**Metadata**

Each italicized heading represents a different flat sheet (i.e., a CSV file) that is linked by a unique identifier for each SR (‘id’).

An asterix beside heading indicates that coding is plural (i.e., multiple element levels recorded from the same SR).

*1) Publication\_info:*

Details relating to the publication

**id:** File name used as a unique identifier for each individual SR

**title:** title of SR

**year:** year of publication

**journal\_name:** the name of the journal that the SR was published in

**SR\_type:** The dominant review method within the SR. For example, if a SR is dominated by a meta-analysis but includes a small section of vote counting, this will be coded as 1 for meta-analysis. Note that all SRs generally include a narrative portion, so the SR will only be coded as 4 if a narrative form of reporting is the dominant form.

MA = formal or informal meta-analysis (i.e., weighted or unweighted regression statistical model), broad = a broad quantitative systematic review not including a formal or informal meta-analysis (i.e., vote counting), map = a systematic map, narrative = narrative SRs

**timeframe\_start:** the earliest year that the literature covers. This can be taken as the earliest publication year from the primary literature included in the SR

**timeframe\_end:** when was the last date (year) that the literature search covers (usually the date of the search)

**n\_studies:** the totalnumber of original studies included in the SR that met their study selection criteria for the dominant review method within the SR. If the study reported human studies versus animal studies separately, only the number of animal studies was recorded. We report the total number of animal studies that met the included SRs study criteria even if some of the included animal studies within the included SR did not meet our criteria. We only report the number of studies that also met our criteria if results were separated in SR (e.g., SR runs sub analyses on offspring prenatal exposure versus offspring postnatal exposure)

**k\_effect\_sizes:** number of effect sizes (if meta-analysis), NA = if the SR was not a meta-analysis. If the SR was comprised of multiple sub-analyses with no overlap of *k,* the number of effect sizes should be summed to get a total. If the study comprised of multiple sub-analyses with overlapping effect sizes included, the maximum number of effect sizes from the largest analysis should be taken.

*2) Review\_info:*

Details relating to the SR

**topic\_code:** unique identifier for broad category of the main topic:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| adaptive | adaptive non-genetic effects i.e., ‘anticipatory effects’ and ‘condition-transfer effects’ (i.e. if the SR examines where descendant are reared in a similar vs different environment from F0 or if F0 exposed to a high quality environment confers a benefit to descendants) |
| non-adaptive | maladaptive/negative transgenerational effects such as exposure to stressors that are predicted to disrupt descendant health/fitness relative to a control |
| unclear | unspecified/unclear |

**discipline\_code:** What research field is the SR from:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| eco evo | ecology and evolution |
| biomed | biomedicine (human-centric environments such as tobacco, alcohol and Western diets) |
| toxicology | (eco-) toxicology (pollution and contaminants) |
| agriculture | agriculture/aquaculture |
| crossdisciplinary | cross-disciplinary (i.e., mixture of environmental factors that span multiple disciplines) |
| unclear | other/unclear |

**terminology\_code:** Does the terminology used to describe the non-genetic inheritance match our definition of inter- vs -transgenerational inheritance:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| yes | yes |
| no | no |
| not used | does not use these terms |
| unclear | unclear |

**mutagen\_code:** Does the SR include any primary studies that may be exposing animals to mutagenic factors (including carcinogens)?

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| yes | yes |
| no | no |
| unclear | unclear |

*3) Species\_info\*:*

Details of species covered in the SR (i.e., the species from the primary literature). NA if no species lists were provided in SRs (did not record species if the paper mentioned a species but did not provide species list when methods state that more than one species was eligible for inclusion, also did not record species if common names that were not clear enough to be converted to Latin names were provided):

**species\_name:** Latin species name

Note that some SRs report common names for some widely used model study systems. If this is the case, we will convert this to the Latin name. For example, vinegar fly = Drosophila melanogaster, lab rat = Rattus norvegicus domestica, mouse = Mus musculus etc.

*4) Higher\_taxon\_code\*:*

What are the broad taxonomic groups included in the SR?

**taxon\_code**: which broad taxonomic groups do the species in the study belong to:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| vertebrates | vertebrates |
| invertebrates | invertebrates |
| plants | plants |
| other | other |
| unclear | unclear |

*5) Transmission\_info\*:*

What modes of transmission (maternal vs. paternal, etc.) were included in the SR?

**transmission\_code:** did the SR focus on the effects of environmental exposures of:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| matriline | matriline |
| patriline | patriline |
| not separated | not separated (i.e., the primary studies used do not enable matriline and patriline effects to be distinguished, e.g., if both sexes exposed) |
| unclear | unclear/unspecified |

*6) Inter\_vs\_trans\_info\*:*

Was the type of reviewed non-genetic inheritance inter-generational or trans-generational based on the F0 sex and broad taxonomic group of the studied species (See main text Fig. 1)?

**inter\_vs\_trans\_code:**

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| inter | inter-generational |
| trans | trans-generational |
| unclear | unclear |

*7) Env\_mismatch\_info\*:*

Did the descendants’ environment match or mismatch the F0 environment? In the case on treatment and controls, does the offspring environment match that of the treatment parents?

**env\_mismatch\_code:**

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| match | match (descendants environment matched F0 environment) |
| mismatch | mismatch (descendants do not experience same environment as F0) |
| unclear | unclear |

*8) F0\_env\_info\*:*

What was the type of reviewed environmental factor that varied in the F0 generation?

**F0\_env\_code:** Unique identifier for the broad category of environmental variable:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| diet | diet |
| human induced | human induced pollutant/toxin |
| environmental composition | natural variation in environmental composition (e.g., salt, nitrogen etc) |
| psychological stress | psychological stress (e.g., post-natal separation) |
| temperature | temperature |
| human health | ‘human health’ related environments (e.g., tobacco, alcohol etc.) |
| population demographic | differences in population demographics (e.g., population density, predators, sex-ratio etc.) |
| light | light and/or photoperiod |
| unclear | other/unclear |

*9) Env\_eff\_direction\_info\*:*

What was the expected direction of the effects of the F0 environment on descendants:

**env\_eff\_direction\_code:** The overall effect on the F0 environment:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| negative | stressful/negative |
| positive | beneficial/positive |
| unclear | neutral/unclear |

*10) Exposure\_timing\_info\*:*

At what life stage was the F0 exposed to the environmental factor?

**exposure\_timing\_code:** when was the F0 exposed to the environmental factor?

*Note that some SRs may include a mixture of primary studies where the F0 was exposed to the environment at a variety of different lifestages*

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| pre-natal | pre-natal (i.e., when mother or father is developing) |
| post-natal | post-natally before sexual maturity |
| post-sexual maturity | after sexual maturity but before gestation |
| gestation | during gestation |
| unclear | other/unclear |

*11) Descendant\_trait\_code\*:*

What were the descendant traits included in the SR?

**descendent\_trait\_code:** a unique identifier of the broad descendant trait that was included:

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| physiological | physiological (e.g., immune function, insulin levels, hormone levels) |
| morphological | morphological (e.g., body size, adiposity, colouration, anogenital distance) |
| reproductive | reproductive (e.g., fecundity and sexual trait measures) |
| life history | life-history (e.g., developmental rate, aging and lifespan) |
| survival | descendant survival/aging (must be measured post-natally) |
| behavioural | behavioural (e.g., response to stimuli, anxiety, learning and memory) |
| molecular | molecular (e.g., gene expression, DNA methylation) |
| health | health and disease (e.g., disease prevalence) |
| unclear | other/unclear |

*12) descendant\_sex\_info\*:*

Which descendant sex was included in the SR?

**descendant\_sex\_code:** what was the sex of the descendant in the SR. 1 = males, 2 = females, 3 = unclear

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| males | males |
| females | females |
| unclear | unclear |

*13) Descendant\_age\_info\*:*

At what life stage were the descendant traits measured:

**descendant\_age\_code:** The age at which the descendants were measured for studied traits:

*Note that some SRs may include a mixture of primary studies with traits measured at different life stages including as fetuses.*

|  |  |
| --- | --- |
| Controlled vocabulary | Description |
| foetal | foetal/embryonic |
| juvenile | juvenile (post-embryonic/birth prior to sexual maturity) |
| adult | adult |
| ongoing | ongoing |
| unclear | other/unclear |

*14. Descendant\_generat\_info\*:*

What generation(s) were included in the SR?

**Descendant\_generat\_code:** the generational for which outcome traits were measured (F1, F2, F3 etc).