wspec Documentation

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Matthias Flor

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CONTENTS

This is the Wolbachia speciation (wspec) module for numerical simulations of speciation events driven by Wolbachia-induced cytoplasmic incompatibility (CI) and reinforcement processes.

Contents:

ANALYTICAL

Analytical solutions for stability of cytoplasmic incompatibility (CI) patterns, gene flow, and reproductive values of migrants between populations with different infection states.
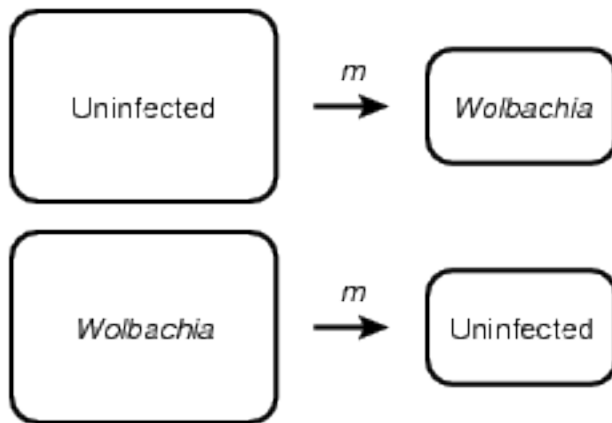
wspec.analytical.**dynamics_IM** (f, ci, m, t, x)

> Infection dynamics of Wolbachia for the scenario with an infected mainland (IM), iterative map.

> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **m: float in interval [0, 1]** migration rate
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>>
>> **x: float in interval [0, 1]** infection frequency of Wolbachia
>
> **Returns:**
>
>> **out: float** infection frequency in the next generation

wspec.analytical.**dynamics_SP** (f, ci, t, x)

> Infection dynamics of Wolbachia in a single host population (SP), iterative map returns the infection frequency in the next generation.

> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia

> **x: float in interval [0, 1]** infection frequency of Wolbachia

> **Returns:**

>> **out: float** infection frequency in the next generation

wspec.analytical.**dynamics_UM**(*f*, *ci*, *m*, *t*, *x*)
> Infection dynamics of Wolbachia for the scenario with an uninfected mainland (UM), iterative map returns the infection frequency in the next generation.

> **Args:**

>> **f: float in interval [0, 1]** fecundity reduction in infected females

>> **ci: float in interval [0, 1]** level of CI

>> **m: float in interval [0, 1]** migration rate

>> **t: float in interval [0, 1]** transmission rate of Wolbachia

>> **x: float in interval [0, 1]** infection frequency of Wolbachia

> **Returns:**

>> **out: float** infection frequency in the next generation

wspec.analytical.**fix1_IM**(*f*, *ci*, *m*, *t*)
> Fixpoint x_1^* for the scenario with an infected mainland (IM).

> **Args:**

>> **f: float in interval [0, 1]** fecundity reduction in infected females

>> **ci: float in interval [0, 1]** level of CI

>> **m: float in interval [0, 1]** migration rate

>> **t: float in interval [0, 1]** transmission rate of Wolbachia

> **Returns:**

>> **out: float** critical migration rate

wspec.analytical.**fix1_SP**(*f*, *ci*, *t*)
> Infection frequency fixpoint x_1^* for a single host population (SP).

> **Args:**

>> **f: float in interval [0, 1]** fecundity reduction in infected females

>> **ci: float in interval [0, 1]** level of CI

>> **t: float in interval [0, 1]** transmission rate of Wolbachia

> **Returns:**

>> **out: float** equilibrium frequency of Wolbachia

wspec.analytical.**fix1_UM**(*f*, *ci*, *m*, *t*)
> Fixpoint x_1^* for the scenario with an uninfected mainland (UM).

> **Args:**

>> **f: float in interval [0, 1]** fecundity reduction in infected females

>> **ci: float in interval [0, 1]** level of CI

>> **m: float in interval [0, 1]** migration rate

>> **t: float in interval [0, 1]** transmission rate of Wolbachia

> **Returns:**
>
>> **out: float** equilibrium frequency of Wolbachia

wspec.analytical.**fix2_IM**(*f*, *ci*, *m*, *t*)

> Fixpoint x_2^* for the scenario with an infected mainland (IM).
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **m: float in interval [0, 1]** migration rate
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** critical migration rate

wspec.analytical.**fix2_SP**(*f*, *ci*, *t*)

> Infection frequency fixpoint x_2^* for a single host population (SP).
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** equilibrium frequency of Wolbachia

wspec.analytical.**fix2_UM**(*f*, *ci*, *m*, *t*)

> Fixpoint x_2^* for the scenario with an uninfected mainland (UM).
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **m: float in interval [0, 1]** migration rate
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** equilibrium frequency of Wolbachia

wspec.analytical.**fix3_IM**(*f*, *ci*, *m*, *t*)

> Fixpoint x_3^* for the scenario with an infected mainland (IM).
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **m: float in interval [0, 1]** migration rate
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** critical migration rate

wspec.analytical.**fix3_SP**(*f*, *ci*, *t*)

Infection frequency fixpoint x_3^* for a single host population (SP).

Args:

> **f: float in interval [0, 1]** fecundity reduction in infected females
>
> **ci: float in interval [0, 1]** level of CI
>
> **t: float in interval [0, 1]** transmission rate of Wolbachia

Returns:

> **out: float** equilibrium frequency of Wolbachia

wspec.analytical.**fix3_UM**(*f*, *ci*, *m*, *t*)

Fixpoint x_3^* for the scenario with an uninfected mainland (UM).

Args:

> **f: float in interval [0, 1]** fecundity reduction in infected females
>
> **ci: float in interval [0, 1]** level of CI
>
> **m: float in interval [0, 1]** migration rate
>
> **t: float in interval [0, 1]** transmission rate of Wolbachia

Returns:

> **out: float** equilibrium frequency of Wolbachia

wspec.analytical.**fix_SP**(*f*, *ci*, *t*)

Infection frequency fixpoints for a single host population (SP).

Args:

> **f: float in interval [0, 1]** fecundity reduction in infected females
>
> **ci: float in interval [0, 1]** level of CI
>
> **t: float in interval [0, 1]** transmission rate of Wolbachia

Returns:

> **out: tuple of three floats** equilibrium frequencies x_1^*, x_2^*, and x_3^* of Wolbachia

wspec.analytical.**fix_UM**(*f*, *ci*, *m*, *t*)

Infection frequency fixpoints for the scenario with an infected mainland (IM).

Args:

> **f: float in interval [0, 1]** fecundity reduction in infected females
>
> **ci: float in interval [0, 1]** level of CI
>
> **m: float in interval [0, 1]** migration rate
>
> **t: float in interval [0, 1]** transmission rate of Wolbachia

Returns:

> **out: tuple of three floats** equilibrium frequencies x_1^*, x_2^*, and x_3^* of Wolbachia

wspec.analytical.**gff_DS**(*m*, *s*)

Gene flow factor (gff) for the case of divergent selection (DS). Residents have a viability advantage of *s* over migrants, equivalent to migrants having a viability cost of $\frac{s}{1+s}$. Derived from fitness graph for the reproductive value of a migrant.

> **Args:**
>
> > **m: float in interval [0, 1]** migration rate
> >
> > **s: positive float** selection coefficient
>
> **Returns:**
>
> > **out: float** gene flow factor

wspec.analytical.**lcrit_SP**(*f*, *t*)

> Critical CI level (lcrit) for a single host population (SP).
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** critical CI level

wspec.analytical.**lcrit_UM**(*f*, *m*, *t*)

> Critical CI level (lcrit) for the scenario with an uninfected mainland (UM).
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **m: float in interval [0, 1]** migration rate
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** critical CI level

wspec.analytical.**mcrit_IM**(*f*, *ci*, *t*)

> Critical migration rate (mcrit) for the scenario with an infected mainland (IM).
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** critical migration rate

wspec.analytical.**mcrit_IMA**(*f*, *ci*, *s*, *t*)

> Critical migration rate (mcrit) for the scenario with an infected mainland (IM) with local host adaptation (A).
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **s: positive float** selection coefficient
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** critical migration rate

wspec.analytical.**mcrit_UM**(*f*, *ci*, *t*)

    Critical migration rate (mcrit) for the scenario with an uninfected mainland (UM).

    Args:

        f: float in interval [0, 1] fecundity reduction in infected females

        ci: float in interval [0, 1] level of CI

        t: float in interval [0, 1] transmission rate of Wolbachia

    Returns:

        out: float critical migration rate

wspec.analytical.**mcrit_UMA**(*f*, *ci*, *s*, *t*)

    Critical migration rate (mcrit) for the scenario with an uninfected mainland (UM) with local host adaptation (A).

    Args:

        f: float in interval [0, 1] fecundity reduction in infected females

        ci: float in interval [0, 1] level of CI

        s: positive float selection coefficient

        t: float in interval [0, 1] transmission rate of Wolbachia

    Returns:

        out: float critical migration rate

wspec.analytical.**meff_DS**(*m*, *s*)

    Effective migration rate (meff) for the case of divergent selection (DS). Residents have a viability advantage of s over migrants, equivalent to migrants having a viability cost of $\frac{s}{1+s}$. Derived from fitness graph for the reproductive value of a migrant.

    Args:

        m: float in interval [0, 1] migration rate

        s: positive float selection coefficient

    Returns:

        out: float effective migration rate

wspec.analytical.**prcrit**(*ci*, *q*, *s*)

    Minimal rejection probability (pr) of a mutant allele at the locus for female mating preference to spread in an uninfected island receiving migration from an infected mainland.

    Args:

        ci: float in interval [0, 1] level of CI

        q: float in interval [0, 1] transition probability to a new mating round

        s: positive float selection coefficient

    Returns:

        out: float minimal rejection probability

wspec.analytical.**reproval_DS**(*s*)

    Reproductive value of a migrant for the case of divergent selection (DS). Residents have a viability advantage of s over migrants, equivalent to migrants having a viability cost of $\frac{s}{1+s}$. Derived from fitness graph.

    Args:

> **s: positive float** selection coefficient
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_FUHETCL** (*f*, *ci*, *t*)

> Reproductive value of an uninfected female (FU) in a heterogenous host population (HET), *per class* (CL) reproductive value (as opposed to *per capita*). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_FUHETCP** (*f*, *ci*, *t*)

> Reproductive value of an uninfected female (FU) in a heterogenous host population (HET), *per capita* (CP) reproductive value (as opposed to *per class*). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_FUHOMW** (*f*, *ci*)

> Reproductive value of an uninfected female migrant (FU) in a homogenous Wolbachia infected population (HOMW). This applies to the case of perfect Wolbachia transmission, $t = 1$. Derived from fitness graph:
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_FWHETCL** (*f*, *ci*, *t*)

> Reproductive value of an infected female (FW) in a heterogenous host population (HET), *per class* (CL) reproductive value (as opposed to *per capita*). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

`wspec.analytical.`**`reproval_FWHETCP`** (f, ci, t)

> Reproductive value of a Wolbachia infected female (FW) in a heterogenous host population (HET), *per capita* (CP) reproductive value (as opposed to *per class*). Derived from fitness graph.
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** reproductive value

`wspec.analytical.`**`reproval_FWHOMU`** (f, ci, t)

> Reproductive value of a Wolbachia infected female migrant (FW) in a homogenous uninfected population (HOMU). Derived from fitness graph.
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** reproductive value

`wspec.analytical.`**`reproval_IPHOMU`** (f, ci, t)

> Average reproductive value of a migrant from an infected population (IP), i.e. where the Wolbachia infection is at a stable frequency below 1 due to imperfect transmission, in a homogenous uninfected population (HOU). Averaged over sexes (F/M) and cytotypes (U/W). Derived from fitness graph.
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** reproductive value

`wspec.analytical.`**`reproval_MUHETCL`** (f, ci, t)

> Reproductive value of an uninfected male (MU) in a heterogenous host population (HET), *per class* (CL) reproductive value (as opposed to *per capita*). Derived from fitness graph.
>
> **Args:**
>
>> **f: float in interval [0, 1]** fecundity reduction in infected females
>>
>> **ci: float in interval [0, 1]** level of CI
>>
>> **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
>> **out: float** reproductive value

`wspec.analytical.`**`reproval_MUHETCP`** (f, ci, t)

> Reproductive value of an uninfected male (MU) in a heterogenous host population (HET), *per capita* (CP) reproductive value (as opposed to *per class*). Derived from fitness graph.

Args:

> **f: float in interval [0, 1]** fecundity reduction in infected females
>
> **ci: float in interval [0, 1]** level of CI
>
> **t: float in interval [0, 1]** transmission rate of Wolbachia

Returns:

> **out: float** reproductive value

wspec.analytical.**reproval_MUHOMW** (*f*, *ci*)

> Reproductive value of an uninfected male migrant (MU) in a homogenous Wolbachia infected population (HOMW). This applies to the case of perfect Wolbachia transmission, t=1. Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_MWHETCL** (*f*, *ci*, *t*)

> Reproductive value of an infected male (MW) in a heterogenous host population (HET), *per class* (CL) reproductive value (as opposed to *per capita*). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_MWHETCP** (*f*, *ci*, *t*)

> Reproductive value of a Wolbachia infected male (MW) in a heterogenous host population (HET), *per capita* (CP) reproductive value (as opposed to *per class*). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_MWHOMU** (*f*, *ci*, *t*)

> Reproductive value of a Wolbachia infected male migrant (MW) in a homogenous uninfected population (HOMU). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia

Returns:

> **out: float** reproductive value

`wspec.analytical.`**`reproval_UHETCL`** (*f*, *ci*, *t*)

> Average reproductive value of an uninfected host (U) in a heterogenous population (HET), *per class* (CL) reproductive value (as opposed to *per capita*). Derived from fitness graph. Averaged over the two sexes.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

`wspec.analytical.`**`reproval_UHETCP`** (*f*, *ci*, *t*)

> Average reproductive value of an uninfected host (U) in a heterogenous population (HET), *per capita* (CP) reproductive value (as opposed to *per class*). Derived from fitness graph. Averaged over the two sexes.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

`wspec.analytical.`**`reproval_UHOMW`** (*f*, *ci*)

> Reproductive value of an uninfected migrant (U) in a a homogenous Wolbachia infected population (HOMW). This applies to the case of perfect Wolbachia transmission, t=1. Derived from fitness graph. Averaged over the two sexes.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
>
> **Returns:**
>
> > **out: float** reproductive value

`wspec.analytical.`**`reproval_WHETCL`** (*f*, *ci*, *t*)

> Reproductive value of an infected host (W) in a heterogenous host population (HET), *per class* (CL) reproductive value (as opposed to *per capita*). Derived from fitness graph.
>
> **Args:**
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> **Returns:**
>
> > **out: float** reproductive value

wspec.analytical.**reproval_WHETCP** (*f*, *ci*, *t*)

> Average reproductive value of a Wolbachia infected host (W) in a heterogenous population (HET), *per capita* (CP) reproductive value (as opposed to *per class*). Derived from fitness graph. Averaged over the two sexes.
>
> Args:
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> Returns:
>
> > **out: float** reproductive value

wspec.analytical.**reproval_WHOMU** (*f*, *ci*, *t*)

> Reproductive value of a Wolbachia infected migrant (W) in a homogenous uninfected population (HOU). Derived from fitness graph. Averaged over the two sexes.
>
> Args:
>
> > **f: float in interval [0, 1]** fecundity reduction in infected females
> >
> > **ci: float in interval [0, 1]** level of CI
> >
> > **t: float in interval [0, 1]** transmission rate of Wolbachia
>
> Returns:
>
> > **out: float** reproductive value

wspec.analytical.**xPref** (*ci*, *pr*, *q*, *s*)

> Approximated equilibrium frequency of a mutant allele at the locus for female mating preference in an uninfected island receiving migration from an infected mainland.
>
> Args:
>
> > **ci: float in interval [0, 1]** level of CI
> >
> > **pr: float in interval [0, 1]** rejection probability of mating preference mutant allele
> >
> > **q: float in interval [0, 1]** transition probability to a new mating round
> >
> > **s: positive float** selection coefficient
>
> Returns:
>
> > **out: float** equilibrium frequency of mutant preference allele

wspec.analytical.**xTprefEQ** (*pr*, *s*, *xPref*)

> Modified from Kirkpatrick (1982), equation (2).
>
> Args:
>
> > **pr: float in interval [0, 1]** rejection probability of mating preference mutant allele
> >
> > **s: positive float** selection coefficient
> >
> > **xPref: float in interval [0, 1]** frequency of preference allele in Kirkpatrick's model
>
> Returns:
>
> > **out: float** equilibrium frequency of preferred trait

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