

The two dimensional fold test in paleomagnetism using ipython notebook

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Abstract. One aspect of paleomagnetic analysis prone to controversy is the result of the fold test used to evaluate the age of a magnetisation component relative to the age of a structural event. Initially, the fold test was conducted by comparing the Fisherian precision parameter (k) to results from different limbs of a fold structure before and after tilt adjustment. To accommodate synfolding magnetisation, the tilt correction can be performed in stepwise fashion to both limbs simultaneously, here called one dimensional (1D) fold test. The two dimensional (2D) fold test described in this paper is carried out by applying stepwise tilt adjustment to each limb of the fold separately. The rationale for this is that tilts observed on contrasting limbs of deformed structure may not be synchronous or even belong to the same episode of deformation. A program for the procedure is presented here which generates two dimensional values of the k -parameter visually presented in contoured form. The use of ipython notebook enables this 2D fold test to be performed interactively and yield a more precise evaluation than the primitive 1D fold test.

1. Introduction

The paleomagnetic fold test can be a powerful means for establishing the age of a magnetisation in a rock relative to an episode of deformation. It relies on adjusting the paleomagnetic directions from a distributed set of locations for geologic tilt and resolving whether they converge or disperse. The test was first suggested by Graham [1] and an example showing that magnetisation can survive stresses produced during folding was illustrated in Keweenaw sediments by Du Bois [2]. The test was placed on a statistical basis by McElhinny [3]. The Fisherian precision parameter of the directions of magnetisation in situ (k_b) is compared with their precision following tilt adjustment (k_a) and the ratio k_a/k_b is compared with F -ratio tables with equal degrees of freedom ($2N-1$), where N is the number of directions of magnetisation being tested. McElhinny [3] tabulated 95% and 99% confidence limits from application of this fold test for a range of N values.

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Although the simple test of McElhinny [3] is often still used for cursory analysis of magnetisations in deformed rocks it was shown by McFadden and Jones [4] that the test is invalid, most importantly because the population of magnetisations either before or after adjustment cannot be Fisherian. The authors conclude “The correct statistical procedure for applying the fold test is to determine whether the mean direction of a group of sites from one limb may be distinguished from the mean direction of a group of sites from another limb of the fold”. They showed that the test of McElhinny is in general too stringent so a positive result will almost certainly reflect a magnetisation that has survived folding. Unfortunately the new test of McFadden and Jones required a complicated sampling scheme which included several sites with the same tilt corrections [5].

With advancing research in the paleomagnetism of deformed rocks, complex deformation settings were encountered in which the McFadden and Jones [4] analysis was found to be no longer appropriate. As a result for a while workers tended to revert to application of the McElhinny test on the basis that the results produced were conservative and therefore at least dependable. To improve this situation McFadden [6] developed a further test which now satisfactorily covers most geological situations and numerous examples of application and discussion of this now widely-applied test can be found elsewhere e.g. in [7, 8, 9].

The basic assumption of all fold tests is that the rocks being tested were folded synchronously so that each tilt correction must be corrected with the same percentage unfolding. This condition requires that the rocks are embraced by a single fold structure and it excludes the possibility that one limb may have been more deformed than the other. To address this issue the present study embraces the possibility that the rock was originally magnetized in any configuration. Instead of using a complex statistical analysis, we take a visual approach in handling the fold test by making use of k contoured graphs generating by the data after executing stepwise tilt adjustments to the paleomagnetic data from both limbs. However, for full analysis we require information on the expected inclination, in term of an inclination band which can often be supplied from another source such as the paleomagnetic inclination from undisturbed layers or an estimate from the regional apparent polar wander path for the study area. In our opinion, an accurate inclination frame becomes a necessary condition for performing a fold test especially in regions of complex deformation. For a positive 2D fold test the age of magnetisation predates the age of folding and this is indicated by the condition where the point of 100% unfolding becomes the center of the k contours and is covered by the expected inclination band. If the age of magnetisation postdates the age of folding, the graph will show this when the point of 0% unfolding (i.e. *in situ* data) becomes the center of the k contours and is covered by the expected inclination band. The other configurations of the graph otherwise indicate synfolding magnetisations.

To find the preferred mean directions, data falling within the expected inclination band and having k -parameters greater than 95% of k_{max} , here called the target directions, were analysed using a bootstrap technique by calling sub-program `pmag.di.boot` [10]. The target directions are then resampled up to 5000 and the mean direction sought. The obtained means do not however, differ very much from the arithmetic means of the target directions. So, in this 2D fold test we only take the arithmetic mean by averaging the mean directions fulfilling the imposed k -parameter and inclination criteria because the process is much simpler and faster by calling `object.mean()`.

This 2D fold test program makes use of python sub-programs (`pmag`) written by Prof. Tauxe of Scripps Institutes of Oceanography (SIO) [10]. Python is a free scripting modern computer language and has a simple and clean syntax. The 2D fold test program is carried out within the ipython notebook environment. The ipython notebook is also freely available and has cross platforms which can be run under Linux, Apple OS and Windows. It provides a modern computation environment where the user can work in a shell basis so corrections can be done interactively without compilation and can run processes as in traditional computing. By using this technology, researchers can look at

data, test new ideas and evaluate their outcomes and of course much of their time will be invested in solving the problem rather than in writing the computer program. It is estimated that the ipython notebook has now been used by 500,000 – 1.5 million people [11,12].

2. Application Examples of the 2D Fold Test

2.1. An example from the Devonian ('Old Red Sandstone') sediments of South Wales, United Kingdom

The Llanstephan fold is located in Lower Devonian redbeds near the northern margin of the Late Palaeozoic Variscan fold belt in South Wales at 51.76 °N and 355.59 °E. This fold belt is useful for demonstrating the present method because the folds are typically asymmetric with northern limbs tending to be steeper than southern limbs. The Llanstephan fold structure is well exposed and ideally selected for performing a fold test with the aim of dating the magnetisation relative to regional deformation. Paleomagnetic directions from seven sites were taken from the southern limb and four sites from the northern limb and analysed using the 2D fold test. These paleomagnetic data were reported by Setiabudidaya [13] as part of a wider investigation of the magnetisation record in the Devonian "Old Red Sandstone" sediments at the northern margin of the Variscan Belt in Britain [14] and originally analysed using the FOLDCONT program written in fortran. The site mean data are listed in Table 1.

Table 1. Paleomagnetic directions and field orientations of (a) the north limb (b) and the south limb of the Llanstephan fold, South Wales [13]. 'Site' = site number, 'Dec' = declination and 'Inc' = inclination of the magnetisation, 'Azm'=azimuth and 'Dip'= tilt of formation. All figures are in degrees (except for site numbers).

(a)					(b)				
Site	Dec	Inc	Azm	Dip	Site	Dec	Inc	Azm	Dip
1	206.9	-13.5	330	54	1	208.0	-6.3	166	25
2	209.1	-18.4	327	41	2	209.4	3.6	168	48
3	210.0	-12.8	324	32	3	208.8	1.2	190	10
4	197.7	-2.9	342	65	4	210.4	-1.4	167	18
5	208.6	-3.4	349	45					
6	203.1	-5.0	333	64					
7	206.8	-12.8	340	40					

In the first shell (Table 2) modules `matplotlib.pyplot`, `pmag`, `numpy`, `pandas` and `itertools` are imported. The last line `%matplotlib inline` should be assigned for the resulting graph to be shown on the computer screen. Table 3 shows the module `pandas` reading the datafile in this example residing in folder `Data/SouthWales/Llanstephan` with the subfilenames `northlimb.txt` and `southlimb.txt` respectively. The last two lines extract the numeric values of the data. The next shell shown in Table 4 assigns the expected inclinations in terms of an inclination band with the center `i0`.

Table 2. Instructions in python for importing the modules used in the 2D fold test.

```
import matplotlib.pyplot as plt
import pmag
```

```

import numpy as np
import pandas as pd
import itertools
%matplotlib inline

```

Table 3. Instructions in python for reading the data.

```

data_n_limb = pd.read_csv('Data/SouthWales/Llanstephan/
                        north_limb.txt', sep=r"\s+")
data_s_limb = pd.read_csv('Data/South Wales/Llanstephan/
                        south_limb.txt', sep=r"\s+")
data_n_limb = data_n_limb[['Dec', 'Inc', 'Azm', 'Dip']].values
data_s_limb = data_s_limb[['Dec', 'Inc', 'Azm', 'Dip']].values

```

Table 4. Instructions in python for assigning the expected inclination (in degrees).

```

i0 = -7.5
imin = -10.0
imax = -5.0

```

The python codes listed in Table 5 perform the stepwise tilt correction. In this example we take an nstep value of 50 so that the program calculates the k parameter, mean declination and mean inclination for each 2% of step of untilting in addition to *in situ* (0% unfolding). Table 6 shows the python codes used to plot the contour diagram of the data from Table 5 together with relevant attributes.

Table 5. Codes in python used to generate 2D data for k -values, mean declinations and mean inclinations following stepwise tilt corrections.

```

nstep = 50
data_n_limb = data_n_limb.transpose()
data_s_limb = data_s_limb.transpose()
data_n_limb_temp = data_n_limb.copy()
data_s_limb_temp = data_s_limb.copy()
x = np.linspace(0,1,nstep+1)
k = np.zeros((nstep+1,nstep+1))
k1d=np.zeros(nstep+1)
inc = np.zeros((nstep+1, nstep+1))
dec = np.zeros((nstep+1, nstep+1))
for i in range(nstep+1):
    data_n_limb_temp[3]=data_n_limb[3]*x[i]
    for j in range(nstep+1):
        data_s_limb_temp[3]=data_s_limb[3]*x[j]
        data_n_limb_final=data_n_limb_temp.transpose()
        data_s_limb_final=data_s_limb_temp.transpose()
        data_final=np.array([item for item in
                            itertools.chain(data_n_limb_final,
                            data_s_limb_final)])

```

```
data_untilt=pmag.dotilt_V(data_final)
data_untilt=np.array(data_untilt)
tilted_direction=data_untilt.transpose()
tilted_mean=pmag.fisher_mean(tilted_direction)
k[i,j]=tilted_mean.get('k')
inc[i,j]=tilted_mean.get('inc')
dec[i,j]=tilted_mean.get('dec')
if i==j:
    kld[i]=k[i,j]
```

Table 6. Codes in python used to plot contours of k , declination and inclination after executing instructions in the previous shell (Table 5).

```
fig = plt.figure(figsize=(8, 8), dpi=100)
X,Y= np.meshgrid(x,x)
CS1=plt.contour(X,Y,k,colors='g')
CS2=plt.contour(X,Y,inc, levels=[imin, i0,imax],
    colors='k')
CS3=plt.contour(X,Y,dec,colors='r')
for c in CS2.collections:
    c.set_dashes([(0, (5.0, 5.0))])
for c in CS3.collections:
    c.set_dashes([(0, (20.0, 10.0))])
plt.xlabel('Unfolding North Limb(x 100%)')
plt.ylabel('Unfolding South Limb(x 100%)')
plt.clabel(CS1, inline=1,fmt='%1.0f', fontsize=10)
plt.clabel(CS2, inline=1, fmt='%1.1f',fontsize=10)
plt.clabel(CS3, inline=1, fmt='%1.1f',fontsize=10)
plt.title('Contour of k- and Dec-values and Expected Mean
Inclination')
```

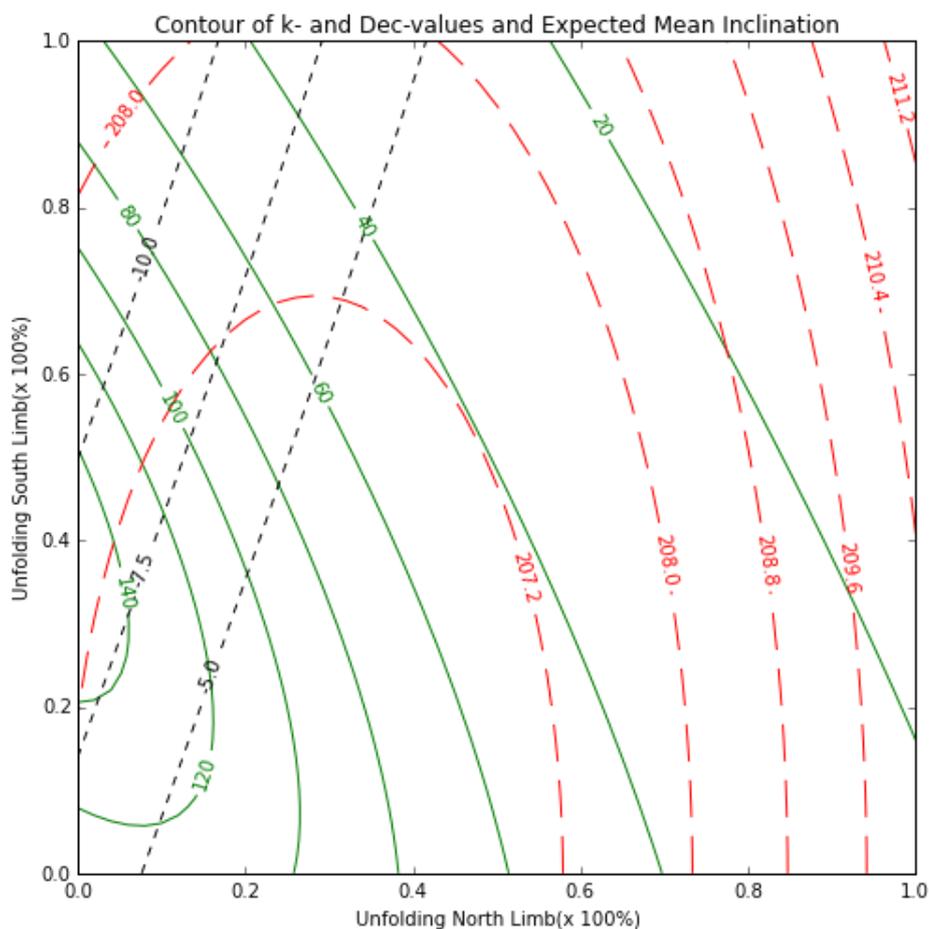


Figure 1. Contour diagram of k -parameters (solid green lines), three expected inclinations (short black dashed lines) and declinations (long red dashed lines) from the 2D fold test of the data shown in Table 1. Numbers shown are in degrees except k values.

The results illustrated in Figure 1 demonstrate that the age of magnetisation here is synfolding. The python codes used to find the mean paleomagnetic direction are listed in Table 7. Only data having k -values more than 95% of k -maximum and inclinations between -5.0° and -10° will be further analysed. In this example, there are 26 data conforming to these criteria. These 26 data have declinations ranging from 207.11° to 207.45° , inclinations ranging from -9.89° to -7.70° and k -values ranging from 143.39 to 150.77. These mean directions are obtained from configurations of 24% to 48% unfolding of the northern limb and 0% to 4% unfolding on the southern limb. For finding the mean direction a function mean is applied to each group of data according to the instructions listed in Table 8.

Table 7. Codes in python used to find the target directions with their corresponding k and unfolding configurations.

```

nstep=50
x = np.linspace(0,1,nstep+1)
k = np.zeros((nstep+1,nstep+1))
inc = np.zeros((nstep+1, nstep+1))
dec = np.zeros((nstep+1, nstep+1))
target_i = []
target_j =[]
target_dec = []
target_inc = []
target_k = []
for i in range(nstep+1):
    data_n_limb_temp[3]=data_n_limb[3]*x[i]
    for j in range(nstep+1):
        data_s_limb_temp[3]=data_s_limb[3]*x[j]
        data_n_limb_final=data_n_limb_temp.transpose()
        data_s_limb_final=data_s_limb_temp.transpose()
        data_final=np.array([item for item in itertools.
            Chain(data_n_limb_final, data_s_limb_final)])
        data_untilt=pmag.dotilt_V(data_final)
        data_untilt=np.array(data_untilt)
        tilted_direction=data_untilt.transpose()
        tilted_mean=pmag.fisher_mean(tilted_direction)
        k[i,j]=tilted_mean.get('k')
        inc[i,j]=tilted_mean.get('inc')
        dec[i,j]=tilted_mean.get('dec')
        if (k[i,j]>(0.95*kmax) and imax>inc[i,j]>imin):
            #we change the order of index i and j to fit the
            #graph ref. http://eli.thegreenplace.net/2014/
            #meshgrids-and-disambiguating-rows-and-columns-
            #from-cartesian-coordinates/
            target_i +=[(j*0.02)]
            target_j +=[(i*0.02)]
            target_dec +=[(dec[i,j])]
            target_inc +=[(inc[i,j])]
            target_k +=[(k[i,j])]
target_i=np.array(target_i);target_j=np.array(target_j);
target_dec=np.array(target_dec);
target_inc=np.array(target_inc);
target_k=np.array(target_k)

```

Table 8. Instructions in python for calculating the means.

```

print 'unfolding-x =', "%0.2f" %target_i.mean(),
        'unfolding-y =', "%0.2f" %target_j.mean()
print 'dec =', "%0.2f" %target_dec.mean(), 'inc =', "%0.2f"
        %target_inc.mean(), 'k =', "%0.2f" %target_k.mean()
print 'paleolatitude_2D =', "%0.2f",
        %pmag.plattarget_inc.mean()

```

Table 9. Output display of the result from applying the instructions of Table 8. The value of unfolding should be multiplied by 100%. The values of 'dec', 'inc' and 'paleolatitude_2D' are

in degrees.

```
unfolding-x = 0.01 unfolding-y = 0.35
dec = 207.27 inc = -8.69 k = 146.76
paleolatitude_2D = -4.37
```

For a comparison, the mean direction from the 1D fold test is sought in terms of the maximum (1D) k value. The command and the printed output instructions are listed in Tables 10 and 11.

Table 10. Instructions in python for printing the results of the 2D fold test.

```
print 'unfolding =', "%0.2f" %(float(k1d.argmax())/nstep)
print 'dec =', "%0.2f" %dec[k1d.argmax(), k1d.argmax()],
      'inc =', "%0.2f" %inc[k1d.argmax(), k1d.argmax()],
      'k =', "%0.2f" %k1dmax
print 'paleolatitude_1D =', "%0.2f",
      %(pmag.plat(inc[k1d.argmax(), k1d.argmax()])))
```

Table 11. Output display of the 1D fold test. The value of unfolding should be multiplied by 100%. The values of 'dec', 'inc' and 'paleolatitude_1D' are in degrees.

```
unfolding = 0.10
dec = 206.84 inc = -5.24 k = 124.41
paleolatitude_1D = -2.62
```

The mean inclination derived from the 2D fold test is seen to be steeper than the mean inclination from the 1D fold test and places South Wales at a slightly more southerly paleolatitude during Permo-Carboniferous times than indicated by the result of the 1D fold test. The 2D fold test also predicts that the southern limb of the fold has experienced more stress than the northern limb since the formation was magnetized which is consistent with plate convergence from the south during the Variscan Orogeny and the frequent structural asymmetry observed in this region.

2.2. An example from Western Sumba, Indonesia

The Lasipu formation in Western Sumba is located at 9.7 °N and 119.6 °E. The formation is mildly deformed by open folding [15]. The azimuth information listed by the author assumed that the samples were taken from the same limb of a fold. Samples from site SL.D and SL.E revealed positive inclinations (normal) and samples from SL.F and SL.G yielded negative inclinations (reversed). Table 12 lists the paleomagnetic results where the reversed directions have been converted to equivalent normal polarity by adding 180° to the declinations and changing signs of the inclination. The expected inclination values for input are listed in Table 13.

Table 12. *In situ* paleomagnetic directions and orientation of (a) the normal limb and (b) the reversed limb of a fold structure at Lasipu, Western Sumba, studied by

Wensink [15]. The *in situ* direction was obtained by this author following untilting of the paleomagnetic directions by a minus dip in the azimuth direction. See also the caption of Table 1.

(a)					(b)				
Site	Dec	Inc	Azm	Dip	Site	Dec	Inc	Azm	Dip
SL.D	239.4	21.2	106	12.5	SL.F	245.0	40.3	149	26
SL.E	236.1	10.0	112	40.0	SL.G	235.2	29.8	113	16

Table 13. Instructions in python for assigning the expected inclination (in degrees).

```
i0=32.5
imin=30.0
imax=35.0
```

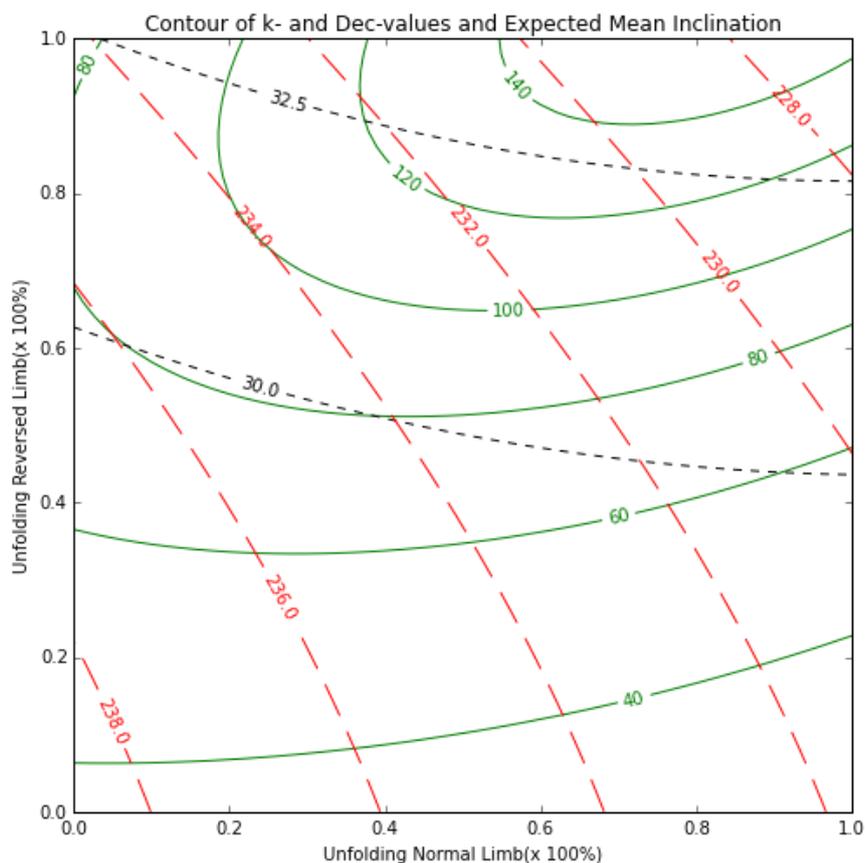


Figure 2. Contour figure of k -parameters (solid green lines), two expected inclinations (short black dashed lines (the third lies outside the range)) and declinations (long red dashed lines) from the 2D fold test applied to the data as listed in Table 2. Numbers shown are in degrees except k values.

The results of this test are shown in Figure 2. Using python code as in Table 7, we find that there are 51 data with $k > 95\%$ from k_{max} ranging from 146.69 to 154.19, the declination ranging from 227.13° to 229.65° and the inclination ranging from 33.14° to 33.58°. These mean directions are

obtained from configurations of 94% up to 100% unfolding the normal limb and 62% up to 96% unfolding of the reversed limb. To find the mean, a function mean is applied to each group of data (cf. Table 9) and the results are listed in Table 14. For comparison the output from the 1D fold test is listed in Table 15. This 2D fold test shows that the predicted tectonic rotation of the study area is just 2° less than that predicted by the 1D fold test.

Table 14. Output from the 2D fold test: the value of unfolding should be multiplied by 100%. The values of ‘dec’, ‘inc’ and ‘paleolatitude_2D’ are in degrees.

```
unfolding-x = 0.78  unfolding-y = 0.98
dec = 228.63  inc = 33.40  k = 149.97
paleolatitude_2D = 18.24
```

Table 16. Output of the 1D fold test. The value of unfolding should be multiplied by 100%. The values of ‘dec’, ‘inc’ and ‘paleolatitude_1D’ are in degrees.

```
unfolding = 1.00
dec = 226.83  inc = 33.58  k = 143.98
paleolatitude_1D = 18.37
```

3. Conclusion

The 2D fold test, based on this pictorial approach shows more possibilities for adjusted mean paleomagnetic directions after executing stepwise tilt corrections than the 1D fold test. The expected inclination constraint is added together with a search for the highest k values. The mean paleomagnetic directions derived from the 2D fold test are more accurate and can therefore be used to revise paleomagnetic directions arising from the 1D fold tests. Hence, the paleolatitude and the amount of block rotation of the study area and the configuration of the limbs of a fold can collectively provide additional information to workers investigating the kinematics of complex deformed areas.

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