

# infercnvpy\_heatmap\_color\_fix

August 24, 2022

```
[1]: import scanpy as sc
import infercnvpy as cnv
import matplotlib.pyplot as plt
```

```
sc.settings.set_figure_params(figsize=(5, 5))
```

```
[2]: sc.logging.print_header()
```

```
scanpy==1.9.1 anndata==0.8.0 umap==0.5.3 numpy==1.22.4 scipy==1.8.1
pandas==1.4.2 scikit-learn==1.1.1 statsmodels==0.13.2 python-igraph==0.9.10
pynndescent==0.5.7
```

```
[3]: adata = cnv.datasets.maynard2020_3k()
adata.var.loc[:, ["ensg", "chromosome", "start", "end"]].head()
```

```
[3]:
```

symbol	ensg	chromosome	start	end
AL645933.5	ENSG00000288587.1	chr6	31400702	31463705
AC010184.1	ENSG00000288585.1	chr3	141449745	141456434
AC023296.1	ENSG00000288580.1	chr8	2923568	2926689
AL117334.2	ENSG00000288577.1	chr20	3406380	3410036
AC107294.4	ENSG00000288576.1	chr3	184778723	184780720

```
[4]: # We provide all immune cell types as "normal cells".
```

```
cnv.tl.infercnv(
    adata,
    reference_key="cell_type",
    reference_cat=[
        "B cell",
        "Macrophage",
        "Mast cell",
        "Monocyte",
        "NK cell",
        "Plasma cell",
        "T cell CD4",
        "T cell CD8",
        "T cell regulatory",
        "mDC",
```

```

        "pDC",
    ],
    window_size=250,
)

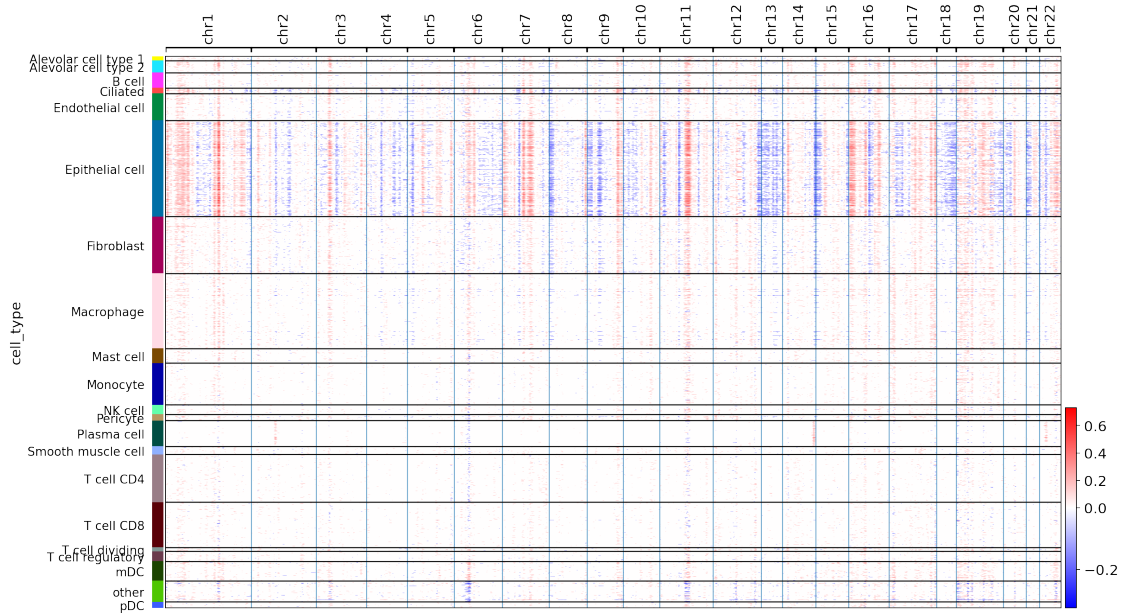
```

0% | | 0/1 [00:00<?, ?it/s]

```
[5]: cnv.pl.chromosome_heatmap(adata, groupby="cell_type")
```

/home/cody/.virtualenvs/scanpy/lib/python3.8/site-packages/infercnvpy/pl/\_chromosome\_heatmap.py:59: FutureWarning: X.dtype being converted to np.float32 from float64. In the next version of anndata (0.9) conversion will not be automatic. Pass dtype explicitly to avoid this warning. Pass `AnnData(X, dtype=X.dtype, ...)` to get the future behaviour.

```
tmp_adata = AnnData(X=adata.obsm[f"X_{use_rep}"], obs=adata.obs)
```



```
[6]: # these should match colors in above heatmap
adata.uns["cell_type_colors"]
```

```
[6]: array(['#FFFF00', '#1CE6FF', '#FF34FF', '#FF4A46', '#008941', '#006FA6',
        '#A30059', '#FFDBE5', '#7A4900', '#0000A6', '#63FFAC', '#B79762',
        '#004D43', '#8FB0FF', '#997D87', '#5A0007', '#809693', '#6A3A4C',
        '#1B4400', '#4FC601', '#3B5DFF', '#4A3B53', '#FF2F80', '#61615A',
        '#BA0900', '#6B7900', '#00C2A0', '#FFAA92', '#FF90C9', '#B903AA',
        '#D16100', '#DDEFFF', '#000035', '#7B4F4B', '#A1C299', '#300018',
        '#0AA6D8', '#013349', '#00846F', '#372101', '#FFB500', '#C2FFED'],
        dtype=object)
```

```
[7]: # define custom color dictionary for a couple cell types
colordict = {
    "Epithelial cell": "#e377c2", # pink
    "Endothelial cell": "#d62728", # red
}
# let's change colors for cell_type in adata
for x in list(colordict.keys()):
    adata.uns["cell_type_colors"][list(adata.obs.cell_type.cat.categories).
    ↪index(x)] = colordict[x]
```

```
[8]: # indexes 4 and 5 should be updated now
adata.uns["cell_type_colors"]
```

```
[8]: array(['#FFFF00', '#1CE6FF', '#FF34FF', '#FF4A46', '#d62728', '#e377c2',
        '#A30059', '#FFDBE5', '#7A4900', '#0000A6', '#63FFAC', '#B79762',
        '#004D43', '#8FB0FF', '#997D87', '#5A0007', '#809693', '#6A3A4C',
        '#1B4400', '#4FC601', '#3B5DFF', '#4A3B53', '#FF2F80', '#61615A',
        '#BA0900', '#6B7900', '#00C2A0', '#FFAA92', '#FF90C9', '#B903AA',
        '#D16100', '#DDEFFF', '#000035', '#7B4F4B', '#A1C299', '#300018',
        '#0AA6D8', '#013349', '#00846F', '#372101', '#FFB500', '#C2FFED'],
        dtype=object)
```

```
[9]: # now, Epithelial cell should be pink and Endothelial cell should be red
cnv.pl.chromosome_heatmap(adata, groupby="cell_type")
```

```
/home/cody/.virtualenvs/scanpy/lib/python3.8/site-
packages/infercnvpy/pl/_chromosome_heatmap.py:59: FutureWarning: X.dtype being
converted to np.float32 from float64. In the next version of anndata (0.9)
conversion will not be automatic. Pass dtype explicitly to avoid this warning.
Pass `AnnData(X, dtype=X.dtype, ...)` to get the future behaviour.
    tmp_adata = AnnData(X=adata.obsm[f"X_{use_rep}"], obs=adata.obs)
```

