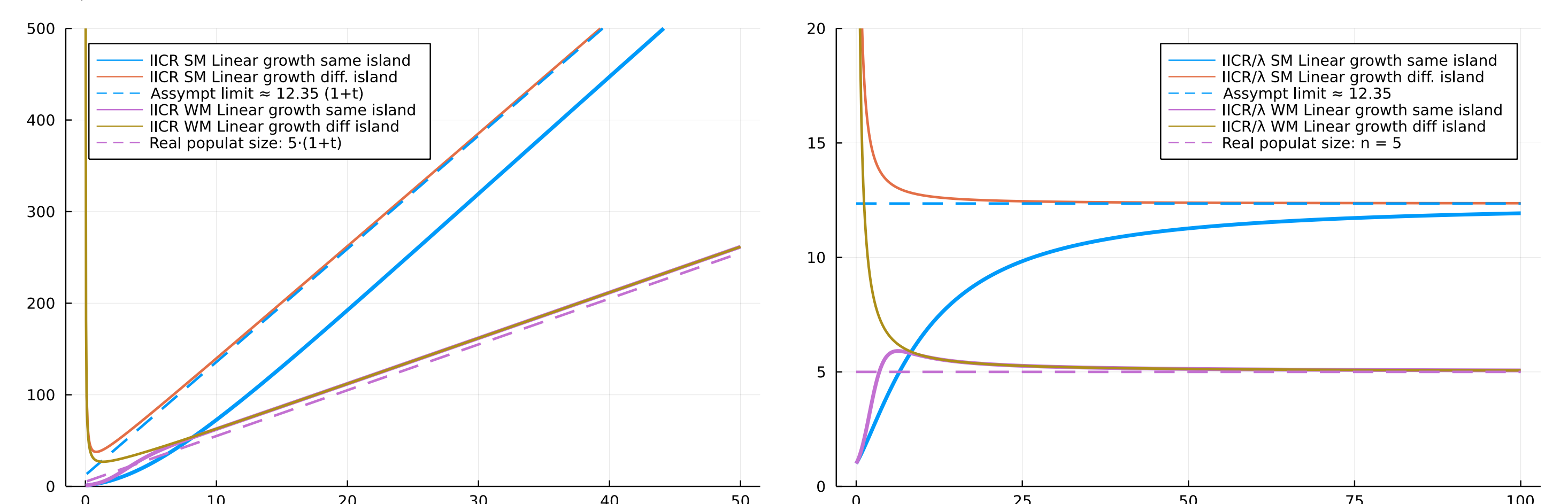


The migration rate is  $M = 0.5$  and the number of islands is  $n = 43$ . Also,  $\alpha = 125.91$  and  $T = 4$ . See [3].



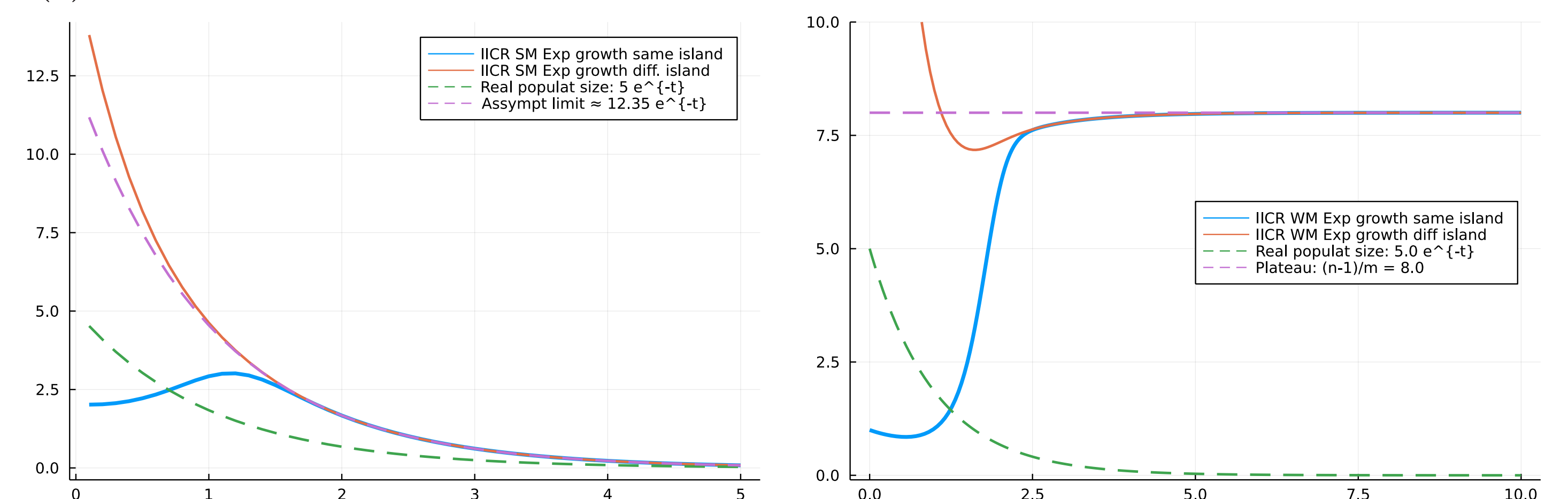
**Linear growth:**  $\lambda(t) = 1 + t$

The migration rate is  $M = 0.5$  and the number of islands is  $n = 5$ .



**Exponential growth:**  $\lambda(t) = e^{-t}$

The migration rate is  $M = 0.5$  and the number of islands is  $n = 5$ .



The IICR of structured populations with size change behave differently under weak and strong migration. Note that an exponential growth and weak migration produce an IICR with a plateau unrelated to  $\lambda$ .

## Discussion

- the IICR of structured model can behave completely differently to the real population size
- the weak and strong migration hypothesis produce different IICR function behaviors under the same structure and the same population size change
- demographic inference on these models is challenging
- this is a work in progress, future work should include the study of more realistic scenarios [1, 5, 6]

The Notebook for generating the plots:

[www.github.com/JosueCorujo/structured\\_pop\\_with\\_size\\_change](http://www.github.com/JosueCorujo/structured_pop_with_size_change)

