

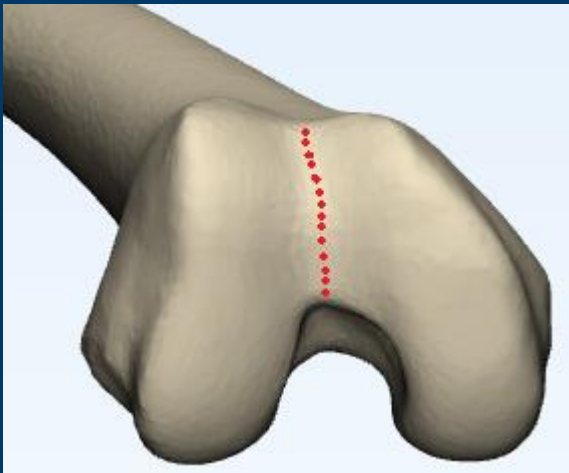


FINDING THE PERFECT FIT

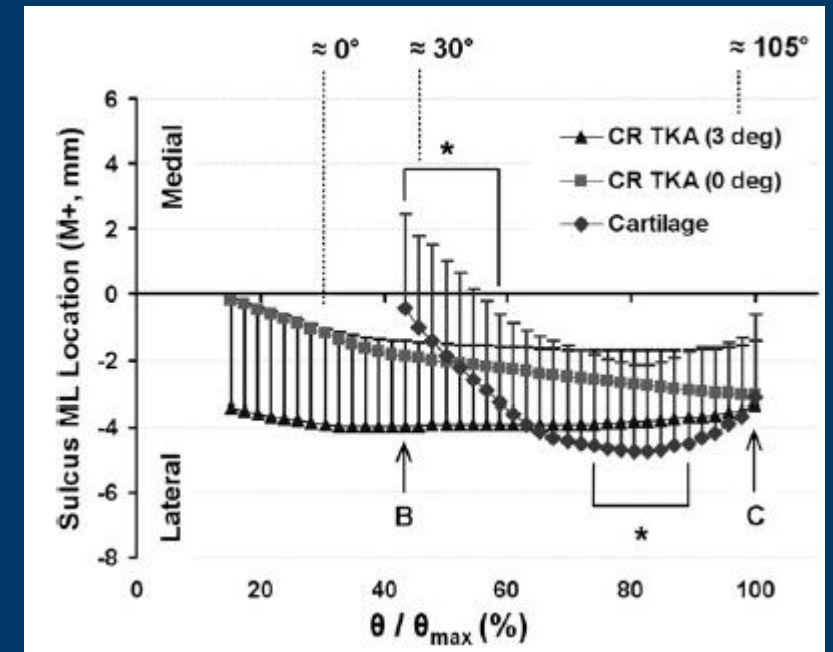
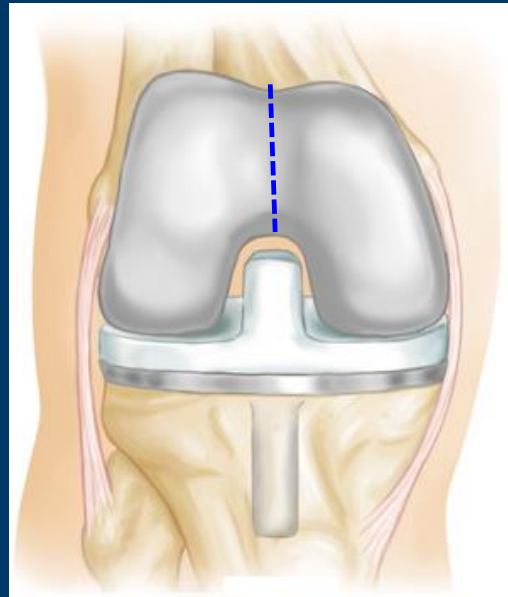
An anatomical population study into the trochlear groove orientation and modern femoral implant designs

A solid red horizontal bar is positioned below the subtitle text.

Optimized surgical technique \neq patellofemoral tracking restored to physiological values



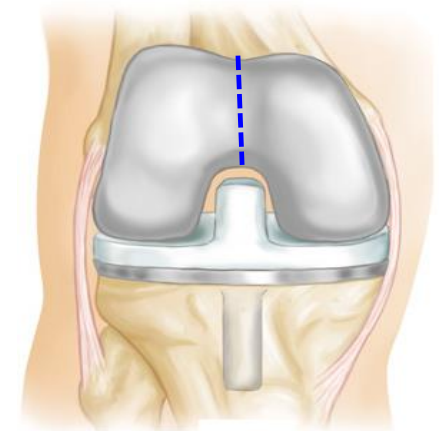
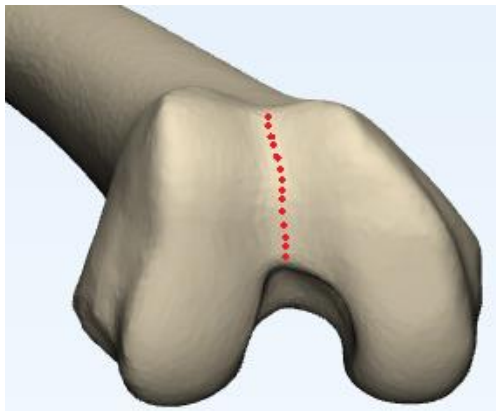
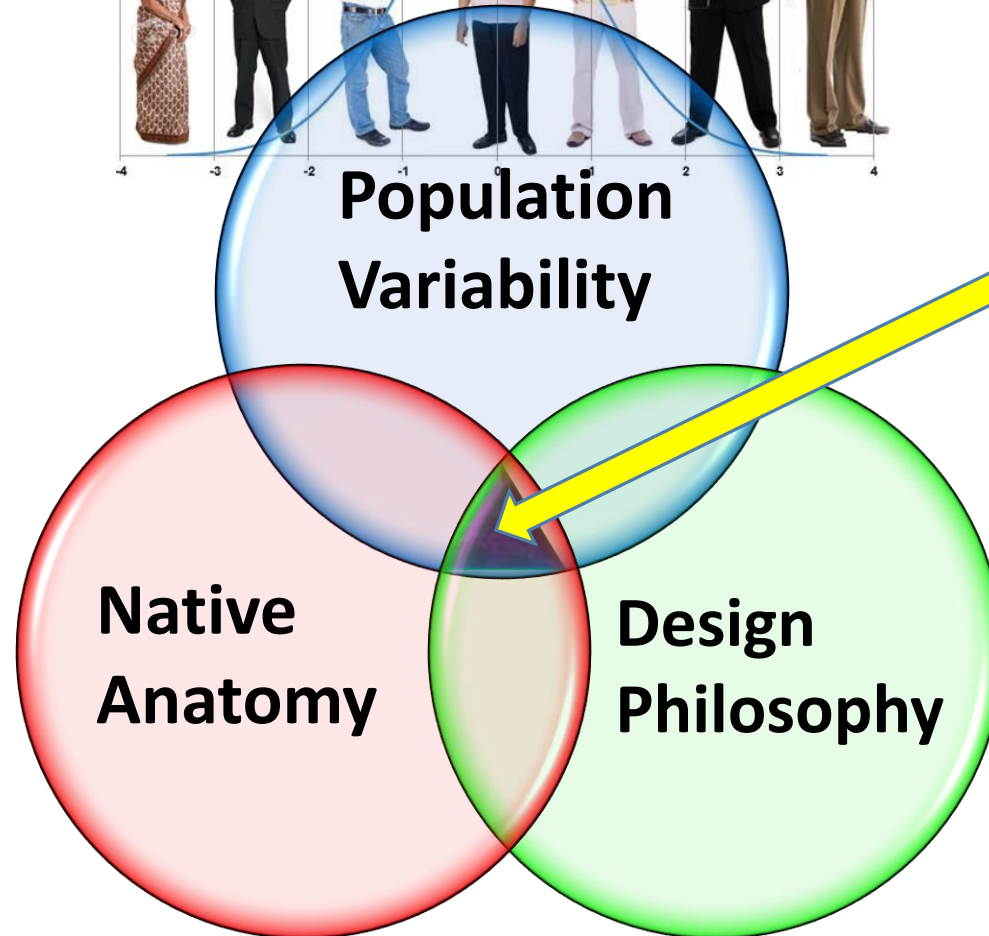
VS



Varadarajan et al. 2011



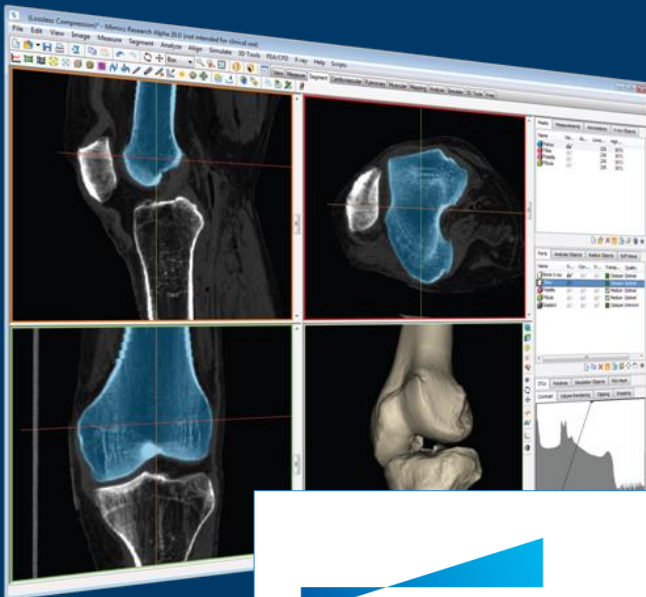
The “Perfect Fit”



Our Study

Materials

- 100 CT based femoral surfaces
 - 50 Male, 50 Female
 - 50 Asian, 50 Caucasian



materialise mimics
innovation suite

```
1 import time
2 import numpy as np # for the math
3 import numpy.linalg as la # for the math as well
4
5 #####
6 def compute_angle_signed_on_plane(v1, v2, normal):
7     """ Returns the angle in angles between vectors 'v1' and 'v2'
8     """
9     cross = np.cross(v1, v2)
10     cosang = np.dot(v1, v2) / (la.norm(v1) * la.norm(v2))
11     sinang = la.norm(cross)
12     angle = np.arctan2(sinang, cosang) * 180 / np.pi
13     if np.dot(normal, cross) < 0:
14         angle = -angle
15     return angle
16
17 #####
18 def angle_signed_on_plane(line1, line2, plane_name):
19     normal = trimatic.find_plane(plane_name).normal
20     l1 = (line1.get_point(0), line1.get_point(1))
21     l2 = (line2.get_point(0), line2.get_point(1))
22     v1 = np.subtract(l1[1], l1[0])
23     v2 = np.subtract(l2[1], l2[0])
24     return compute_angle_signed_on_plane(v1, v2, normal)
25
26 #####
27 def cho_plane(p1, p2, plane_name):
28     find_plane(plane_name).normal
29     normal = find_plane(plane_name).normal
30     normal = normal / la.norm(normal)
31     normal = str(type(normal))
32     return normal
33
34 #####
35 def sjoerds_point(plane_name):
36     find_plane(plane_name).normal
37     normal = find_plane(plane_name).normal
38     normal = normal / la.norm(normal)
39     normal = str(type(normal))
40     return normal
```

Materialise
ADaM



Population
Variability

Native
Anatomy

3-matic Scripting

- Rotated a plane around transepicondylar axis in 5° steps
- Generate finely sampled curves representing trochlear region

```
1 import trimatic
2 import csv
3 import numpy as np
```

```
for file in os.listdir(path):

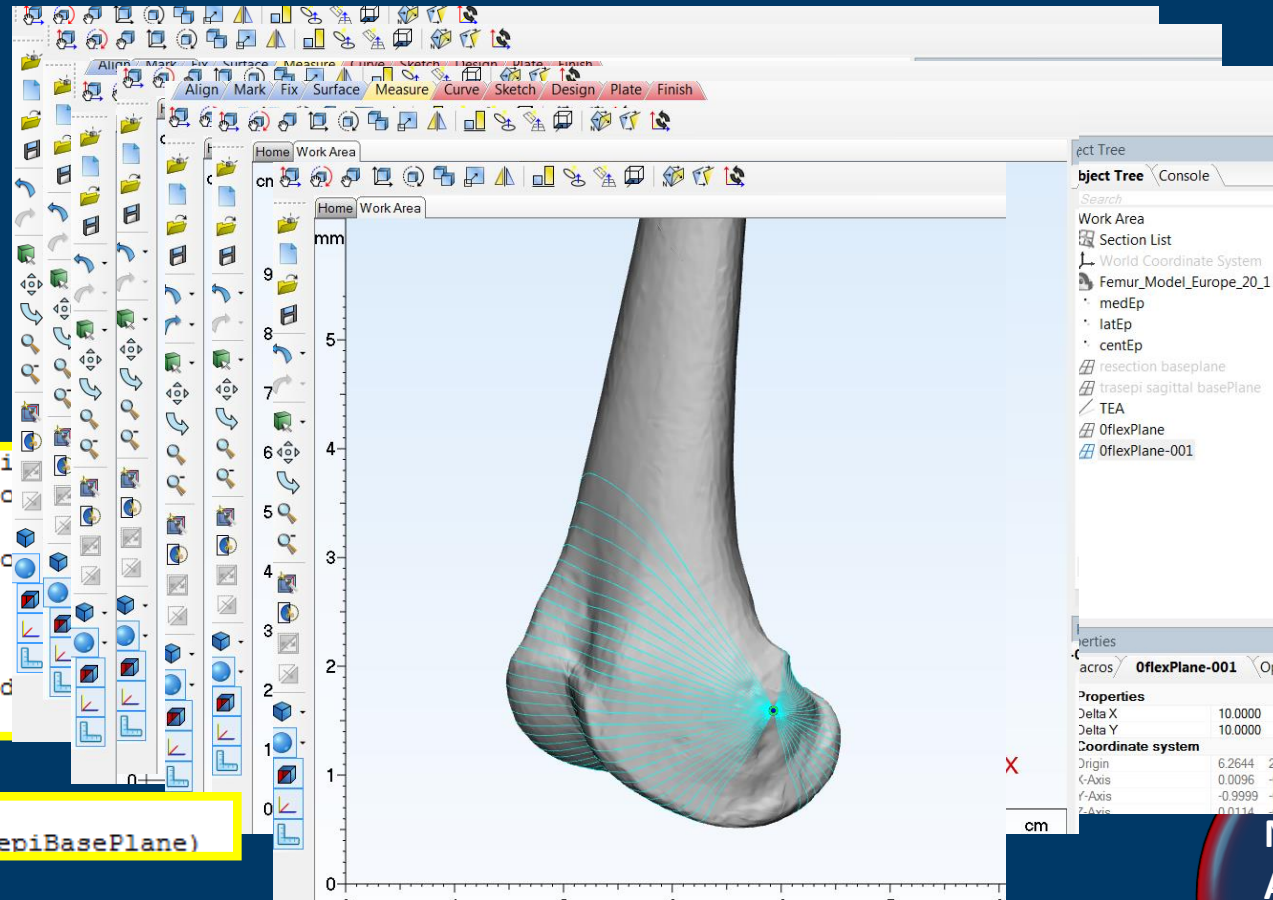
    trimatic.new_project()
    trimatic.import_part_stl(file)
    Femur=trimatic.data.parts()[0]
```

```
mpt=trimatic.create_point([mEpix,mEpiy,mEpiz])
lpt=trimatic.create_point([lEpix,lEpiy,lEpiz])
```

```
PlaneNormal = Femur.object_coordinate_system.z_axis
resbasePlane=trimatic.design.create_plane_normal_c
resbasePlane.name='resection baseplane'
sagbasePlane=trimatic.design.create_plane_normal_c
sagbasePlane.name='trasepi sagittal basePlane'

# create 0deg flexion plane
epiBasePlane=trimatic.create_plane_1_point_perpend
epiBasePlane.name='OflexPlane'
```

```
trimatic.rotate(epiBasePlane,5,cpt,TEA,0)
profile=trimatic.create_intersection_curve(Femur,epiBasePlane)
```

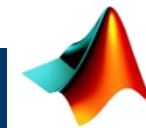
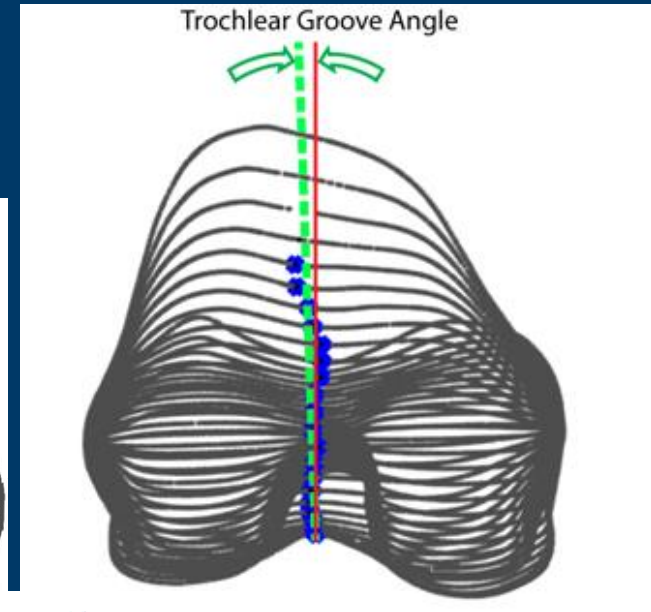
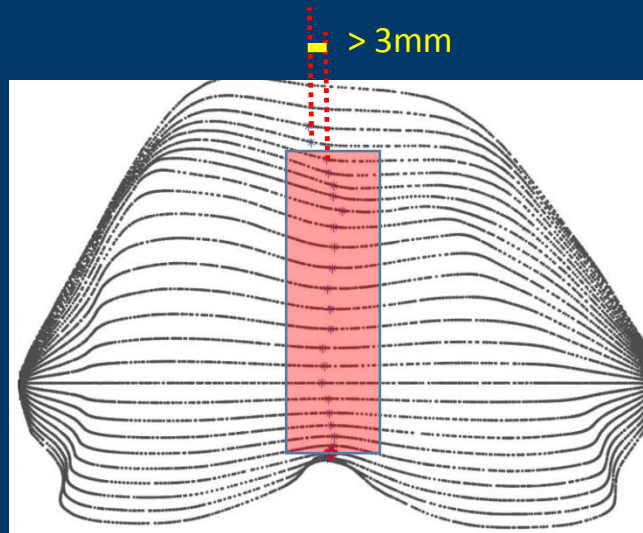
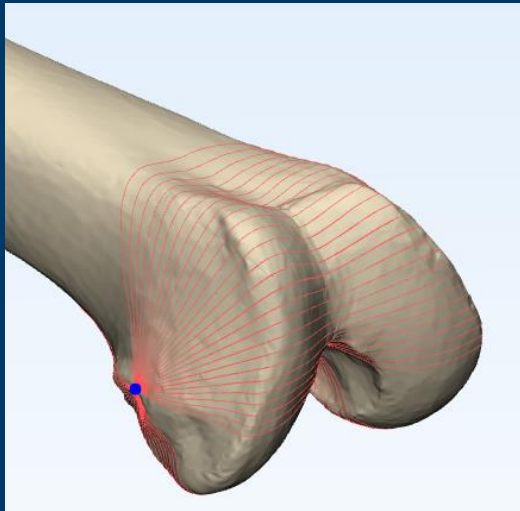


Population
Variability

Native
Anatomy

3-matic Scripting

- Deepest points identified on trochlear curves
- Best fitted line for trochlear orientation referencing mechanical axis



MATLAB

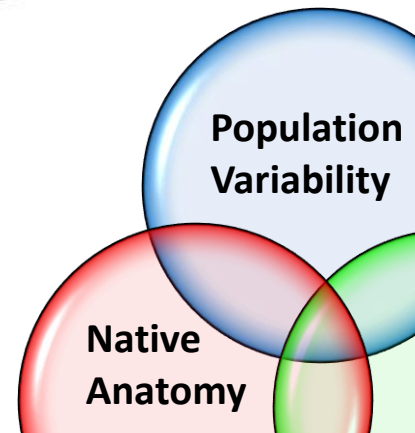
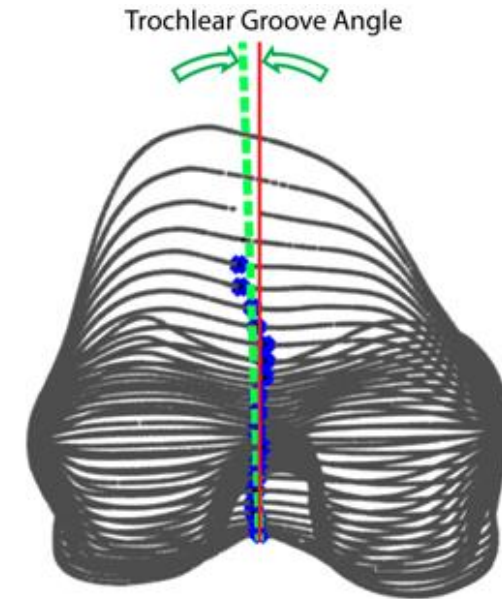
Population
Variability

Native
Anatomy

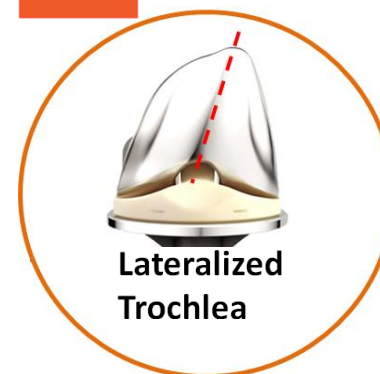
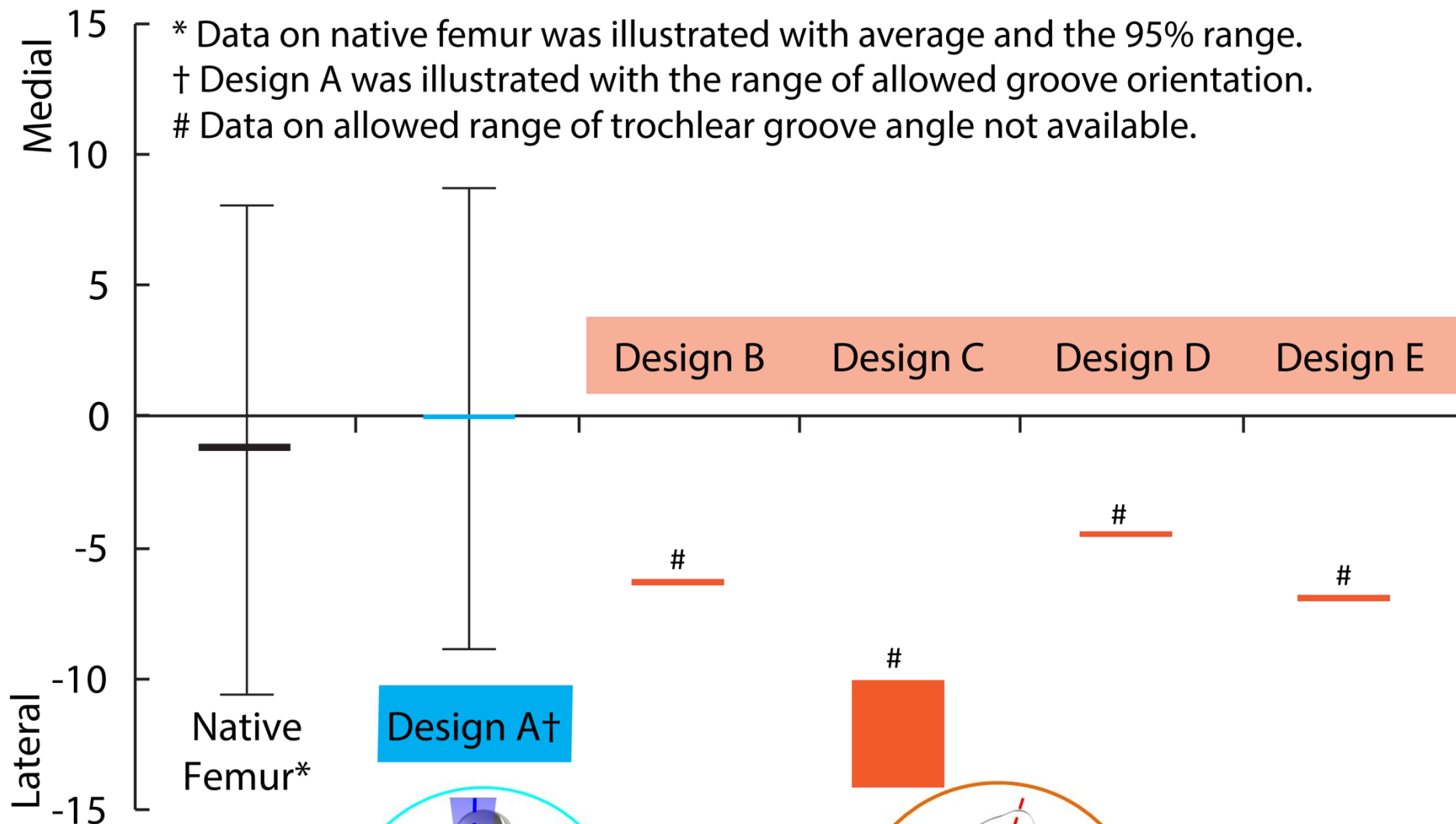
Native Trochlear Orientation

Trochlear Groove Orientation (°) † Mean ± Standard Deviation [95% range]		
Pooled	$-1.4^{\circ} \pm 4.7^{\circ}$ [-10.8°, 8.0°]	
Female	$-1.0^{\circ} \pm 4.8^{\circ}$ [-10.6°, 8.6°]	N.S.
Male	$-1.8^{\circ} \pm 4.6^{\circ}$ [-11.0°, 7.4°]	
Asian	$-2.1^{\circ} \pm 3.9^{\circ}$ [-9.9°, 5.7°]	N.S.
Caucasian	$-0.6^{\circ} \pm 5.3^{\circ}$ [-11.2°, 10.0°]	

† Negative values indicate that the trochlear groove was tilted laterally in distal to proximal direction.

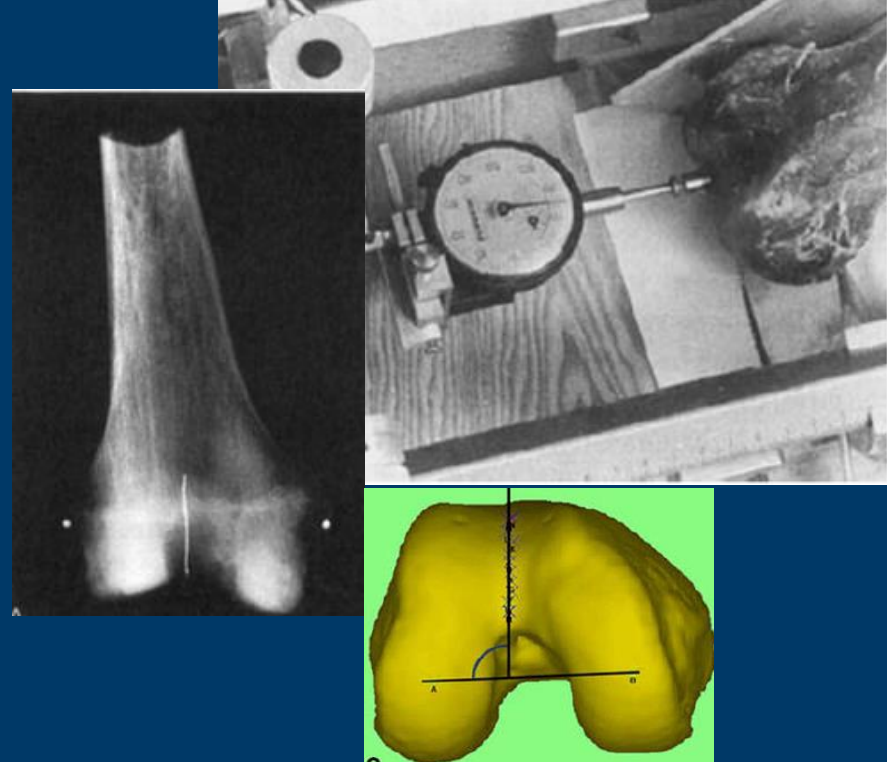
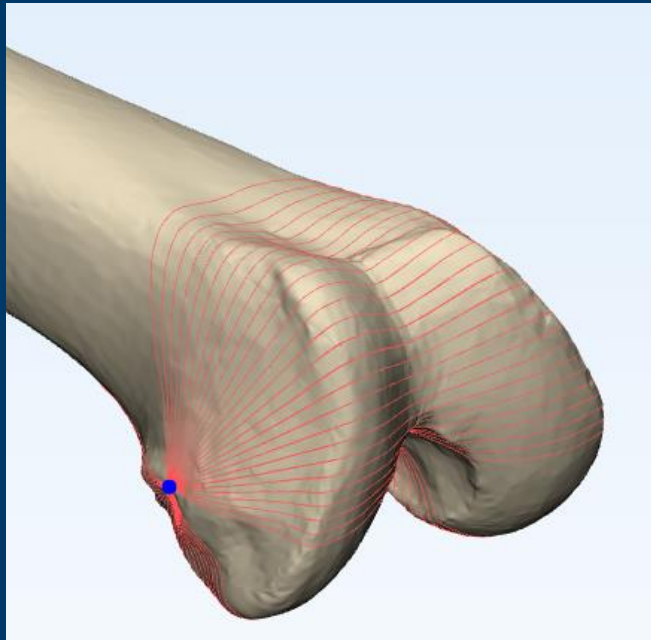


Trochlear Groove Orientation (°)



Summary of User Experience

- Short script: ~60 lines for this study
- Highly efficient: < 2 minutes per bone for ~30 curves
- Offered easy data I/O based on Python platform
- Projects saved for validation activities, future reference and demo
- Versatile and easy customization of workflow and study variables
- Functions ready to use in a commercially available package



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