

Constraining tip dates to non-zero values using tsinfer/tsdate? Part II.

```
In [28]: import tsinfer
import tskit
import tsdate
import numpy as np
import pandas as pd
import datetime as dt
import time
```

infer tree sequence

```
In [29]: vdata = tsinfer.VariantData("chr1/chr1.vcf",
                                     ancestral_state="variant_AA")

In [30]: inferred_ts = tsinfer.infer(vdata)
print(f"Inferred a genetic genealogy for {inferred_ts.num_samples} (haploid) genomes")

Inferred a genetic genealogy for 29 (haploid) genomes
```

store tip dates in sampling_times array

```
In [31]: metadata = pd.read_table("data/filtered_metadata.tsv")

In [32]: # get sampling times
metadata['time'] = metadata['date'].str[:4].astype(float)
# set time as N years since most recent sample
metadata['time'] = max(metadata['time']) - metadata['time']
#metadata['time'] = 2025 - metadata['time']

In [33]: # create sample:time dictionary
accession_to_time = dict(zip(metadata['experiment_accession'], metadata['time']))

# match tip names and sampling times to nodes names
individuals_list = {}

for s in inferred_ts.samples():
    individuals_list[s] = inferred_ts.individual(inferred_ts.node(s).individual).metadata['variant_data_sample_id']

sampling_times = np.full(inferred_ts.num_individuals, tskit.UNKNOWN_TIME)

for sample in inferred_ts.samples():
    id = individuals_list[sample]
    sampling_times[sample] = accession_to_time[id]

In [34]: sampling_times

Out[34]: array([17., 49., 35., 32., 4., 38., 28., 29., 50., 43., 22., 44., 16.,
                30., 26., 52., 49., 30., 30., 33., 10., 10., 37., 33., 86., 48.,
                2., 0., 9.] )
```

reinfer tree sequence with sampling_times array

```
In [35]: vdata = tsinfer.VariantData("chr1/chr1.vcf",
                                     ancestral_state="variant_AA",
                                     individuals_time = sampling_times)

In [36]: # inferred_ts = tsinfer.infer(vdata, # tip dates are stored in vdata
#                                           time_units = "years")

# print(f"Inferred a genetic genealogy for {inferred_ts.num_samples} (haploid) genomes")
```

(1) generate ancestors

```
In [37]: anc = tsinfer.generate_ancestors(vdata)
```

(2) match ancestors

```
In [38]: anc_m = tsinfer.match_ancestors(vdata, anc, time_units = "years")
anc_m.tables.nodes.time

Out[38]: array([[1.11405836, 1.0397878 , 0.96551724, 0.93103448, 0.65517241,
                0.62068966, 0.55172414, 0.34482759, 0.31034483, 0.27586207,
                0.27586207, 0.20689655, 0.17241379, 0.17241379, 0.17241379,
                0.13793103, 0.13793103, 0.13793103, 0.10344828, 0.10344828,
                0.10344828, 0.10344828, 0.06896552, 0.06896552, 0.06896552,
                0.06896552, 0.06896552, 0.06896552])
```

(3) match samples [error]

```
In [39]: anc_ts = tsinfer.match_samples(vdata, anc_m, force_sample_times=True)

-----
ValueError                                Traceback (most recent call last)
Cell In[39], line 1
----> 1 anc_ts = tsinfer.match_samples(vdata, anc_m, force_sample_times=True)

File ~/tsinfer-env/lib/python3.11/site-packages/tsinfer/inference.py:1629, in match_samples(variant_data, ancestors_ts, recombination_rate, mismatch_ratio, path_compression, indexes, post_process, force_sample_times, num_threads, overlay_non_inference_sites, recombination, mismatch, precision, extended_checks, engine, progress_monitor, simplify, record_provenance, results)
    1622 sample_times = variant_data.individuals.time[:] [individuals]
    1624 # Here we might want to re-order sample_indexes and sample_times
    1625 # so that any historical ones come first, any we bomb out early
    1626 # if they conflict but that would mean re-ordering the sample
    1627 # nodes in the final ts, and we sometimes assume they are in
    1628 # the same order as in the file
-> 1629 manager.match_samples(sample_indexes, sample_times, results)
    1630 ts = manager.finalise(overlay_non_inference_sites)
    1631 if post_process:

File ~/tsinfer-env/lib/python3.11/site-packages/tsinfer/inference.py:2766, in SampleMatcher.match_samples(self, sample_indexes, sample_times, results, slice_)
    2764 if slice_ is None:
    2765     slice_ = slice(0, len(sample_indexes))
-> 2766 return self.match_samples(sample_indexes[slice_], results)

File ~/tsinfer-env/lib/python3.11/site-packages/tsinfer/inference.py:2735, in SampleMatcher._match_samples(self, sample_indexes, results)
    2733 if np.any(times[node_id] > times[result.path.parent]):
    2734     p = result.path.parent[np.argmax(times[result.path.parent])]
-> 2735     raise ValueError(
    2736         f"Failed to put sample {j} (node {node_id}) at time "
    2737         f"{times[node_id]} as it has a younger parent (node {p})."
    2738     )
    2739 builder.add_path(
    2740     result.node,
    2741     result.path.left,
    2742     (...)
    2744     compress=self.path_compression,
    2745 )
    2746 builder.add_mutations(
    2747     result.node,
    2748     result.mutations_site,
    2749     result.mutations_derived_state,
    2750 )

ValueError: Failed to put sample 0 (node 28) at time 17.0 as it has a younger parent (node 26).
```

With "force_sample_times = True", throws "ValueError: Failed to put sample 0 (node 28) at time 17.0 as it has a younger parent (node 26)." It seems that due to the uncalibrated times given by tsinfer, my real tip ages are always much older than any internal nodes.

```
In [40]: # Now match_samples without forcing sample times
anc_ts = tsinfer.match_samples(vdata, anc_m) # ,force_sample_times=True)
anc_ts.tables.nodes.time

Out[40]: array([[0., 0., 0., 0., 0.,
                0., 0., 0., 0., 0.,
                0., 0., 0., 0., 0.,
                0., 0., 0., 0., 0.,
                0., 0., 0., 0., 0.06896552,
                0.06896552, 0.06896552, 0.06896552, 0.06896552,
                0.10344828, 0.10344828, 0.10344828, 0.10344828, 0.10344828,
                0.13793103, 0.13793103, 0.13793103, 0.17241379, 0.17241379,
                0.17241379, 0.20689655, 0.27586207, 0.27586207, 0.31034483,
                0.34482759, 0.55172414, 0.62068966, 0.65517241, 0.93103448,
                0.96551724, 1.0397878 ]])

In [41]: inferred_ts = tsinfer.match_samples(vdata, anc_ts, force_sample_times=True)
```

```
-----
ValueError                                Traceback (most recent call last)
Cell In[41], line 1
----> 1 inferred_ts = tsinfer.match_samples(vdata, anc_ts, force_sample_times=True)

File ~/tsinfer-env/lib/python3.11/site-packages/tsinfer/inference.py:1599, in match_samples(variant_data, ancestors_ts, recombination_rate, mismatch_ratio, path_compression, indexes, post_process, force_sample_times, num_threads, overlay_non_inference_sites, recombination, mismatch, precision, extended_checks, engine, progress_monitor, simplify, record_provenance, results)
    1597 variant_data._check_finalised()
    1598 progress_monitor = _get_progress_monitor(progress_monitor, match_samples=True)
-> 1599 manager = SampleMatcher(
    1600     variant_data,
    1601     ancestors_ts,
    1602     recombination_rate=recombination_rate,
    1603     mismatch_ratio=mismatch_ratio,
    1604     recombination=recombination,
    1605     mismatch=mismatch,
    1606     path_compression=path_compression,
    1607     num_threads=num_threads,
    1608     precision=precision,
    1609     extended_checks=extended_checks,
    1610     engine=engine,
    1611     progress_monitor=progress_monitor,
    1612 )
    1613 sample_indexes = check_sample_indexes(variant_data, indexes)
    1614 sample_times = np.zeros(
    1615     len(sample_indexes), dtype=variant_data.individuals.time.dtype
    1616 )

File ~/tsinfer-env/lib/python3.11/site-packages/tsinfer/inference.py:2668, in SampleMatcher._init__(self, variant_data, ancestors_ts, **kwargs)
    2664 self.ancestors_ts_tables = ancestors_ts.dump_tables()
    2665 super().__init__(
    2666     variant_data, self.ancestors_ts_tables.sites.position, **kwargs
    2667 )
-> 2668 self.restore_tree_sequence_builder()
    2669 # Map from input sample indexes (IDs in the SampleData file) to the
    2670 # node ID in the tree sequence.
    2671 self.sample_id_map = {}

File ~/tsinfer-env/lib/python3.11/site-packages/tsinfer/inference.py:2341, in Matcher.restore_tree_sequence_builder(self)
    2336 raise ValueError(
    2337     "Ancestors tree sequence not compatible: sequence length is different to"
    2338     " sample data file."
    2339 )
    2340 if np.any(tables.nodes.time <= 0):
-> 2341     raise ValueError("All nodes must have time > 0")
    2343 edges = tables.edges
    2344 # Get the indexes into the position array.

ValueError: All nodes must have time > 0
```

run tsdate

```
In [42]: # somehow this is still running despite ValueError from match_samples

simplified_ts = tsdate.preprocess_ts(
    inferred_ts,
    erase_flanks=True
)

dated_ts, fit = tsdate.date(simplified_ts,
                             mutation_rate=6.1e-7,
                             time_units="years",
                             return_fit=True,
                             match_segregating_sites = True,
                             #constr_iterations=100 # no effect on tip dates
                             )

In [47]: dated_ts.nodes_time

Out[47]: array([[ 0., 0., 0., 0.,
                0., 0., 0., 0.,
                0., 0., 0., 0.,
                0., 0., 0., 0.,
                0., 0., 0., 0.,
                0., 0., 0., 0.,
                0., 8.1101485 , 1.9017355 , 9.54585197,
                0.92320977, 1.5683697 , 5.42048973, 2.1821495 ,
                3.3631714 , 3.84439326, 6.10075609, 2.21114753,
                17.71661843, 7.72050752, 5.87168088, 11.11856677,
                10.35199326, 9.95833546, 13.01286384, 11.0493302 ,
                13.87701521, 14.74093075, 16.83053289, 17.89812799,
```


19.76832641, 21.66212157, 22.93135039, 24.58521966,
807.29412396, 10.66932169))